## 070600-01-10

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

August 13, 2004, 17:03:51 ; Search time 678.508 Seconds Run on:

(without alignments) 2504.436 Million cell updates/sec

US-10-029-020-14\_COPY\_1\_400 2143 1 MDVKERKPYRSLTRRRDAER......BITEDTASSWPVPTDVSLXP 400 Title: Perfect score: Sequence:

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext Ygapext Fgapext Xgapext **BLOSUM62** Scoring table:

3373863 seqs, 2124099041 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

N Geneseg 29Jan04: Database :

geneseqn2001as:\* geneseqn2001bs:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2004s:\* geneseqn2003cs:\* geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\* geneseqn2002s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Abs52100 Human TEN	Aav19251 Human gam	Aax87705 Gamma-her	Aad00791 Human Her	Aas18526 DNA encod	Abn85378 Human NOV	Abs78652 Human cDN	Aav19252 Human gam
	ID	ABS52100	AAV19251	AAX87705	AAD00791	AAS18526	ABN85378	ABS78652	AAV1.9252
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* č	Match	100.0	8.66	8.66	8.66	8.66	6.76	97.2	0.09
	Score	2143	2138	2138	2138	2138	2098	2082	1285
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## ALIGNMENTS

ABS52100 standard; DNA; 8354 (first entry) 05-NOV-2002 ABS52100; RESULT 1 ABS52100

Human TEN-M4-like gene.

Human, NOVX, NOVX-associated disorder, cardiomyopathy; atherosclerosis, cell signal processing; metabolic pathway modulation; metabolic disorder, obesity; diabetes; infectious disease; neurodegenerative disorder; acne; Alzheimer's disease, parkinson's disease, immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health; gastro-intestinal disease, reproductive, neurological disease; health; nephrological disorder; expreductive; neurological disease; nephrological disorder; system disorder; age-related disorder; neuropsychiatric disorder; payered disorder; ade-related disorder; adipocyte complement-related clq tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6/ekk-2; glucose transporter; type la membrane sushi-containing domain; butyrophilin; type la membrane-sushi domain containing; SNP; gene; ds; single mucleotide polymorphism. 

Homo sapiens

Location/Qualifiers replace(117,G) variation

COCTACACCAGCTCGTCCCCCGGACAGGCGAAAGCCCCGCAGAATCGTACACCC

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ArgTyrThrSerSerAlaAspSerGluGluGlyLysAlaProGlnLysSerTyrSer

LysaspileValProGlnGluAlaGluGluPheCysArgThrGlyAlaAsnPheThrLeu

SerSerGluThrLeuLysAlaTyrAspGlnAspAlaArgLeuAlaTyrGlySerArgVal

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useful for treating or preventing a NOVA purpylptices. The invention is useful for treating or preventing a NOVA sportpetities. The invention is cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, preferably human. The invention is also useful for treating metabolic disorders (e.g. Alzheimer's disease, infectious disease, neurodegenerative disorders, haematopolicit disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, pancreatitis, learning and memory defects, infertility, congenital heart of defects, ance, hair growth, pigmentation disorders, endocrine disorders, reproductive, health, conrological diseases, bone marrow transplantation, endocrine diseases, allergy and inflammation, nephrological disorders, urinary system disorders, neuropsychiatric disorders and age-related disorders. The present nucleic acid sequence represents a NOVX gene. This sequence encodes a NOVX protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease or
                                                 "Single nucleotide polymorphism (SNP)"
                                                                                                     "Single nucleotide polymorphism (SNP)"
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Liu
"Single nucleotide polymorphism (SNP)
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Anderson D, Shimkets RA, Burgess CE, Zerhusen BD,
Casman SJ, Boldog FL, Smithson G, Li L, Ji W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to new NOVX polypeptides.
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20-DEC-2000; 2000US-0257314P.
22-MAY-2001; 2001US-0294075P.
24-JUL-2001; 2001US-031550P.
10-AUG-2001; 2001US-0311590P.
10-AUG-2001; 2001US-0311590P.
29-AUG-2001; 2001US-0311613P.
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P-PSDB; ABG70388
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                                                                      variation
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AsnArgGlyAsnPheThrProArgSerAsnProSerProAlaProThrAspHisSerLeu

635 AACCGGGGGAACTTCACGCCGAGGAGCAACCCCAGGCCCGGCCCCCACGGACCACTCGCTC SerGlyGluProProAlaGlyGlyAlaGlnGluProAlaHisAlaGlnGluAsnTrpLeu

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ASDThrGluThrAspHisProGlyGlyLeuGlnAsDHisAlaArgLeuArgThrProPro 180

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181 575 201

ProProLeuSerHisAlaHisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeu 

120

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ThrValLeuSerProGluHisProValArgLeuTrpGlyArgSerThrArgSerGlyArg 140

335 GGCCTGCCCCAATGCGGCTACTCCATGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC

GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp

101

121 395 141 455 161

SerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGlu 160

AGCTCCTGCCTGTCCAGCCGGGCCAATTCCAATTCTCACACTCACGACACACGAGCATGAA

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ArgGluLeuGlyLeuGluGluValThrProProHisGlyThrLeuTyrArgThrAsplle

AAGGACATTGTGCCCCAGGAGGCCGAGGAATTCTGCCGCACAGGTGCCAACTTCACCTG

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                                                  CTCAACAGCAACATCCCCCTGGAGACCAGGAACCTAGGCAAGCAGCAGTTCCTAGGGACA
                                                                                                                                                                              AGTGACGGGCACTTCCTCTTCAAGCCTGGAGGCACCTCCCCGGTCTTCTGCACACATCA
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LeuGlnAspAsnLeuIleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyr
                                                                                                                                                   SerAspGlyHisPheLeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSer
                                                                                                                                                                                                                                            SerThrPheAlaArgProAlaPheAsnLeuLysLysProSerLysTyrCysAsnTrpLys
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                                 LeuAsnSerAsnIleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThr
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2.42e-127 2143.00 100.00% 100.00%

Percent Similarity: Best Local Similarity:

Query Match:

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334 ATGGACGTGAAGGAGGAGGAGGCCTTACCGCTCGCTGACCCCGGCGCCGCGACGCCCGAGCGC 393

MetAspValLysGluArgLysProTyrArgSerLeuThrArgArgArgAspAlaGluArg

ArgTyrThrSerSerSerAlaAspSerGluGluGlylysAlaProGlnLysSerTyrSer

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CECTACACCAGCTCCGCCGCACAGCGAGGGCCAAAGCCCCCGCAGAAATCGTACAACC

454 TCCAGGAGACCCTGAAGGCCTACGACCAGGACGCCCGCCTATGGCAGCCGCGTC LysAspileValProGluAlaGluAlaGluBheCysArgThrGlyAlaAsnPheThrLeu

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ArgGluLeuGlyLeuGluGluValThrProProHisGlyThrLeuTyrArgThrAspIle

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GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp

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GGCCTCCCCACGGGGTACTCCATGGGGGCTGGTCTGATGCCGACATGGAGGCTGAC

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ACGGTGCTGTCCCCCTGAGCACCCCGTGCGTCTGTGGGCCGGGAGCACACGGTCAGGGCGC

ThrValLeuSerProGluHisProValArgLeuTrpGlyArgSerThrArgSerGlyArg

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160 813 AsnThrGluThrAspHisProGlyGlyLeuGlnAsnHisAlaArgLeuArgThrProPro 180

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814 AACACTGAGACTGATCATCGGGCGGCCTGCAGAACCACGCGCGGGCTCCGGACGCCGCG ProProLeuSerHisAlaHisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeu 874 CCGCCGCTCTCGCACACCCCCACACCACACCACGCGCGCCTCCATTAACTCCCTG AsnArgGlyAsnPheThrProArgSerAsnProSerProAlaProThrAspHisSerLeu

754 AGCTCCTGCCTGTCCAGCCGGGCCAATTCCAATCTCACCACTCACCGACACACGAGCATGAA

SerSerCysLeuSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGlu

873

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(See AAW44817), a movel member of the heregulin superfamily, that has a unique N-terminal domain not present in previously identified heregulins. Gamma-HRG is secreted by human breast cancer MDA-MB-175 cells. It leads to the formation of a constitutive active receptor complex and stimulates the growth of these cells in an autocrine manner. The mucleic acid was isolated by screening a MDA-MB-175 with a probe corresponding to the EGP-like domain and part of the N-terminal sequences of HRG-beta-3. It can be used for the recombinant production of gamma-HRG, or for in vivo or exvivo gene therapy. A claimed mucleic acid, which is complementary to the mucleic acid sequence encoding the N-terminal domain of gamma-HRG, is able to reduce production of gamma-HRG by MDA-MB-175 cells. The invention provides claimed methods for activating an BEDB receptor and for provider claimed methods for activating an BEDB receptor and for provider claimed methods for activating an BEDB receptor and for provider claimed methods for activating an BEDB receptor and for provider claimed methods for activating an BEDB receptor and for provider claimed methods for activating an BEDB receptor and for provider claimed methods for activating and BEDB receptor and for provider claimed methods for activating and provider claimed methods for activating and for activating and for provider claimed methods for activating and for provider claimed methods for activating and for activating and for provider claimed methods for activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gamma-heregulin; gamma-HRG; human; autocrine growth factor; breast cancer; MDA-MB-175 cell; diagnosis; gene therapy; ErbB receptor; cell proliferation; cell differentiation; cell sifferentiation; neurological disorder; muscular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enhancing proliferation, differentiation or survival of a cell by contacting the cell (preferably a glial or muscle cell) with gamma-HRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This nucleic acid molecule codes for human gamma-heregulin (gamma-HRG)
GlulleThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to
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934 AACCGGGCAACTICACGCCGAGGAGCAACCCCAGCCCGGCCCCCACGGACCACGCTC

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361 ValAlaMetHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyr 380

JS-10-029-020-14\_COPY\_1\_400 (1-400) x AAV19251 (1-3111)

Query Match:

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SerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGlu 160
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                                               334 ATGGACGTGAAGGAAGCCTTACCGCTCGCTGACCCGGCGCCGCGACGCCGAGGCGC
                                                                                ArgTyrThrSerSerSerAlaAspSerGluGluGlyLysAlaProGlnLysSerTyrSer
                                                                                                                                                                                                                                                                                                       634 GOCTICCCCCACTGCGGCTACTCCATGGGGCTGCTCTGATGCCGACATGGAGGCTGAC
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                                                                                                                                                                             rccaecgagacccrgaaggccracgaccaggacgcccgccragccrargccaggcggcgrc
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                  1473
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                                                                                                                                                                                                                                                                           Gamma-heregulin; HRG-alpha; human; ligand; HER2; HER3; HER4; receptor;
lung surfactant; respiratory distress syndrome; emphysema;
epithelial growth factor; therapy; ss.
1474 GAGATCACGGAGGACACAGCCAGTAGGCTGTGCCAACCGACGTTCCCTATACCCC
                                                  GluileThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heregulin ligands can be used to induce epithelial cell growth, and promote repair and healing of tissue damage or injury.
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(IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                              Gamma-heregulin cDNA
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Query Match:
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The patent discloses a method for inducing hair cell generation, or inner-
ear-supporting cell growth, regeneration, and/or proliferation, by
heregulins (HRG), the ligand for HRZ2/HER3 dimeric receptors. Heregulin
contains function as activators of HBR-2 concogene and result from
alternate splicing of a single gene mapped to chromosome Bp. The two
major types, alpha and beta HRG's are based on two variant Esf-like
(epidermal growth factor) domains, that differ in their C-terminal ends.
This method can be used to increase the number of inner-ear-supporting
cells and for treatment of hair cell related hearing disorders and
clisease states associated with tissue damage, e.g. ototoxic injury,
acoustic assault, degenerative hearing loss, balance impairments, damage
associated with surgery or physical injury and inner ear disorders
cell dysfunction. The present sequence is the human
heregulin variant, gamma-HRG protein encoding cDNA, isolated from a
contained to hair cell dysfunction. The present sequence is the human
heregulin variant, gamma-HRG protein encoding cDNA, isolated from a
contained to hair cell by human MDA-MB-175 cells. It has atleast one
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/product= "Human Heregulin variant, gamma-HRG protein"
                  1414 GTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGCAGCTGTAT
ValAlaMetHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyr
                                                                        GlulleThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro
                                                                                                             1474 GAGATCACGGAGGACACAGCAGCAGTTGGCCTGTGCCAACCGACGTCTCCCTATACCCC
                                                                                                                                                                                                                                                                                                                                                   Heregulin; variant; gamma-HRG; human; inner-ear-supporting cell; activator; HER2 receptor; HER3 receptor; HER-2 oncogene; chromosome hair cell related hearing disorder; octoxic injury; tissue damage; acoustic assault; degenerative hearing loss; balance impairment; treatment; hair cell; surgical injury; physical injury; inner ear disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for inducing hair cell generation and inner-ear-supporting egrowth regeneration and proliferation, useful for treating hearing
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cobstructive pulmonary disease (COPP) e.g. chronic bronchitis, asthma, neonatal pulmonary diseases including neonatal respiratory distress syndrome, meconium aspiration syndrome, chronic lung disease of the neonate, congenital diaphragmatic hernia and acute lung injuries conducte, congenital diaphragmatic hernia and acute lung injuries conduction, near drowning, cystic fibrosis and other epithelial cell trauma diseases including injuries associated with surgical wounds and researchions, ulcers, lesions and tissue tears as normal epithelial cell growth factors. For treating infants/neonates with respiratory distress cas well as youth and adult with poor lung function due to lung injury or danage. The HRG binds with varying and very high affinity to the HER2, HER3 and/or HER4 receptors. The method stimulates growth and collinar barriers of organs and allowing the affected tissue to develop collular barriers of organs and allowing the affected tissue to develop cormal physiological functions more quickly. Hence the method improves oxygenation and speeds of the development of a barrier to infection while treating lung cells that are damaged by inhalation of smoke resulting in complysema. It also facilitates regeneration of epithelial cells. The method human heregulin gamma-
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121 ThrValLeuSerProGluHisProValArgLeuTrpGlyArgSerThrArgSerGlyArg 140
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                                                                                                                                                                                                                                                                                                                          NOVX polypeptides and encoding polynucleotides, useful for preventing treating NOVX-associated disorders e.g. cancer, inflammation, or Alzheimer's disease, and in chromosome mapping, tissue typing or
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Zhong M, Gangolli BA, Burgess CE, Patturajan M, Vernet CAM;
Taylor S, Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse I
Alsobrook JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman l
Macdougall J, Malyankar U, Millet I, Peyman J, Smithson G;
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              09-JAN-2001; 2001US-0260417P.
10-JAN-2001; 2001US-0260831P.
28-FEB-2001; 2001US-027338P.
09-MAR-2001; 2001US-0284704P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCACCTTCGCCCGGCCGGCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAG
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AsnArgGlyAsnPheThrProArgSerAsnProSerProAlaProThrAspHisSerLeu
                AACCGGGGCAACTTCACGCCGAGGAACCCCAGCCCGGCCCCCACGACCACCTC
                                                                SerGlyGluProProAlaGlyGlyAlaGlnGluProAlaHisAlaGluAsnTrpLeu
                                                                                       TCCGGAGAGCCCCCTGCCGGCGGCGCCCAGGAGCCTGCCCCAGGAGAACTGGCTG
                                                                                                                                  LeuAsnSerAsnIleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThr
                                                                                                                                                                  CTCAACAGCAACATCCCCTGGAGACCAGAAACCTAGGCAAGCAGCCATTCCTAGGGACA
                                                                                                                                                                                                      LeuGlnAspAsnLeuIleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyr
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/trans_except= (pos: 1138. .1147,aa:Met)
/product= "NOV1 protein"
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                                 SerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGlu
                                                                                                                                                                                                   SerGlyGluProProAlaGlyGlyAlaGlnGluProAlaHisAlaGlnGluAsnTrpLeu
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424 AGCTCCTGCCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACACGGCACACGGAGCATGAA
                                                                                               AACACTGAGACTGATCATCCGGGCGGCCTGCAGAACCACGCGGGGCTCCGGACGCCGCCG
                                                                                                                                    CCGCCGCTCTCGCACGCCCCAACCAGCACCACGCGCCCCCCTTTAACTCCCTG
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                                                                                                                  ProProLeuSerHisAlaHisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeu
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The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to CGDD, a biologically active fragment or an immunogenic fragment. Also included are the fragment or an immunogenic fragment. Also included are the comprising a promoter sequence operably linked to the CGDD produclectides and promoter sequence operably linked to the CGDD produclectide or a transgenic organism comprising the recombinant polymuclectide, an anticomprising for compounds which bind to/modulate or are antibody, screening for compounds which bind to/modulate or are antiposists of CGDD or alter the expression of CGDD polymuclectide and antagonists are useful for diagnosing, treating or cGDD polymuclectide and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of CGDD, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia or vera, psoriasis, primary thromobocytopaenia or cancer), developmental disorders (e.g. Alzheimer disease, Parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. Albs), (acquired immunodeficiency syndrome) allergies, asthma, autoimmune thyroiditis, contact dermatitis, contact dermatitis, contact dermatitis, contact dermatitis, phymometrial arteriors.
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renal tubular acidosis; anaemia; mental retardation; epilepsy, AIDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma; reproductive disorder; infertility, autoimmune disorder; allergy; inflammatory disorder; acquired immunodeficiency syndrome; uveitis; autoimmune thyroditis, contact dermatitis; Crohn's disease; infection; diabetes mellitus; glomerulonephritis; irritable bowel syndrome; multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
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Burford N;
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or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8645 BP; 2060 A; 2494 C; 2319 G; 1771 T; 0 U; 1 Other,
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TY, Lal PG, Duggan
Khare R, Walia NK;
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23-FEB-2001; 2001US-0271T5P.
08-MAR-2001; 2001US-0274552P.
09-MAR-2001; 2001US-0274552P.
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Xu Y, Gietzen KJ,
Richardson TW, Tra
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Length: Matches:

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1071 AGCACCTTCGCCCGGCCGTTTTAACCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAG 1130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are claimed, together
on, differentiation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insoluble when expressed as a thioredoxin fusion protein in Bscherichia coli cells. Gamma-HRG nucleic acid and polypeptide are claimed, together with their uses e.g. for enhancing the proliferation, differentiation or survival of glial or muscle cells
                                                                                                                                                                                                                                                                                                                                              Gamma-heregulin; gamma-HRG; human; autocrine growth factor; breast cancer; MDA-WB-175 cell; diagnosis; gene therapy; BrbB receptor; cell proliferation; cell differentiation; cell survival; neurological disorder; muscular disorder; ss.
                                                                                                        GAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCGACGTCTCCCTATACCCC
                                CysAlaAlaLeuSerAlaIleValIleSerAlaThrLeuValIleLeuLlaTyrPhe
                                                           rececaeccricaccercercarcreaccacrerearerrecreerescaractrr
                                                                                       ValAlaMetHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyr
                                                                                                                                              GluileThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding gamma-heregulin - used to activate ErbB receptor and nnce proliferation, differentiation or survival of a cell.
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                                                                                                                                                                                                                                                                                                                     Human gamma-heregulin cDNA clone 20.
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                                                                                                                                                                                                                                   standard; cDNA; 2387
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P-PSDB; AAW44818.
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                                                                                                                       ArgTyrThrSerSerAlaAspSerGluGluGluGlyLysAlaProGlnLysSerTyrSer
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                                                                    COPY_1_400 (1-400) x ABS78652 (1-8645)
 Conservative:
Mismatches:
Indels:
98.25%
98.25%
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Similarity:
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                                                                                                                                                                                                                                                                                                New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                     Wang J;
Wang Z;
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TTTACCCTAAGGCAGTTAGGAGTTTGTGAACCAGCAACTCGAAGGAACTGGCATTTTGT
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Drmanac RT,
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                                                                                                                                                                                                     RW, Ren F, Zhang
Weng G, Zhou P,
Boyle BJ;
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Mismatches:
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Matches:
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Gaps:
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                                                                                                                                                                                                                Wehrman T,
en R, Xu C,
                                                 10-DEC-2001; 2001US-0339739P.

11-DEC-2001; 2001US-0339453P.

14-MAR-2002; 2002US-036591P.

14-MAR-2002; 2002US-0365384P.

12-APR-2002; 2002US-0372381P.

12-APR-2002; 2002US-037261SP.

22-APR-2002; 2002US-0012858

24-APR-2002; 2002US-0012858
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Chen R,
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                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                                                           ThrProArgSerAsnProSerProAlaProThrAspHisSerLeuSerGlyGluProPro
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chromosome marker; genetic disorder; gene; ds.
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where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, notropic, anticonvulsant, cerebroprotective, noctropic, cardiovascular, antidated antidated antidated antidated antidated antidated and antidated and antidated and can be used in gene protozoacide and antihelminthic activities, and can be used in gene manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers (e.g. leuksemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Altheimer's disease or pick's disease, altheimer's disease or pick's altheim of the control o
                          cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy;
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kets RA, Tchernev VI, Spaderna SK, Gorman L;
ijan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
ijan M, Care V, Burqess CE, Edinger S, Ellerman K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
                                                                        Pick's disease; vesicular transport disease; cystic fibrosis; goitre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia;
          gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes novel human proteins designated NOVX
        antihelminthic;
                                                                                                                                                                           rheumatoid arthritis; gene; chromosome 4; ss.
        protozoacide;
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                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "NOV15b"
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29-MAR-2001; 2001US-0279833P.
13-ARR-2001; 2001US-0283889P.
18-ARR-2001; 2001US-0286889P.
25-ARR-2001; 2001US-0286683P.
29-MAY-2001; 2001US-029680P.
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2001US-0259785P.
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17-SEP-2001;
26-NOV-2001;
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04-JAN-2001;
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29-MAR-2001;
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diabetes mellitus, Grave's disease, or gitte', gastrointestinal disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. allorgic reactions, autoimmune haemolytic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic

Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide;

Human NOV15b encoding cDNA SEQ ID NO:37.

(first entry)

17-DEC-2002

ABQ82344;

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and protozoal infections. The NOVX proteins can be used as immunogens produce antibodies and as vaccines. The NOVX nucleotide sequences may lused in chromosome mapping, identifying individuals from minute biological samples (tissue typing), and in forensic identification of biological sample. The present sequence encodes human NOV15b, which is located on chromosome 4
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AACTGGCAGCTACAGCAGACTGAAAATGACACATTTGAGAATGGAAAAGTGAATTCTGAT 1218
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                                                                                                   Gly---GlyThrSerProLeuPheCysThrThrSerProGlyTyrProLeuThrSerSer 308
                                                                                                                          1039 AAATTCAAGAAGTCTTCAAAGTACTGTAGCTGGAAATGCACTGCACTGTGTGCCGTAGGG
                                IleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAspGlyHisPheLeuPheLysPro
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/transl_excert
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2001US-0259814P.
2001US-0279863P.
2001US-0279863P.
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02-JAN-2001; 2
04-JAN-2001; 2
20-FEB-2001; 2
9-MAR-2001; 2
29-MAR-2001; 2
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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, noticopic, cardiovascular, artidiabetic, anticonvulsant, cerebroprotective, noticopic, cardiovascular, antidiabetic, antidiabetic, antidiaterinitic, virucide, immunosuppressive, antidialergic, antidiaterial, fungicide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the mandiscure of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers of e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or pick's cischaemic cerebrovascular transport (e.g. cystic fibrosis, diseases), disorders (e.g. allergic reactions, autoimmune haemolypic autoimmune diseases (e.g. allergic reactions, autoimmune haemolypic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be produce antibodies and as vaccines. The NOVX nucleotide sequences may be biological samples (tissue typing), and in forensic identification of a biological samples (tissue typing), and in forensic identification of a biological sample.
                                                                                                                                                                                                                                                   Wolenc AR, Vernet CAM, Eisen A, Liu X;
kets RA, Tchernev VT, Spaderna SK, Gorman L;
jan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
no G, Millet I, Macdougall JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New NOVX polypeptides and polymucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 110-112; 444pp; English
                                                                                                                                                                                                                                                 Spytek KA, Li L, Wolenc AR, Vern
Malyankar U, Shimkets RA, Tcherne
Kekuda R, Patturajan M, Gusev V,
Rastelli L, Casman SJ, Boldog F,
Gunther E, Smithson G, Millet I,
13-APR-2001; 2001US-0283889P.
25-APR-2001; 2001US-0286683P.
29-MAY-2001; 2001US-0296683P.
16-AUG-2001; 2001US-023480P.
17-AUG-2001; 2001US-0313355P.
17-SEP-2001; 2001US-0333350P.
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P-PSDB; ABP53586.
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Sequence 8675 BP; 2362 A; 2067 C; 2201 G; 2041 T; 0 U; 4 Other;

sample. The present sequence encodes human NOV15a, which is

biological sample. The located on chromosome

8675 212 49 90 64 12 Length:
Matches:
Conservative:
Mismatches: Indels: 2.43e-53 987.00 62.89% 51.08% 46.06% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: ÿ. Pred

US-10-029-020-14\_COPY\_1\_400 (1-400) x ABQ82343 (1-8675)

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- 1 MetAspVallysGluArgLysProTyrArgSerLeuThrArg---ArgArgAspAlaGlu 19
- 211 CGGCGCTACACACAATTCCTCCGCAGACAATGAGGAGTGCCGGGTACCCACAGAAGTCC 270 20 ArgArgTyrThrSerSerSerAlaAspSerGluGluGlyLysAlaPro---GlnLysSer 38
- 57

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1 TACAGIICCAGCGAGACAITGAAAGCITITGAICAIGAITCCICGCGGCIGCTITACGGC	58 SerargValLysAspIleValProGlnGlualaGluGluPheCysArgThrGlyAlaAsn 77	PheThrLeuArgGluLeuGlyLeuGluGluValThrProProHisGlyThrLeuTyrArg	:::      :::   TTTACCCTAAGGCAGTTAGGAGTTTGTGAACCAGCAACTCGAAGAGGACTGGCATTTGT	8 ThrAspileGlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMet	1 OCCOMMAN GOGGET LECEL TO ACADAGO TALICIA IL AGIGEAGGGILAGAGILGENGA IN ACADAGO TALICIA IL AGIA AGIA AGIA AGIA AGIA AGIA AGIA	1 GAAAATGAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		1 TCAGGCCGCAGCTCCTGCCTGTCAAGTCGGTCCAACTCAGCCCTCACCCTGACAGATACG	8 GluHisGluAsnThrGluThrAspHisProGlyGlyLeuGlnAsnHisAla              1 GAGCACGAAACAAGTCCGACAGGAATGAGCAACCTGCAAGCAA	5 ArgLeuArgThrProProProProLeuSerHisAlaHisThrProAsnGlnHisHisAla	1 ACCCTGCAGCCCTTGCCGCCTTCCCATAAGCAGCACTCTGCACAGCATCAT	5 AlaSerIleAsnSerLeuAsnArgGlyAsnPheThrProArgSerAsnProSerProAla	z ccatocateacticicicadagaaacteccigaecaatagaaggaaccagagtegggee	5 ProThrAspHisSerLeuSerGlyGluProProAlaGlyGlyAlaGln	1GluProAlaHisAlaGluGluAsnTrpLeuLeuAsnSerAsnIleProLeuGluThr		0 ArgAsnLeuGlyLysGlnProPheLeuGlyThrLeuGlnAspAsnLeuIleGluMetAsp	8 AGG	0 IleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAspGlyHisPheLeuPheLysPro	1	0 GlyGlyThrSerProLeuPheCysThrThrSerProGlyTyrProLeuThrSerSer		9 ThrValTyrSerProProArgProLeuProArgSerThrPheAlaArgProAlaPhe	CONTINUE CONTROLL CONTROLL CONTROLL CONTROL CO	9 AsnLeuLysLysProSerLysTyrCysAsnTrpLysCysAlaAlaLeuSerAlaIleVal	9 AAATICAAGAAGICTICAAAGIACIGIIIIIIIIIIIIII		gretegengerectegeaanacreergretatttanagaangearetettegeeere	9 AsnTrpHisLeuGlnProMetGluGlyGlnMetTyrGluIleThrGluAsp	AACTGGCAGGTACAGACAGACTGAAAATGACACATTTGAGAATGGAAAAGGGAATGGAATTCTGAT	ThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro 400	ACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynuclectides which are differentially-regulated in breast cancer. The methods and compositions of the present invention are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and/or treating diseases and conditions relating to breast cancer, and may be used in gene therapy or antisense therapy. They can also be used in research, drug discovery, clinical medicine and forensis medicine. Sequences given in records ACC72012-ACC72074 represent polynucleotides of the invention that are this patent and the form part of the printed specification, but was obtained in electronic format directly from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38
                                                                                                                                                                                                                                                                                                                                                    New isolated human differentially-regulated breast cancer polynucleotide and polypeptide, useful for diagnosing, staging, prognosticating, preventing and/or treating diseases and conditions relating to breast
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                                                                                                                  Breast cancer; cytostatic; gene therapy; antisense therapy; regulated; drug discovery; clinical medicine; forensic medicine; gene; chromosome 5q33.3; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 AlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsnIleProLeuGluThrArgAsnLeu
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                                                                                                                                                                   213 ProAlaProThrAspHisSerLeuSerGlyGluProProAlaGlyGlyAlaGlnGluPro
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ArgvalLysAspileValProGlnGluAlaGluGluPheCysArgThrGlyAlaAsnPhe
                                                                               ThrieuArgGluLeuGlyLeuGluGluValThrProProHisGlyThrLeuTyrArgThr
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Human; FCTRX; myelogenous leukaemia; carcinoma; melanoma; glioma; ds; astrocytoma; congenital neonatal alloimmune thrombocytopaenia; infection; neurological disorder; neurodegenerative disorder; neuropathy; familial myelodysplastic syndrome; familial myelodysplastic syndrome; familial myelodysplastic syndrome; familial myelodysplastic syndrome; mental health condition; immunological disorder; allergy; infertility; bronchial asthma; Avellino type eosinophilia; lung disease; deafness; reproductive disorder; alsorder; alloropy; affertility; gasmoditive disorder; processis, hepatitis C; virucide; gastric disorder; pancreatic disease; Schistosoma mansoni infection; Spinocerebellar ataxia; plasmodium falciparum parasiteemia; diabetes; corneal dystrophy-lattice type I; Corneal dystrophy-lattice type I;
                                                                                                                                                                                                                                                                                                                                               Reis-Bucklers corneal dystrophy, cytostatic; immunosuppressive; antiallergic; autiasthmatic; antiinfertility; antiinflammatory; antidiabetic; protozoacide; hepatotropic; virucide; ophthalmological; gynaecological; antiinfertility; immunostimulant; auditory; haemostatic; gene therapy; FCTR3a; neurestin-like protein; FCTR3f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides designated as FCTRX polypeptides, useful in detection, prevention and treatment of a broad range of pathological states.
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1494 GGAAACGATGATGTGGCAACAATGCCA 1520
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8385. .9729
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2000US~0186718P.
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                                                       AAS14089 standard; DNA; 9729
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2000US-0196018P.
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5'UTR
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The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the nucleic acids encoding them. These sequences are useful for the treatment or prevention of numerous disorders including myelogenous leukaemia, carcinomas, melanomas, gliomas, astrocytomas, congenital neonatal

Claim 9; Page 37-39; 215pp;

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disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Marie-Tooth neuropathy, demyelinating Gardner syndrome, familial myelodysplastic syndrome, mental health conditions, immunological disorders, allergy and infection, bronchial asthma, Avellino type eosinophila, lung diseases, reproductive disorders, infertility, male and female reproductive disorders, glacoprotein la deficiency, desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric disorders, pancreatic diseases such as diabetes, Schistosoma mansoni infection Spinocerebellar ataxia, Plasmodium falciparum parasitemaia, Corneal dystrophy-Greonouw type I, Corneal dystrophy-lattice type I and Reiss Bucklers corneal dystrophy. This sequence represents DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 Anggangrahakgacckgcca---cacckcrcrrrcaccakkgakcgcrcrgcgcaaakkg 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        804 CCATTGCTAGACAGCAGCTCCCATCAAATCATGGACACCAACCCTGATGAGGAATTC 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 864 TCCCCCAATTCATACCTGCTCAGAGCATGCTCAGGGCCCCCAGCAAGCCTCCAGCAGTGGC 923
alloimmune thrombocytopaenia, neurological disorders, neurodegenerative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 GlyArgSerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGlu
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839.00
54.42%
43.14%
39.15%
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Best Local Similarity:
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                          924 CCTCCGAACCACCACCACTGGAGGCCCCCTCTCCCACC--CCTCACAAC 980
                                                                                                                                                       GluProProAlaGlyGlyAlaGluGluProAlaHisAlaGlnGluAsnTrpLeuLeuAsn 242
                                                                                                                                                                                                     SerAsnileProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThrLeuGln 262
                                                                                                                                                                                                                                                   263 AspAsnLeuIleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAsp 282
           LeuGlnAsnHis-----AlaArgleuArgThrProProProProLeuSerHisAla 186
                                                                                                        207 ProArgSerAsn------ProSerProAlaProThrAspHisSerLeuSerGly 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene; ss; FCTR3f; colorectal cancer; adenomatous polyposis coli; myelogenous leukaemia; congenital neonatal autoimmune thrombocytopenia; ovarian cancer; brain tumour; breast cancer; glioma; astrocytoma; renal cell carcinoma; melanoma; clear cell carcinoma; granular cell carcinoma; neurological disorder; neurodegenerative disorder; nerve trauma; familial myelodysplastic syndrome; charcot-Marie-Tooth neuropathy; Gardner syndrome; mental health condition; immunological disorder; allergy; asthma; lung disease; reproductive disorder; deafness; alycoprotein deficiency; desmoid tumour; turcot syndrome; liver cirrhosis; hepatitis C; gastric disorder; pancreatic disease; diabetes; schistosoma mansoni infection; spinocerebellar ataxia; plasmodium falciparum infection; Groenouw's corneal dystrophy;
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                                                          HisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsnPheThr
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GTGCCCTGGTCGTTGAAA 1412
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US2003087816-A1

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The invention relates to FCTRX polypeptides and the polynucleotides
encoding them. The sequences of the invention are useful for the
manufacture of a medicament for diagnosing and treating disorders
associated with the FCTRX polypeptide, such as colorectal cancer,
adenomatous polyposis coli, myelogenous leukaemia, congenital neonatal
cutcommune thrombocytopenia, malignant ovarian tumours, malignant brain
tumours, breast adenocarcinoma, ovarian carcinoma, melanomas, clear
carcinoma, breast adenocarcinoma, ovarian carcinoma, melanomas, clear
carcinoma, breast adenocarcinoma, neurological disorders,
cell and granular cell carcinomas, neurological disorders,
cell and granular cell associates, nerve trauma, familial myelodysplastic
syndrome, Charcot-Marie-Tooth neuropathy, Gardner syndrome, mental health
conditions, immunological disorders, allersy and infection, asthma, lung
diseases, male and female reproductive disorders, dasherss, schistosoma mansoni
cinfection, spinocerebellar ataxia, plasmodium falciparum infection,
dronenced conneal dystrophy and lattice corneal dystrophy. This sequence
corrections corneal dystrophy and lattice corneal dystrophy. This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New FCTRX polypeptide and encoding polynucleotide, useful for preventing or treating FCTRX-related disorders, such as cancer, autoimmune, neurodegenerative, gastrointestinal, reproductive and inflammatory
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                                                                                                                                                                                                                                                                                                                                                                             Majumder K;
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Rastelli L;
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Mismatches:
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Matches:
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Mezes PS,
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                                                                                         03-MAR-2000; 2000US-0186592P.
                                            05-MAR-2001; 2001US-00800198.
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FERNANDES E.
SHIMKETS R.
HERRMANN J.
MAJUMDER K.
MACDOUGALL J.
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MEZES P S.
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Best Local Similarity:
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P-PSDB; ADB32029.
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/*tag= a
/product= "Human FCTR3b"
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03-MAR-2000; 2000US-0186718P.
06-MAR-2000; 2000US-0187294P.
17-MAR-2000; 2000US-019440P.
17-AR-2000; 2000US-019610P.
03-JAN-2001; 2001US-0259548P.
                                                                                             AAS14085 standard; DNA; 9826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; FCTRX; myelogenous leukaemia; carcinoma; melanoma; glioma; ds;
astrocytoma; congenital neonatal alloimmune thrombocytopaenia; infection;
neurological disorder; neurodegenerative disorders; nerve trauma;
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Majumder K;
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Mezes PS, Rastelli L;
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The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the nucleic acids encoding them. These sequences are useful for the treatment or prevention of numerous disorders including myelogenous leukaemia, carcinomas, melanomas, gliomas, astrocytomas, congenital meonatal alloimmune thrombocytopaenia, neurological disorders, neurodegenerative disorders, nerve trauma, familial myelodysplastic syndrome, chanisating dardner syndrome, familial myelodysplastic syndrome, mental health conditions, immunological disorders, allergy and infection, bronchial asthma, Avellino type cosinophilia, lung diseases, reproductive disorders, infertility, male cosinophilia, lung diseases, reproductive disorders, infertility, male disorders, panoreatic diseases such as diabetes, Schistosoma mansoni infection Spinocerebellar ataxia, plasmodium falciparum parasitaemia, corneal dystrophy-Greonouw type I, Corneal dystrophy-lattice type I and Febise Bucklers conneal dystrophy. This sequence represents DNA encoding CFCTR3b, a neurestin-like protein
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Sequence 9826 BP; 2567 A; 2643 C; 2479 G; 2137 T; 0 U; 0 Other;

Cores: 8.38-44 Length: 9826 839.00 Matches: 195 ilarity: 54.42% Conservative: 51 Similarity: 43.14% Mismatches: 76 Indels: 130 5.0-14_COPY_1_400 (1-400) x AAS14085 (1-9826)	MetaspValLysGluargLysProTyrArgSerLeuThrArgArgArgAspAlaGlu	0 ArgargTyrThrSerSerSerBeaspSerGluGluGluGlyLysalaProGlnLySSer 	9 TyrSerSerGluThrLeuLysAlaTyrAspGlnAspAlaArgLeuAlaTyrGlySer 	9 ArgvallysAspilevalProGlnGluAlaGluGluPheCysArgThrGlyAlaAsnPhe	9 ThrleudrgGluleuGlyLeuGluGluValThrProProHisGlyThrLeuTyrArgThr                    :::       :::		9 AlaAspThrValLeuSerProGluHisProValArgLeuTrpGlyArgSerThrArgSer	9 GlyArgSerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGlu	9 HisGluasnThrGluThrAspHisProGly	80	4 CTCCTCCCATCTGCTCAGCTGCCTAGCTCCCCATAATCCTCCACCAGTTAGCTGCCAGATG	890
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Title: Perfect score:

on:

Scoring table: Sequence:

Searched:

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APPLICANT: Alsobrook II, John et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE
FILE REFERENCE: 21402-568A
CURRENT APPLICATION NUMBER: US/10/383,201
CURRENT FILING DATE: 2003-03-06
PRIOR PLICATION NUMBER: 10/029020
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2002-03-20
PRIOR FILING DATE: 2002-04-12
PRIOR PLICATION NUMBER: 60/365,984
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-15
PRIOR FILING DATE: 2002-06-16
                                                                       Sequence 3, Appli
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appli
Sequence 1, Appli
Sequence 12, Appli
Sequence 55, Appl
Sequence 11, Appli
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Sequence 37, Appli
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Sequence 36, Appli
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18 US-10-04-415-17

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      13 US-10-383-201-43

13 US-10-290-120-13

15 US-09-773-517-12

9 US-09-773-517-12

9 US-09-773-61-12

15 US-09-782-025-12

15 US-09-649-668-12

15 US-10-290-578-1

13 US-10-453-183-12

14 US-10-485-1

17 US-10-042-865-1

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18 US-09-808-135-1

19 US-09-800-198-66

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US-09-977-418-21
US-09-977-033A-21
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; Publication No. US20040029226A1
; GENERAL INFORMATION:
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USTPETO spool/USI0029020/runat 06082004 112218 29331/app query.fasta_1.3519
-Q=/cgn2 1/USTPETO spool/USI0029020/runat 06082004 112218 29331/app query.fasta_1.3519
-DB=Published Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LCCAL -OUTFMT=pto -NORM=ext -HEAPSTIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US10029020 @CGN 1 1 2156 @runat -06082004 112218 _29331
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NG SCORES=0 -WAIT -DSPBLOCK=100
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DBV_TINEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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2448.158 Million cell updates/sec
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1 MDVKERKPYRSLTRRRDAER......EITEDTASSWPVPTDVSLYP 400
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/DSO7_NEW PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/DSO7_NEW PUB.seq:*
7/cgn2_6/ptodata/2/pubpna/DSO8_NEW PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                     OM protein - nucleic search, using frame_plus_p2n model
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Jatabase

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1175 GAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCGACGTCCCTATACCCC 1234
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                                                                                                                                                                                                                                                                                                                                                                                                             301 ProGlyTyrProLeuThrSerSerThrValTyrSerProProArgProLeuProArg 320
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LeuGlnaspasnLeulleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 SerThrPheAlaArgProAlaPheAsnLeuLysLysProSerLysTyrCysAsnTrpLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 GlulleThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro
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                                                                                     LeuAsnSerAsnIleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThr
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; Publication No. US20040033971A1
; GENERAL INFORMATION:
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CRGANISM: Homo sapiens
US-10-029-020-13
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Matches:
Conservative:
Mismatches:
Indels:
        PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 10/051,874
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 60/366,928
PRIOR APPLICATION NUMBER: 10/055,877
PRIOR APPLICATION NUMBER: 10/055,877
PRIOR FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 43
LENGTH: 8354
TYPE: DNA
CORANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (35)
US-10-383-201-43
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                                                                                                                                          GTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGCAGATGTAT 1174
                     AGCACCTTCGCCCGGCCGGCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAG 1054
                                                                                                                        ValAlaMetHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyr 380
                                                                                                                                                                                        GlulleThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro 400
                                                      CysAlaAlaLeuSerAlaIleValIleSerAlaThrLeuValIleLeuLeuAlaTyrPhe
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 US-10-029-020-14_COPY_1_400 (1-400) x US-10-290-578-3 (1-1680)
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399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/290,578
FILING DATE: 08-No. US20030078389A1-2002
CLASSIFICATION: <unknown>
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/891,845
FILING DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                             Sliwkowski, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
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REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/021640 FILLING DATE: 12-121-96 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10290578
Publication No. US20030078389A1
GENERAL INFORMATION:
APPLICANT: Schaefer, Gabriele M.
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TELEPHONE: 415/225-1994
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TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415/952-9881
TELEX: 910/371-7168
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SEQUENCE CHARACTERISTICS
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                                                                                                   US-10-029-020-14_COPY_1_400 (1-400) x US-10-029-020-13 (1-8354)
                 Conservative:
Mismatches:
 Matches:
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2143.00
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               Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
       REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1145
TELECOMMUNICATION INFORMATION:
TELEFRAX: 650/225-7467
TELEFRAX: 650/952-981
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3111 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                          MOLECULE TYPE: nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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SerGlyGluProProAlaGlyGlyAlaGlnGluProAlaHisAlaGlnGluAsnTrpLeu
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/792,025
FILING DATE: 23-Feb-2001
CLASSIFICATION: <UNKNOWN>
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FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
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STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
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ArgGluLeuGlyLeuGluGluValThrProProHisGlyThrLeuTyrArgThrAsplle
                                                                                                                       GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp
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                                                                                        US-10-290-578-1
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Matches:
Conservative:
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Indels:
Gaps:
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PACHELL NO. USZ0020081299A1

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: HAIR CELL DISORDERS
FILE REFERENCE: GENENT 035VPC
CURRENT APPLICATION NUMBER: US/09/849,868
CURRENT FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 12
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; LOCATION: (334)...(2637)
US-09-849-868-12
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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TYPE: DNA
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Sequence 12, Application US/10453183

Publication No. US20030199428A1

GENERAL INFORMATION:

APPLICANT: Sliwkowski, Mark

APPLICANT: Sliwkowski, Mark

APPLICANT: Sliwkowski, Mark

APPLICANT: Sliwkowski, Mark

PETER REPRENCE: PI145R1

FILE REPERENCE: PI145R1

CURRENT PILING DATE: 2003-06-03
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/290, 578
FILING DATE: 08-No. US20030078389A1-2002
CLASSIFICATION: vUNKnown>
PRIOR APPLICATION DATA:
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Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/891,845
FILING DATE: -CUMCHOWNS
APPLICATION NUMBER: 60/021640
FILING DATE: 12-Jul-96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                    APPLICANT: Schaefer, Gabriele M.
Sliwkowski, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 3111 base pairs
            Sequence 1, Application US/10290578 Publication No. US20030078389A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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2138.00
99.75$
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Query Match:
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Pred. No.:
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GURREAU INVENTALION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILLE REFRENCE: 12402-5684

FILLE REPRENCE: 21402-5684

CURRENT APPLICATION NUMBER: US/10/393,201

CURRENT PELING DATE: 2000-03-06

PRIOR PELICATION NUMBER: 60/365,984

PRIOR PELING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: 60/372,022

PRIOR PELING DATE: 2002-01-20

PRIOR PELING DATE: 2002-01-2

PRIOR PELING DATE: 2002-01-2

PRIOR PELING DATE: 2002-01-3

PRIOR PELING DATE: 2002-01-3

PRIOR FILING DATE: 2002-01-3

PRIOR FILING DATE: 2002-01-3

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PRIOR PELING DATE: 2002-01-3

PRIOR PELING DATE: 2002-01-16

PRIOR PELING DATE: 2002-01-16

PRIOR PELING DATE: 2002-01-16

PRIOR FILING DATE: 2002-01-16

PRIOR PELING DATE: 2002-
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               LeuGlnAspAsnLeuIleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyr
                                           SerAspGlyHisPheLeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSer
                                                                                                                                                                                         ProGlyTyrProLeuThrSerSerThrValTyrSerProProArgProLeuProArg
                                                                                                                                                                                                                         1234 CCAGGGTACCCACTGACGTCCAGCACAGAGTACTCTCCGCCCCGACCCCTGCCCCGC
                                                                                                                                                                                                                                                                           SerThrPheAlaArgProAlaPheAsnLeuLysLysProSerLysTyrCysAsnTrpLys
                                                                                                                                     AGTGACGGCACTTCCTCTTCAAGCCTGGGGGCACCTCCCCGGCTCTTCTGCACCACTACA
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 55, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Percent Similarity:
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NAME/KEY: CDS
LOCATION: (1).
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US-10-383-201-55
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: US/09/243,198
PRIOR FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: US 60/073,866
PRIOR FILING DATE: 1998-02-04
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 12
LENGTH: 3111
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                                                                                                                                                                                                                                                                                      2138.00
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                                                                                                                                                   TYPE: DNA
) ORGANISM: Homo sapiens
US-10-453-183-12
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Best Local Similarity:
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Pred. No.:
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964 AGCACCTCGCCCGGCCCTTAAACCTCCAAGAAGCCCTCAAAGAAGCCTCCAAGAAG 1023  QV 341 CychallewserAllewserAllewillseerAlamtrewallleteubalayrba 360  1024 TGCCAACCTCGAACGCATCGTCATCACCACTCGCACTCGGCAACTTT 1083  361 VallabateHisteubheGlyteuasmrpHisteuGlprowalprowertcludlyGlnMet 379  1064 GTGCCACCTCGAACGCTCAACCTCAACCTCCACCTCGACCACTCGGCAACTTG 1083  1064 GTGCCACCTCGAACGCATCGTCAACTCGACCCCATCGACCACTCGGCAACTTG 1083  1064 GTGCCATCGACCCTCAAACTCGACCCCATCGACCCCACTCGACCCATCGACACTTGGCCCATCGACCACTTGGCCCATCGACCACTTGGCCCATCGACCCACTTGGCCCATCGACCCACTTGGCCCTAAATGCCCCTTAAACTCGACCCCATAAATGCCCCTTAAACTCC 1203  QV 380 UTYTEO 400  BD 1204 ATACCCC 1210  RESULT 11  UBS-10-20-59-11  SGLWCCC 1210  RESULT 11  UBS-10-20-59-11  UBS-10-20-59-11  UBSTATTA CATTATCAACTCGCACACACCCCACCACTCGACCCCACCCCACCCTCCACCCCACCTCCACCCCACCTCCACCCTCACCCCACCTCCACCCTCACCCCACCTCCACCCCACCCTCCACCCCACCTCCACCCCACCTCCACCCTCACCCCACCTCCACCCTCCACCCTCACCCCACCCTCCACCCCACCCCCACCCTCCACCCCACCCCCACCCTCCACCCCACCCCCACCCCCACCCTCCACCCCACCTCCACCCCACCTCCACCCCACCCTCCACCCCACCTCCACCCCACCTCCACCCCACCCTCCACCCCACCTCCACCCCACCTCCACCCCACCCTCCACCCCACCCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCACCTCCACCCCCACCCCCACCCCCACCCCCACCCCCACCCCCACCCC	TELEFAX: 415/952-9881     TELEFAX: 415/952-9881     TELEFAX: 415/952-9881     TELEFX: 910/371-7168     SEQUENCE CHARACTERISTICS:     SEQUENCE CHARACTERISTICS:     SEQUENCE SINGLE Acid     STRANDEDNESS: Single     TOPOLOGY: Linear     SEQUENCE DESCRIPTION: SEQ ID NO: 11:     US-10-290-578-11     Alignment Scores:   1.77e-120   Matches:     Pred. No.:   1285.00   Matches:     Score:   100.00
cent Similar tr Local Sim rry Match: 10-029-020- 10-029-020- 114 441 41 41 41 124 124 121 124 121 124 121 124 121 124 121 124 121 121	1yThr 

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                                                                                                                                           APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Sabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILS ERFERENCE: 2140-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2000-12-29
PRIOR PILING DATE: 2001-01-02
PRIOR PLILNG DATE: 2001-01-04
PRIOR PLILNG DATE: 2001-01-04
PRIOR PLILNG DATE: 2001-03-29
PRIOR PLILNG DATE: 2001-03-29
PRIOR PLING DATE: 2001-04-13
PRIOR PLING DATE: 2001-04-13
PRIOR PLING DATE: 2001-04-18
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Edinger, Shlomit R
                                                                                     Ellerman, Karen
Gunther, Erik
Smithson, Glennda
Millet, Isabelle
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                                                                                        Thr ProArgSerAsnProSerProAlaProThrAspHisSerLeuSerGlyGluProPro
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US-10-029-020-14_COPY_1_400 (1-400) x US-10-290-578-11 (1-2387)
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Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Wolenc, Adam R
APPLICANT: Wolenc, Adam R
APPLICANT: Wenet, Corine
APPLICANT: Bisen, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Tin, Xiaohong
APPLICANT: Tin, Xiaohong
APPLICANT: Tin, Xiaohong
APPLICANT: Tohernev, Velizar
APPLICANT: Spaderna, Steven K
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Gusev, Vladimir Y
Gangolli, Esha A
Guo, Xiaojia S
Shenoy, Suresh G
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Kekuda, Ramesh
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Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
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Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
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Gusev, Vladimir Y
Gangolli, Esha A
Guo, Xiaojia S
Shenoy, Suresh G
Rastelli, Luca
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NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
APPLICANT: Smither, Ella
APPLICANT: Smither, Ella
APPLICANT: Smither, Ella
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/259,928
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR PILING DATE: 2001-01-02
PRIOR PILING DATE: 2001-01-02
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-18
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ORGANISM: Homo sapiens
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Sequence 35, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION,
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Woienc, Adam R
APPLICANT: Woienc, Adam R
APPLICANT: Wenet, Corine
APPLICANT: Bisen, Andrew J

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AGGCCCCCTCTCCCACCC---CTCACACACACGCTGTCCCATCACCAC---TCGTCC 1022
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                                                                                                 APPLICANT: Origene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer
FILE REFERENCE: 3U 103 R1
CURRENT APPLICATION NUMBER: US/10/144,194A
CURRENT FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin version 3.0
                                                              Sequence 81, Application US/10144194A Publication No. US20030215809A1 GENERAL INFORMATION:
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64.06%
50.61%
44.24%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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  TyrSerSerSerGluThrLeuLysAlaTyrAspGlnAsp---AlaArgLeuAlaTyrGly
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Alignment Scores: Pred. No.: Pred. No.: 920.00 Score: Score: Score: Percent Similarity: Percent Similarity: 94.03\$ Mismatches: 90 Query Match: 9 Gaps: 126 US-10-029-020-14_COPY_1_400 (1-400) x US-09-808-602-78 (1-8689)  Qy 1 MetAspVallysGluArglysProTyrArgSerLeuThrArgArgArgArgAspAlaGlu 19	20 ArgargTyThrSerSerala 20 ArgargTyThrSerSerala 190 TGTGGTACACACCTCTCTG 39 TyrSerSerSerGluThrLeuLys (		4 1 4	Qy 139 GlyArgSerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrLeuThrClu 158	Db   607 ATGADATAAATGGATGACGACAATGGTCGACCTACCTCGTCTGGC 666     Qy   168	169Gly 16  787 TCCCTAATTCATACCTGCTCAGAGCATGCTCAGGGCCCCAGCAAGCCTCCAGTAGTGGC 84  170 LeuGlnAsnHisAlaArgLeuArgThrProProProLeuSerHisAla 18  187 ListhrProAsnGlnHisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsnPheThr 20  187 HisThrProAsnGlnHisHisAlaAlaAserIleAsnSerLeuAsnArgGlyAsnPheThr 20	Db 904 CACACCCTGTCCCACCACCATCCTCTGCCAACTCACTCACAGAAACTCACTGACC 960  Qy 207 ProArgSerAsn
197	1172	Db 1200 AGCACACTTGTTCAGCAGTATACCTTTGACTCAGGAAAGGTTTAC 1259  Qy 312 SerProProArgProLeuProArgSerThrPheAlaArgProAlaPheAsnLeuLys 331  Db 1260 AGCCCCCGCCCCGCCTGCTGCCAGGAATACTTTCTCCAGGAAGGTTTTCAGGTGAAG 1319  Qy 332 LysProSerLysTyrCysAsnTrpLysCysAlaAlaLeuSerAlaIleValIleSerAla 351	ThrLeuVallleLeuLeuAlaTyrPheValAlaMetHisLeuPheGlyLeuAsnTrpHis 371	Db 1440 CTCCAGCTGCAGATGGGCACACCTTTAACAATGGGATAAGGACCGGCTTACCA 1493  QY 392 ValProThrAspValSerLeuTyrPro 400  Db 1494 GGAAACGATGAGGAACAATGCCA 1520	RESULT 15 US-09-808-602-78 Sequence 78, Application US/09808602 Sequence 78, Application US/09808602 GENERAL INFORMATION: APPLICANT: Vernet, Corine A APPLICANT: Fernandes, Elma APPLICANT: Shimkets, Richard A APPLICANT: Herman, Obhn L APPLICANT: Majumder. Kumnd	APPLICANT: Mishra, Vishum APPLICANT: Macs, Peter S APPLICANT: Mezes, Peter S APPLICANT: Mezes, Peter S APPLICANT: Mezongall, John ITLLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same ITLLE OF INVENTION: NO. US20020155115Alel Proteins and Nuclec Acids Encoding Same CURRENT PAPLICATION NUMBER: US/09/808,602 CURRENT FILING DATE: 2001-03-14 PRIOR APPLICATION NUMBER: 00/186,596 PRIOR APPLICATION NUMBER: 60/186,596	FALOR FILING DATE: 2000-03-03  NUMBER OF SEQ ID NOS: 114  SOFTWARE: PatentIn Ver. 2.1  SEQ ID NO 78  TYPE: DNA  CRGANISM: Rattus norvegicus  US-09-808-602-78

AC 1056	ln 262	1080	sp 282	1080	ro 301	CA 1137	er 321	AT 1197	ys 341	3C 1257	Val 361	TA 1317	lu 381	1374	400	1428
3GAGICCGIICAGCICCAGGACAGCIGGGIGCIGAAC 1056	SerAsnIleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThrLeuGln	AGTAACGTGCCGCTGGAGACGCGG	AspAsnLeulleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAsp		283 GlyHisPheLeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSerPro	CACTICCTCTTCAAGACGTCCTCCGGAAGCACACCCCTGTTCAGCAGCTCTTCTCCA	GlyTyrProLeuThrSerSerThrValTyrSerProProProArgProLeuProArgSer	GGATACCCCTTGACCTCAGGGACGTTTATACACCACCACCCCGCCTGCTGCTGCACGGAAT	ThrPheAlaArgProAlaPheAsnLeuLysLysProSerLysTyrCysAsnTrpLysCys	ACATTCTCTAGGAAGGCCTTCAAGCTGAAGAACCCTCCAAATACTGCAGTTGGAAATGC	AlaalaLeuSerAlaIleValIleSerAlaThrLeuValIleLeuLeuAlaTyrPheVal	GCCGCCCTGTTTTGCTGCCGCTGCCCTCTTTTGCTGCCTTTTTGCTGC	AlaMetHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyrGlu	GCAATGCATCTGCTCGGACTCAATTGGCAACTCCAGCCGGCAGATGGACACCTTT	IleThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro 	AACAATGGCGTAAGGACCGGCTTA\CAGGAAACGATGATGTGGCAACAGTGCCA
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US-09-623-326-2

US-09-528-991A-15189

US-09-758-282B-140

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US-09-758-282B-168

US-09-758-282B-183

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US-09-105-537-5

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US-09-657-440-19

US-08-68-657-1

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinDatin (Genentech)
APPLICATION DATA:
APPLICATION NUMBER: US/08/891,845
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Patent No. 6086801
GENERAL INFORMATION
APPLICANT: Schaefer, Gabriele M.
APPLICANT: Slwkcwski, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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REGISTRATION NUMBER: 40,378
REEECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/922-1994
TELEFRAX: 415/952-9881
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT THRORMATION:
                              TELEX: 910/371-7168
          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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-MODEL=frame+ p2n.model - DEW=xlh
-MODEL=frame+ p2n.model - DEW=xlh
-MODEL=frame+ p2n.model - DEW=xlh
-De_cgnz_1/USPTO_spool/US10029020/runat_06082004_112217_29301/app_query.fasta_1.3519
-DB=ISBUGA_PAtentEs NA -OFMT=fastap - SUFFIX=p2n.rni - MINNATCH=0.1 - LOOPCL=0
-DOENTT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi
-LIST=45 - DOCALIGN=200 - THR_SCORE=pct - THR_NAX=100 - THR_NATCH=0 - ALIGN=15
-MODE=LOCAL - OUTPWT=pto - NORN=ext - HEAPSIZE=560 - MINLEN=0 - MAXLEN=200000000
-USRE-WIST0029020 @CGN 1 1 258 @runat 66082004 112217_29301 - NCPU=6 - ICPU=3
-NO _MMAP - LARGEQUERY - NEG_SCORES=0 - WAIT - DSPBICCK=100 - LONGLOG
-DOUTD=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPDP=10 - XGAPEXT=0.5 - FCAPPP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
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Sequence 6, Appli
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Sequence 1, Appli
Sequence 11748, A
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1875.793 Million cell updates/sec
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                                                                                                                                                                                                                                                                                    2143
1 MDVKERKPYRSLTRRRDAER.....EITEDTASSWPVPTDVSLXP 400
                                                                                                                                                                   August 14, 2004, 01:16:21 ; Search time 118.339 Seconds
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seg:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seg:*
5: /cgn2_6/ptodata/2/ina/6B_COMB.seg:*
6: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seg:*
6: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seg:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                      OM protein – nucleic search, using frame_plus_p2n model
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US-09-103-840A-1
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US-09-514-573-3
US-08-1845-1
US-09-514-573-1
US-09-514-573-1
US-09-514-573-11
US-09-623-31-899-69
US-09-051-994-1
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Maximum Match 100%
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seq length: 200000000
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Jatabase :

Result No.

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961 AGCACCTTCGCCCGGCCGGCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAG 1020
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                                                                                                                                                                      ProGlyTyrProLeuThrSerSerThrValTyrSerProProArgProLeuProArg
                                 SerAspGlyHisPheLeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSer
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: (Genetech)
CURRENT APPLICATION DATA:
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1S-09-514-573-3
1S-09-514-573-3
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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FILING DATE: 28 FEB 2000
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/891845
FILING DATE: 10 JULY 1997
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994
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Mismatches:
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Matches:
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2138.00
99.75%
99.75%
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1680 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                         Linear
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Best Local Similarity:
Query Match:
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TOPOLOGY: Lir
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Pred. No.:
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1021 TGCGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCTGGTGGCATACTTT 1080
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                              961 AGCACCTTGGCCCGGCCGGCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAG 1020
                                                                                                                                                                                                                                                                                             381 GluileThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro 400
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                                                                                CysAlaAlaLeuSerAlaIleValIleSerAlaThrLeuValIleLeuLeuAlaTyrPhe
  US-10-029-020-14_COPY_1_400 (1-400) x US-08-891-845-1 (1-3111)
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Mismatches:
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Patent No. 6096873
GENERAL INFORMATION:
APPLICANT: Schaefer, Gabriele M.
APPLICANT: Sliwkowski, Mark
ITILE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,845
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CLASSIFICATION: 435
PION APPLICATION DATA:
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTONEY/ABENT INFORMATION:
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1043
TELEPHONE: 415/225-1994
TELEFRAX: 415/252-1994
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CITY: South San Francisco
STATE: California
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity:
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COMPUTER PROJUCE
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/514,573
FILLING DATE: 28 FEB 2000
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Matches:
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                                                                                                                     GENERAL INFORMATION:
APPLICANT: Schaefer, Gabriele M.
APPLICANT: Sliwkowski, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
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TELEFONE 415/225-1994
TELEFAX: ATENA
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APPLICATION NUMBER: 08/891845
FILING DATE: 10 JULY 1997
APPLICATION NUMBER: 6/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
                                                                                      Sequence 1, Application US/09514573 Patent No. 6500941
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378
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Best Local Similarity:
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CLASSIFICATION:
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US-09-514-573-1
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                                                                                            ACGGGCTGTCCCCCTGACACCCCGTGCGTCTGTGGGGCCCGGAGCACCACGGTCAGGGCGCC
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   ArgTyrThrSerSerAlaAspSerGluGluGlyLysAlaProGlnLysSerTyrSer
                       CGCTACACCCAGCTCGTCCGCGGACAGCGAGGGGCAAAAGCCCCGCAGAAATCGTACAGC
                                                                        SerSerGluThrLeuLysAlaTyrAspGlnAspAlaArgLeuAlaTyrGlySerArgVal
                                                                                                                                           LysAspIleValProGlnGluAlaGluGluPheCysArgThrGlyAlaAsnPheThrLeu
                                                                                                                                                                                                                                                                                                                 SerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGlu
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                       disk
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRINT APPLICATION DATA:
APPLICATION NOMBER: US/08/891,845
FILING DATE:
CLASSIFICATION A435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRAHION NUMBER: 40,378
REGISTRAHION NUMBER: 40,378
REGISTRAHION NUMBER: 40,378
  Gamma-Heregulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                            STREET: 460 Point San Bruno Bl. CITY: South San Francisco STATE: California COUNTRY: USA
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1285.00
100.00%
100.00%
59.96%
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TYPE: Nucleic Acid
STRANDEDNESS: Single
TITLE OF INVENTION: GA
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
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  514 AAGGACATTGTGCCGCAGGAGGCCGAGGAATTCTGCCGCACAGGTGCCAACTTCACCCTG
                                                                                                 GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp
                                                                                                                                                                                                                                                       ThrValLeuSerProGluHisProValArgLeuTrpGlyArgSerThrArgSerGlyArg
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Patent No. 6096873
GENERAL INFORMATION:
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Query Match:   59.964   Indels:   0	; EARLIER FILING DATE: 1997-06-04 ; EARLIER APPLICATION UNMER: 09/090,793 ; EARLIER FILING DATE: 1998-06-04 ; NUMBER OF SEQ ID NOS: 86 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 69 ; LENGTH: 4446
DD 361 CTCTTCAAGCCTGGAAGCACCTCCCCCCTCTTCTGCACCACATCACCAGGGTACCCAGGGTACCCAGGGTACCCAGGGTACCCAGGGTACCCAGGGTACCCAGGGTACCCAGGGTACCCAGGGTACCCAGGGTACCCCAGGGTACCCCCCGCCACCCTCCCCCCCACCCCTCCCCCCCC	US-09-514-573-11 Alignment Scores: 1.66e-108 Length: 2387 Pred. No.: 1285.00 Matches: 235 Score: 100.00\$ Conservative: 0 Bercent Similarity: 100.00\$ Mismatches: 0

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         roAlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsnIleProLeuGluThrArg----
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APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS;
FILE REPERENCE: REG-341-PCT-US
CURRENT APPLICATION NUMBER: US/09/051,994A
CURRENT FILING DATE: 1998-04-24
EARLIER APLICATION NUMBER: CT/US96/17201
EARLIER FILING DATE: 1996-10-25
BARLIER FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
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Patent No. 6602683
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NAME/KEY: modified_base
LOCATION: (1782)
OTHER INFORMATION: n=a,
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NAME/KEY: modified_base
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NAME/KEY: modified_base
LOCATION: (1741)
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NAME/KEY: CDS
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ORGANISM: Homo sapiens
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US-09-231-899-69
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Db	312Prol.  760 CCAIGGGCATITCAGACACAGGTITTCGGGGGGACCCCCCCTCCTGGGACTITGTCCCA  318 euProArgSerThrPheAlaArgProAlaPheAsnLeuLysLysP  [	333 robertysfyrcysdantrpbyscysdladleuseralailevallieserAlaThrb 35 [     :::     640 CCTCCGGGTCCCATC-CGATGTGCCAATGATGTAGTAGTGTGTGTGAGCGAAC 58 353 euVallleLeuLeuAlaTyrPheValalaMetHisLeuPheGlyLeuAsnTrpHisLeuG 37              ::::::::::::::::::::::::	Qy 373 InProMetGluGLyGInMetTyrGluIleThrGluAsp	RESULT 9 US-09-623-326-6 ; Sequence 6, Application US/09623326 ; Patent No. 6607933.	al. Polymerase Chime 4 NUMBER: US/09/622001-02-08		; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: polynucleotide	Alignment Scores:  Alignment Scores:  Pred. No.:  Score:  Score:  Percent Similarity:  Best Local Similarity:  Conservative:  Mismatches:  Distry Match:  115  Conservative:  115  Conservative:  115  Conservative:  115	4 Gaps: -029-020-14_COPY_1_400 (1-400) x US-09-623-326-6	3 VallysGluarglysProTyrargserleuThrargargArgArg		Qy 33LysAlaProGlnLys-SerTyrSerSerGluThrLeuLysAlaTyrAs 49 :::         ::::          :::      :::
Percent Similarity: 32.35% Conservative: 41  Best Local Similarity: 23.74% Mismatches: 173  Query Match: 6.14% Indels: 150  DB: 4 Gaps: 24  US-10-029-020-14_COPY_1_400 (1-400) x US-09-051-994-1 (1-1860)	Oy 1 MetAspValLysGluArgLysProTyrArgSerLeuThrArgArgAspAlaGluArg 20	Qy         41         SerSerGluThrLeuLysAlaTyrAspGlnAspAlaArgLeuAlaTyrGlySerArgVal 60           bb         1555         TCCGGCCCCTAGCTCTGGGTGGGGAC	Qy         75 GlyAlaAsnPheThrLeuArgGluLeuGluGluValThrProProHisGlyThr 94	Qy 103 ProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspWetGluAlaAspThr 121	Qy 122 ValleuSerPro	Db 1240 CACGTGAGAGGCCTCATACTTGTAGTAGATGTTTGGAGGGCTCTGGGGGGGCCCAT 1181  Qy 152LeuThrLeuThrAspThrGluHisGluAsnThrGluThrAspHisProGlyGlyLeu 170  Db 1180 CCTGCACGATATACACAGGATGCCCATAGTCACCACTCACT	Qy 171 GlnAsnHisAlaArgLeuArgThrPro	OY 181 ProProLeuSerHisAlaHisThrProAsnGlnHisHisAlaAlaSerIleAsnSer 199	laHisAlaGlnGluAsnTr          :: GCCACGCCCAGCAAGAGA	Oy 239 pLeuLeuAsnSerAsnIleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGl 259	Qy         259 yThrLeuGlnAspAsnLeuIleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAl         279           Db         867AGGGGGCAGGGGGG         854	Qy 279 aTyrSerAspGlyHisPheLeuPheLysProGlyGly-ThrSerProLeuPheCysThrT 299

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                                                                             uGluPheCysArgThrGlyAlaAsnPheThrLeuArgGluLeuGly---LeuGluGluVa
pGlnAspAlaArgLeuAlaTyrGlySerArgValLysAspIleValProGlnGluAlaGl
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Patent No. 6294328
GENERAL INPORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: PENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
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OTHER INFORMATION: Un' bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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Matches:
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CURRENT APPLICATION NUMBER: US/09/103,840A
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                                                                                                                TYPE: DNA ORGANISM: Mycobacterium tuberculosis
1998-06-24
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130.50
36.72%
23.88%
              CURRENT FILING DATE: 1998-
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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	Qy 270 eLeuGlyAlaSerArgHisAspGly-AlaTyrSerAspGlyHisPheLeuPheLysProG 290	Oy 290 lyGlyThrSerProLeu	Oy 296PheCysThrThrSerProGlyTyrProLeuThrSerSerThrValTyrSerProProP 315	Qy 315 roArgProLeuProArgSerThrPheAlaArgPro 326	RESULT 11 0.56-00-10-10-10-10-10-10-10-10-10-10-10-10-	133 %00/ ACCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG

Best Local Si Query Match: DB:	al Similarity: 22.22\$ Mismatches: 103 tch: 6.07\$ Indels: 124
US-10-02	9-020-14_COPY_1_400 (1-400) x US-09-252-991A-11748 (1-1998)
QY Db	5 GluarglysProTyrargSerLeuThrargArgArgAspAlaGluargArgTyrThrSer 24 US
oy S	SerSerAlaAspSerGluGluG     :::   :::
a &	LeulysalaTyraspGlnAspAlaArgLeuAlaTyrGlySerArgValLysAspIleVal 64
Dp	CTACGCGCCGAGCAAGTCCATCGGTTTCATCCGGCCGGGCGACGCGGTGCTGATCCGCTA 1077
Qy Dp	65 ProGlnGluAlaGluGluPheCysArgThrGlyAlaAsnPheThrLeuArgGluLeuGly 84 ; ;
۲۵ م <u>ر</u>	85 LeuGluGluValThrProProHisGlyThrLeuTyrArgThrAspIleGlyLeuProGln 104 ; ; ; ; ;
δλ	CysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAspThrValLeu 123
ପୁପ ପୂ	7 CAAGGTGCAGTCGATCTCCCGCGCCAGCGTCTCCTATGC 1155
S 8	124
δλ	DE 143 CysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGluAsnThr 162
qq	1210 GCTGTACCGGCTGCGGGTAACCCTCGA
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? <i>\</i>	AlaHisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsnPhe
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Qy Dp	306 ThrSerSerThrValTyrSerProProProArgProLeuProArgSerThrPheAla 324
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GENERAL INFORMATION:

Factoric 11618, Application US/09252991A

Factoric 11618, Application US/09252991A

Factoric No. 6551795

GENERAL INFORMATION:

FAPPLICATION:

MUCHEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

FRIOR PAPLICATION NUMBER: US 60/074,788

FRIOR PAPLICATION NUMBER: US 60/094,190

FRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 11618

LENGTH. 3180
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Best Local Similarity: 2
Query Match: 6
DB:
325 ArgPro 326
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IS-09-252-991A-11618/c
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   ---SerHis 185
                                                                                                                                                                                                        AlaGlyGlyAlaGlnGluProAlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsnIle 245
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                                                                  186 AlaHisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsnPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 ThrSerSerThrValTyrSerProProProArgPro---LeuProArgSerThrPheAla
                                                                                          Sequence 1, Application US/07945283
Patent No. 5352596
GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
APPLICANT: Weeley, Ronald D.
ATILE OF INVENTION: Pseudorabies Virus Deletion Mutants TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants TITLE OF INVENTION: Involving The EPO and LIT Genes NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: CLITIS P. Ribando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
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STREET: 1815 No. 5352596th University Street
CITY: Peoria
                                                                                                                                                                                                                                 1753 CCTGGCGATGATCGCCGGCTACCACGCCACCA
                                                                                                                                                           -----GCTCTCGCCCTGCGCCTGGGCCG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 309-685-4011 ext.513
174 AlaArgLeuArgThrProProPro
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ATTORREY/AGENT INFORMATION:
NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 8438 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: double
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US-07-945-283-1/c
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1504 GACAC-CTTCCTGGGAAGTGCCACCCGGCTCCACTTTCCTCCCAGCCCCTTCCCCAGCTC 1562
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Mismatches:
                                                                                                                                                                             Length:
Matches:
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4456 base pairs
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23.71%
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                                                                     nucleic acid
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Best Local Similarity:
                                                                                    STRANDEDNESS:
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         --9536 GCCGCCACCGTCTCCGCCGCCGCCGCCGCGCGCGCGG--
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APPLICANT: Peles, Eior
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF ALP RELATED DISORDERS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 90071-zvvv
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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SYSTEM: IBM P.C. DOS 5.0
FastSEQ for Windows 2.0
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SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,443
FILING DATE: Herewith
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TELECOMMULICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
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APPLICATION NUMBER: 60/049,477
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09095443 Patent No. 6342593 GENERAL INFORMATION:
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California
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90071-2066
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Search completed: August 14, 2004, 19:39:29 Job time : 5373.34 secs

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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/CQ2121_(USTBPTO spool)/US10029020/runat_06082004_112216_29275/app_query.fasta_1.3519
-DB=GGnEmbl -QFWT=fastap -SUFFIX=p2n.rge -MINMATGH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -RND=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -RND=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITS=bits -START=1 -RND=-1 -MATRIX=B0 - MINLEN=0 -MAXLEN=20000000000
-UNITS=bits -START=1 -RND=-1 - MATRIX=0 -MAXLEN=2000000000000
-USR=USIOC29020_@CGN 1 1.19065_@runat_06082004_112216_29275 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORRS=0 -MAIT_-DSPBLOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG SCORRS=0 -MAIT_-DSPBLOCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                 August 13, 2004, 23:35:57; Search time 7074.72 Seconds (without alignments) 2450.585 Million cell updates/sec
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                           OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delcp 6.0 , Delext
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AF009227 Homo sapi
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AX600210 Sequence
AB022413 Mus muscu
AF059485 Mus muscu
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AJ238613 Gallus ga
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AX662359 Sequence
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ALIGNMENTS

AC079194 Homo sapi AC136801 Rattus no AC134948 Rattus no AC120288 Rattus no

AC084775 F AP002957 F

AP002470

AC079194 AC136801

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Homo sapi Homo sapi

Sequence

RESULT

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CCGCCGCTCTCGCACGCCCACACCCCAACCAGCACCACGCGCCTCCATTAACTCCCTG
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Schaefer,G.M. and Sliwkowski,M.
Gamma-heregulin
Patent: US 6500941-A 3 31-DEC-2002;
Location/Qualifiers
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Sequence 3 from patent US 6500941.
AR270935
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Kekuda, R., Stone, D. J., Anderson, D., Shimkets, R. A., Burgess, C. B.
Zerhusen, B. D., Liu, X., Syytek, K. A., Casman, S. J., Boldog, F. L.,
Smithson, G., Li, L. and Ji, W.
Polypetides and nucleic acids encoding same
Patent: WO 0205743-A 13 25-JUL-2002;
Curagen Corporation (US)
Location/Qualifiers
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        ProProLeuSerHisAlaHisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeu

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
           Sequence 13 from Patent W002057453.
AX556500
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Schaefer,G.M. and Sliwkowski,M.
Gamma-heregulin
Patent: US 6500941-A 1 31-DEC-2002;
Location/Qualifiers
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                                                                                                                                                                                                                                         1354 IGGGGAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCTGCTGGCATACTTT
                                                                                                                                                                                                                                                                                                 1414 GTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGCCAGTGTAT
              TTGCAGGACAACCTCATTGAGATGGACATTCTCGGCGCCTCCCGCCATGATGGGGCCTTAC
                                                     SerAspGlyHisPheLeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSer
                                                                         1174 AGTGACGGGCACTTCCTCTTCAAGCCTGGAGGACCTCCCCCGGCTCTTCTGCACCACCATCA
                                                                                                           ProGlyTyrProLeuThrSerSerThrValTyrSerProProProArgProLeuProArg
                                                                                                                               1234 CCAGGGTACCCACTGACGTCCAGCACAGTGTACTCTCCTCCGCCCCGACCCCTGCCCCGC
LeuGlnAspAsnLeuIleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyr
                                                                                                                                                                     SerThrPheAlaArgProAlaPheAsnLeuLysLysProSerLysTyrCysAsnTrpLys
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                                                                                                                                                                                                                                                                                 361 ValAlaMetHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyr
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
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.nGluAlaGluGluPheCysArgThrGlyAlaAsnPheThrLeu

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CTCAACAGCAACATCCCCCTGGAGACCAGAAACCTAGGCAAGCAGCCATTCCTAGGGAAA 1113
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                                                                                                                                                                                                                                             ArgGluLeuGlyLeuGluGluGluValThrProProHisGlyThrLeuTyrArgThrAspile 100
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                                                                                                                         ACGGTGCTGCTCCCCTGAGCACCCCGTGCGTCTGTGGGGCCGGAGCACACGGTCAGGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnThrGluThrAspHisProGlyGlyLeuGlnAsnHisAlaArgLeuArgThrProPro
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                                 ArgTyrThrSerSerAlaAspSerGluGluGlyLysAlaProGlnLysSerTyrSer
                                                                      cectacaccaectcerceceeaacaecaaeaeaeecaaaaaecceecaaaatcetacae
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BHCGYSMCAGSDADMEADTULSPEHPVRLMGRSTRSGRSCLGSRANSILITITDTEHE
BHCGYSMCAGSDADMEADTULSPEHPVRLMGRSTRSGRSCLGSRANSILITITDTEHE
SIGEPPAGGAGSPADMEADTULSPEHPVRLMGRSTRSGRSCLGSRANSILITITDTEHE
SIGEPPAGGAGEPAHAGENWILLNSNIPLETRNIGKOPFIGTLODNI IERDIIGASRH
DGAYSDGHFIFFFKGGTSPLFCTTSPGTYPLTSSTVYSPPPRPLPRSTFARPAFNLKRPS
KYCNWKCAALSAIVISATIVILLAYPVAMHIRGLNWHLOPMEGQNYEITEDTASSWPY
PTDVSILYPSGGTGLETPDRKGKGTTFGKPSSFPEDSFIDGETDVGRRASGKIPPGT
FWRSQVFIDHPULKFNVSLGGAALVGIYGRSFPEDSFIDGETDVGRRASGKIPPGT
FWRSQVFIDHPWLLKFNVSLGGAALVGIYGRKGLPPSHTQPDFFULLDGRKLLITGAR
SILBGTPRQSRGTVPPSSTBTGFIQYLDSGIWHLAFYNDGCRSBVVSFLTTRIALPPRL
KEMKSQSSAGSKLVIRCETSSEYSSIRFKWFKNGNBLUNKKNVQUIKIQKKFGEL
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ISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKTFCVNGGECFNVKDLSNPSRYLCKCP
NEFTGDRCQNYVMASFYSTSTPFLSLPE"
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Homo.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 3111)
Schaefer, G., Fitzpatrick, V. D. and Sliwkowski, M. X.
Gamma-heregulin: a novel heregulin isoform that is an autocrine growth factor for the human breast cancer cell line, MDA-MB-175
Oncogene 15 (12), 1385-1394 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genentech, Inc., 460
CA 94080, USA
   ValAlaMetHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyr
                       GluIleThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro
                                                                                          1474 GAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCGACGTCTCCCTATACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schaefer, G., Fitzpatrick, V.D. and Sliwkowski, M.X.
Schaefer, G., Fitzpatrick, V.D. and Sliwkowski, M.X.
Direct Submission
Submitted (18-JUN-1997) Protein Chemistry, Genentech
Foint San Bruno Blvd, South San Franciscp, CA 94080,
Location/Qualifiers
Location/Qualifiers
// Mol type="MRNA"
// Mol type="MRNA"
// Mol xref="taxon:9606"
// Chromosome="8"
// Map="8p22-p1"
// Cell line="MDA-MB-175"
// Cell Lipe="MDA-MB-175"
// Cell Lipe="MDA-MB-175"
                                                                                                                                                                               mRNA linear complete cds.
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/product="gamma-heregulin"
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mRNA,
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/db_xref="G1:2406644"
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Homo sapiens gamma-heregulin
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MetaspvallysGluArgLysProTyrArgSerLeuThrArgArgArgAspAlaGluArg 20

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8 6 8 6 8 6 8 6	8 8 8 8 8 8 8 8	4 6 6 6 6 6 6 6 6	RESULT 8 AX600210 LOCUS LOCUS DEFINITION ACCESSION VERYOODS SOURCE ORGANISM REFERENCE AUTHORS
Oy 381 GluileThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro 400  Db 1474 GAGATCACGAGAGCACAGCAGTTGGCCTGTGCCAACCGACGTCTCCTATACCC 1533  RESULT 7  AX67551 LOCUS DEFINITION Sequence 1 from Patent W002055704.  AX67551 GI:2933552 SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human)  REFERENCE Padigaru,M. Li,L., Zerhusen,B.D., Casman,S.J., Shenoy,S., Spytek,K.A., Zhong,M., Gangolli E.A., Burgess,C.E., Patturajan,M., Verlect,C.E., Guo,X., Verlect,C.E., C	DOUGGLY.L., GrOSE, W.M., Alsobrook, J.P., Gerlach, V., Edingermark, S., Rothenberg, M.E., Ellerman, K., Macdougall, J., Malyankar, U., Millet, I., Peyman, J., Smithson, G., Gunther, E. and Stone, D.J.  TITLE Proteins, polynucleotides encoding them and methods of using the same JOURNAL Patent: WO 2025704-A 1 18-JUL-2002;  FEATURES Location/Qualifiers Source Location/Qualifiers   J. 8438     J. 8438     Alignment Scores: 3.61e-99 Length: 8438 Score: 2098.00 Matches: 348	Percent Similarity: 98.76\$   Conservative: 0	Db 124 TcCaGCAGACCTCTAGACGCTCAGGACCCCTTAGGCTTAGGCGCCCTTGTTTGT

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Obbashi, T., Zhou, X., Feng, K., Richter, B., Moergelin, M., Perez, M.T.,
Su, W., Chiquet-Ehrismann, R., Rauch, U. and Faessler, R.
Mouse Ten-m/Odz is a new family of dimeric type II transmembrane
proteins expressed in many tissues
J. Cell Biol. (1999) In press
2 (bases 1 to 8585)
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Submitted (29-MAR-1999) Toshitaka Oohashi, Okayama University
Medical School, Dept. Mol. Biol. & Biochem.; 2-5-1 Shikata-cho,
Okayama, Okayama 700-8252, Japan
SerAspGlyHisPheLeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSer
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Fax:+81-86-222-7768)
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Rodentia;
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Mus musculus
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 CGGGAGCTGGGGCTGGAAGAAGTAACGCCCCCTCACGGGACCCTGTACCGGACAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp
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                                                                                                                                                                                                                                                                                                                                     MetAspValLysGluArgLysProTyrArgSerLeuThrArgArgArgAspAlaGluArg
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Conservative:
Mismatches:
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Gaps:
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Matches:
Conservative:
Mismatches:
Indels: 1.11e-96 2050.00 96.52% 95.02% 95.66% Similarity: Percent Similarity: Alignment Scores: Н 188 248 41 21 Best Local S. Query Match: No.: Pred. d ద à g ò  $\delta$ 

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LysAspIleValProGlnGluAlaGluGluPheCysArgThrGlyAlaAsnPheThrLeu

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1267 140 280 487 547 607 667 727 200 220 300 340 787 847 SerGlyGluProProAlaGlyGlyAlaGlnGluProAlaHisAlaGlnGluAsnTrpLeu 240 360 ROD 15-AUG-1998 907 CTCAACAGTAACATCCCACTGGAAACCAGAAACCTAGGCAAGCCATTCCTAGGGACA 967 ThrValLeuSerProGluHisProValArgLeuTrpGlyArgSerThrArgSerGlyArg cercaacressacressacacacacccccrcaressacrecreassacacacacacac GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp SerSerCysieuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGlu AGTICCIGCCIGICCAGCCGGGCCAACTCCAACTCACACTCACGGACACACAGGAGCATGAG AsnThrGluThrAspHisProGlyGlyLeuGlnAsnHisAlaArgLeuArgThrProPro -Gln ProProLeuSerHisAlaHisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeu AsnArgGlyAsnPheThrProArgSerAsnProSerProAlaProThrAspHisSerLeu LeuAenSerAsn1leProLeuGluThrArgAenLeuGlyLysGlnProPheLeuGlyThr LeuGlnAspAsnLeulleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyr ProGlyTyrProLeuThrSerSerThrValTyrSerProProProArgProLeuProArg SerThrPheAlaArgProAlaPheAsnLeuLysLysProSerLysTyrCysAsnTrpLys CysAlaAlaLeuSerAlaIleValIleSerAlaThrLeuValIleLeuLeuAlaTyrPhe SerAspGlyHisPheLeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSer AGCACCTTCTCCCGACCAGCCTTTAACCTCAAGAAGCCTTCCAAGTACTGCAACTGGAAG ValAlaMetHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGly. linear Mus musulus DOC4 (Doc4) mRNA, complete cds. AF059485.1 GI:3170614 TATCCC 1393 TyrPro 400 488 548 101 121 141 899 1028 1088 1148 1208 609 191 181 728 788 221 848 241 261 281 341 361 1268 201 908 896 301 321 399 1388 RESULT 10
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NTETGAPLHCSSASSTPIEQSPSPPANESQRRLLGNGVAQPTPDSDSEEEFVPN
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                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 9722)
                                                                                                                                                                                                                          Wang, X.Z., Kuroda, M., Sok, J., Batchvarova, N., Kimmel, R., Chung, P., Zinszner, H. and Ron, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang,X.-Z. and Ron,D.
Direct Submission
Submitted (14-APR-1998) Skirball Institute, New York University
Medical Center, 550 First Ave., New York, NY 10016, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                            Identification of novel stress-induced genes downstream of chop EMBO J. 17 (13), 3619-3630 (1998)
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human gamma-heregulin; type II transmembrane protein"
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/ce]1 line="NIH-3T3"
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/strain="NIH/Swiss"
    musculus (house mouse)
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g, X.-Z. and Ron, D.
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AUTHORS
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JOURNAL
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TTAVWTISKHFDAYGRMKEYOYETFRSLMYMTTOYDDWGRVYKKELKVGEYANTTRY
SYEYDADGQLQTVS INDKPLMRYSYDLNGAUHLLASEDRSARLTPLRYDLRDRITTRIGD
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SGRTRRYTDIQLQYRAALCLMYRYGTTVDEEKNRVLELARGRARARGQRIREGE
BGLRAMTDGERQQVLNTGRVQSYDGFFVTSVEDERSDSANNIHFMRQSEMGRR
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375
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Matches:
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1971.00
81.14%
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Query Match:
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Pred. No.:
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Brain Science Institute,

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LORGILI FIDIACODOSANO SELLIANEGI TAVARGUE TEVORGILI TANDA SERIAGUE
LORGILI FIDIACODOSANO SELLIANEGI TAVARGUE TEVORGILI SERHIQUE
LORGILI SELLAGARE SELLO SENTATO SERIAGUE
TAVARE PHECOPECIDHFILVESTA LIAATLES NALAVSHNGLI YI AESDEKKI INRVRQV
STNGEI SILLAGARE SCOCKNDANCOC YSGODOSANA NASHANDE SELAS PEDGELE FADD.
GNINGEI SILLAGARE GADELANTE IS SET IDDELYLEPOWASHVETOSILTYGOYLYNETYS
GEOLISS TIDKWIKRRYSI IRROSTGLPLMM.MGPDGQTEWFTMGTNNALKSVAAQGQEI A
VMTYHES SGOLLATKSNEDGWSTF PEZ ENDY SERLINVYTY PEGRASS SET ROSDSTYRRYQTE
GSTWAPTI SKRNYTLP I DNGLINLYBWRQRKEQARGQOTVYGRRLRYHNRULLSMDFDR
VTRTEKYDDHRKFTLRIHYDHAGREPLARES SELLAGVANYTYS GRAHA AGGOGTOW
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LLB ILLYDTRI I AFSYDESAGMLKTVOLOS SEGRATILI DRQ I FRESERGMV
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                                                                                                                                                                                                                                                                                                                       /note="similar to Drosophila melanogaster tenm/odz and Mus
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                               RIKEN, Lab. for Developmental Gene Regulation; 2-1 Hirosawa,
Wako-shi, Saitama 351-0198, Japan (E-mail:mieda@brain.riken.go.jp,
Tel:81-48-467-9713, Fax:81-48-467-9714)
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              Submitted
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                          GlnAsnHisAlaArgLeuArgThrProProProProLeuSerHisAlaHisThrProAsn
                                                                                                                                                    1363 CAGCATCACGCGGCCTCCATCAACTCCTTGAACAGGGGCAACTTCACCCCCAAGGAGCAAC
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                                                                                                                           GlnHisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsnPheThrProArgSerAsn
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OY 249 ThrArghanLeuGlyLysGlnProPheLeuGlyThrLeuGlnAspAsnLeuIleGluMet 268		388	RESULT 12 AR270936 LOCUS DEFINITION SEQUENCE 11 from patent US 6500941. ACCESSION AR270936 VERSION AR270936.1 GI:29702178 KEYWORDS SOURCE Unknown.	ORGANISM Unknown.  Unclassified.  REFERENCE 1 (bases 1 to 2387) AUTHORS Schaefer,G.M. and Sliwkowski,M.  TITLE Gamma-herequlin JOURNAL Patent: US 650041-A 11 31-DEC-2002; FEATURES 1. 2387  Source //organism="unknown" /mol_type="genomic DNA"	9.1e-58 Length: 1285.00 Matches: 100.00\$ Conserva : 100.00\$ Mismatch : 59.96\$ Indels: 6	US-10-029-020-14_COPY_1_400 (1-400) x AR270936 (1-2387)  Qy
Pred. No.: 5.47e-68 Length: 9264 Score 1455.50 Marches: 287 Best Local Similarity: 70.34\$ Conservative: 45 Best Local Similarity: 60.81\$ Mismatches: 67 Query Match: 69.79\$ Indels: 73 DB: 5 Gaps: 3 US-10-029-020-14_COPY_1_400 (1-400) x AB026980 (1-9264) Qy	Oy 21 ArgTyrThrSerSerSlaAspSerGluGluGluGlyLysAlaProGlnLysSerTyrSer 40		Db   623 GGCCTTCCCCACCGCGACTACTCAGTGGCATCAGAGCGCTGACACAGAAACAGAC 682	160 GluasnThrGluThrAspHisPro	Db   923 AGGGGGCTCAGGCCGGCCGGGATTCGGAGATTGGCCCCCAATTCATTC	189 ProAsnGlnHisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsnPheThrProArg 189 ProAsnGlnHisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsnPheThrProArg 1103 CCAGCACCACACACCCACCCGGGTTCCTGGGCGGAGCAACTACACCCGGGGG 209 SerAsnProSerProAlaProThrAspHisSerLeuSerGlyGluProProAlaGlyGly 1163 AGTAACCCGGGCCCCCCCCGCGTAGTTCAGCTCCCAATAGGGGTCCGACAAGT 229 AlaGlnGluProAlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsnIleProLeuGlu 1220 GCCCAGGACCCCAGGGACCCCAGGACACTGCTCCTAACAGGGTCCCTAGGGGTCCCTAGGGGGCTCCCAAGGGGTCCCCTAGGGGTCCCTAGGGGTCCCTAGGGGCTCCTAGGGGTTCCTCTAACAGGACTTCCTCTAACAGGACTTCCTTAGAGGGTTCCTTAGAGGGTTCCTTAGAGGGCTCCTTAGAGGACAACTGGCTTCCTCTAACAGGACAACTGGCTTCCTTAGAGGGTTCCTTAGAGGGTTCCTTAGAGGGTTCCTTAGAGGGTTCCTTAGAGGGTTCCTTAGAGGGTTCCTTAGAGGGTTCCTTAGAGGACAACTGGCTTCCTCAACACACCAACCTTAGAGGACAACTGGCTTCCTCAACAACACCAACCTTAGAGGGTTCCTTAGAGGGTTCCTTAGAGGGTTCCTTAGAGGTTCCTTAGAGGTTCCTTAGAGGTTCCTTAGAGGTTCCTTAGAGGTTCCTTAGAGGTTCCTTAGAGGTTCCTTAGAGGTTCCTTAGAGGACAACTGGACTACTCTAGAGGTTCCTTAGAGGTTCTTCTAGAGGTTCCTTAGAGGTTCTTCTTAGAGGTTCCTTAGAGGTTCTTCTTAGAGGTTCCTTAGAGGTTCCTTAGAGGTTCCTTAGAGGTTCTTTTAGAGGTTCTTTTAGAGGTTTCTTA

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ETLKAPDHDYSRLLYGNRVKDLVHREADEYTROGONFTLROLGVCESATRRGYAPCAE
BEGLERGYSI SAGSDADTENBAVMSPEHAMELMGCYKSGRSSCLSSRSNSALTLTDT
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GSRLIAREQRNLVESERAGRQARSVSLHEAGFIQYLDSGIWHLAFYNDGKNPEQVSFN
TIVIESVVECPRNCHGNGECVSGTCHCFPGFLGPDCSRAACPVLCSGNGQYSKGRCLC
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VDCGSHGVCMGGSCRCEEGWTGPACNQRACHPRCAEHGTCKDGKCECSQGWNGEHCTI
AHYLDKIVKEGCPGLCNSNGRCTLDQNGWHCVCQPGWRGAGCDVAMETLCTDSKDNEG
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DSTHVLPGESPFNKSLASVIRGQVLTADGTPLIGVNVSFLHYSEYGYTITRQDGMFDL
VANGGASLTLVFERSPFLTQYHTVWIPWNVFYVMDTLVMKKEENDIPSCDLSGFVRPS
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GOLASIQGTTSEKUDYDSQCRIVSRVRADGKTWSYTYLLEKSWYLLLHEADROYT PEYD
MWDELSAITWRSVARHTWOTIRSSGTYVRYNDPESBARSITDYNEEGLILQTRELG
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                                                                                           /translation="MDVKERRPYCSLTKSRREKERRYTNSSADNEECRVPTQKSYSSS
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                                               /protein_id="BAA77398.1"
/db_xref="GI:4760780"
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Mouse Ten-M'Odz is a new family of dimeric type II transmembrane proteins expressed in many tissues
J. Cell Biol. (1999) In press
2. (Dases I to 8964)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Direct Submission
Submitted (29-MAR-1999) Toshitaka Ochashi, Okayama University
Medical School, Dept. Mol. Biol. & Biochem.; 2-5-1 Shikata-cho,
Okayama, Okayama 700-8252, Japan
AlaGlyGlyAlaGlnGluProAlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsnIle
                             GCCGGCGCCCCAGGCCTGCCCACGCCCAGGAGAAACTGGCTGCTCAACAACATC
                                                                                                                             241 CCCCTGGAGACCAGAACCTAGGCAAGCAGCCATTCCTAGGGACATTGCAGGACAACCTC
                                                                                                                                                                      IleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAspGlyHisPhe
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/strain="Balb/c"
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/dev stage="adult"
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50. .8197
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                                                                            Homo sapiens ODZ3 (ODZ3) mRNA, partial cds. AF195420
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Submitted (15-OCT-1999) Faculty of
University, Ramat-Gan, Israel
Location/Qualifiers
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8645 bp
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AX662355
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                                                                 Homo sapiens (human)
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 77
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                                                                                              GCGGAAATGGGGCTCCCTCACAGAGGTTACTCTATCAGTGCAGGGTCAGATGCTGATACT
                                                                                                                                         ThrAspIleGlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMet
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TTTACCCTAAGGCAGTTAGGAGTTTGTGAACCAGCAACTCGAAGAGGACTGGCATTTTGT
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RESULT 15

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                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                        Spytek, K.A., Li, L., Wolenc, A.R., Vernet, C.A., Bisen, A., Liu, X. Malyankar, U., Shimkets, R.A., Tchernev, V.T., Spaderna, S.K., Gorman, L., Rekuda, R., Patturajan, M., Gusev, V., Gangolli, E.A., Guo, X., Shenoy, S., Rastelli, L., Casman, S.J., Boldog, F., Burgess, C.E., Edinger, S., Ellerman, K., Gunther, E., Smithson, G. Miller, T. and Macdougall, J.R.
Proteins and nucleic acids encoding same
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Curagen Corporation (US)
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Mismatches:
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309 ThrValTyrSerProProProArgProLeuProArgSerThrPheAlaArgProAlaPhe 328
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175 ArgLeuArgThrProProProProLeuSerHisAlaHisThrProAsnGlnHisHisAla 194
                691 ACCCTGCAGCCCTTGCCGCCT----TCCCATAAGCAGCACTCTGCACAGCATCAT-- 741
                                                                                                                  231 ---GluProAlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsnIleProLeuGluThr 249
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Search completed: August 14, 2004, 11:51:10 Job time : 7138.72 secs

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Command line parameters:
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-Q=/cgn2 1/USFT0 spool/MITRAQ20/runat_06082004_114100_206/app_query.fasta_1.583
-DEGenEmbl -QFFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEZX=0 -LLOOPEXX=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWHPAD20 @CGN 1_1_3731_@runat_06082004_114100_206 -NCPU=6 -ICPU=3
-UOTFWHPAD20 @CGN 1_1_3731_@runat_06082004_114100_206 -NCPU=6 -ICPU=3
-NO NMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGIAG
-NO NMAP -LARGEQUERY -NEG SCORES=0 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                 August 14, 2004, 12:05:42; Search time 5140 Seconds (without alignments) 3372.999 Million cell updates/sec
                                                                                                                                                                                                           1 MDVKERKPYRSLTRRRDAER........EITEDTASSWPVPTDVSLYP 400
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                  - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                         3470272 seqs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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AB025412 Mis muscu
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AX662353 Sequence
AX64711 Gallus ga
AX250064 Sequence
AX250067 Sequence
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AX250066 Sequence
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ALIGNMENTS

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Sequence Sequence Sequence Sequence

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RESULT

Db   S75 CCGCCGCTCTCGCACGCCCCAACCAGCACCACGCGCCTCCATTAACTCCCTG   S34	QY         321 SerThrPheAlaArgProAlaPhaAsnLeuLysLysProSerLysTyrCysAsnTrpLys         340           Db         995 AGCACCTTCGCCCGGCCGCTTTAACCTCCAAGAACCCTCCAAGTACTGGAAG         1054           QY         341 CysAlaAlaLeuSerAlaIleValileSerAlaThrLeuValileLeuLeuAlaTyrPhe         360           Db         1055 TGCGCAGCCTGGCGCTTCGTCGTCTCTGGTCGTCGTCGTCGTGGTG	NEFERENCE
AX556500  AX556500  AX556500  ACCESSION  AX556500  AX56500  AX56600  AX56600  AX56600  AX56600  AX56600  AX56600  AX5600  AX56600  AX5600  AX600  AX60	Alignment Scores:  Alignment Scores:  Score:  Score:  Score:  Percent Similarity:  99.25%	

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Aco, W.O.

Method of promoting the proliferation of inner ear hairy cells using ligand of FER2 receptor and/or HER3 receptor using ligand of FER2 receptor and/or HER3 receptor and/or HER3 receptor batent: JP 2002529425-A 6 10-SEP-2002;

GENENTECH INC

OS Homo sapiens (human)

PN JP 2002529425-A/6

PD 10-SEP-2002

PP 28-OCT-1999 JP 2000580655

PR 07-NOV-1999 US 60/107522

PR 07-NOV-1999 US 60/107522
      GTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGGCCGATGCAGGGCAGATGTAT 1140
                                                                                                                                                                                                                                                       BD270887
3111 bp DNA linear PAT 17-JUL-2003 Method of promoting the proliferation of inner ear hairy cells using ligand of HER2 receptor and/or HER3 receptor.
BD270887
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                                                                 GlulleThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1
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/mol_type="genomic DNA"
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Homo sapiens (human)
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Unclassified.  AUTHORS Schaefer, G.M. and Sliwkowski, M. TITLE Gamma-heregulin JOURNAL Patent: US 6500941-A 1 31-DEC-2002; FEATURES  1. 3111  Alignment Scores: A.2e-103 Length: 3111 Pred. No.: Core: Percent Similarity: 99.00% Mismatches: 6 Best Local Similarity: 99.00% Mismatches: 7  Query Match: 69.53% Mismatches: 6  SEC14-X-AT-28-64-76 (1-400) x AR270934 (1-3111)	1 MetaspvallysGluarglysProTyrargSerLeuThrargArgArgAspalaGluarg	C 51 C 63 C 63 C 63	Qy         121 ThrValLeuSerProGluHisProValArgLeuTrpGlyArgSerThrArgSerGlyArg 140           Db         694 AcGGTGCTGTCCCCTGAGCACCCGGTGGGTCTGTGGGGCCGAGCACACGGTCAGGGCG 753           Qy         141 SerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrLeuThrAspThrGluHisGlu 160           Db         754 AGCTCCTGCCTGTCCAGCCGGCCCAATTCCAATCTCACACTCACCGACACGAGCATGAA 813           Qy         161 AsnThrGluThrAspHisProGlyGlyLeuGlnAsnHisAlaArgLeuArgThrFroPro           Db         161 AsnThrGluThrAspHisProGlyGlyLeuGlnAsnHisAlaArgLeuArgThrFroPro           Db         814 AACACTGAGACTGATCATCATCACAGCCGGGCCTGCGGGCTCCGGGACGCCGCGG 873	Oy 181 ProProLeuSerHisAlaHisThrProAsnGlnHisHisAlaAlaSerTleAsnSerLeu 200
	Qy         181 ProProLeuSerHisAlaHisThrProAsnGlhHisHisAlaAlaSerIleasnSerLeu         200           By         CCGCCGCTCTCGCACCCCCACCCCCACCCCACGCGGCGCTCCTG         933           Qy         201 AsnArgGlyAsnPheThrProArgSerAsnProSerProAlaProThrAspHisSerLeu         220           Db         934 AACCGGGCACACTCCGAGAGACCCCAGGCCCCCAGGACCACTCCTC         933           Qy         221. SerGlyGluProAraCTCCAGGAGAGCACCCCAGGACCCCAGGACCACTCCTC         993           Qy         222. SerGlyGluProAraCTGAGCCGAGAGACCCCAGGACCCCAGGACCACTCCTC         993           Db         994 TCCGGAGAGAGCCCCTGCGGGCGCGCGCCCAGGAGAACTGGCTG         1053           Db         994 TCCGGAGAGAGCCCCTGCGGGGGCCCCAGGAGACCCCAGGAGAACTGGCTG         1053	241 LeuAsnSerAsnIleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThr	301 ProGlyTyrProLeuThrSerSerThrValTyrSerProProArgProLeuProArg 302 CAGGGGTACCCACTCCAGCCAGTCGTCTCTCTCGCCCGCC	OY 351 VAIALANCH SILVEN STREAM STATEMENT OF THE SECULAR OF THE SECOND STATEMENT 19 1

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251 LeuGlinksphanteulieGluwerkapileteulyalaserArBHisaspolyAlatyr 280 Db 1114	Alignment Scores: 4.2e-103 Length: 3111  Pred. No.: 2122.00 Matches: 396 Score: Similarity: 99.00\$ Conservative: 0  Best Local Similarity: 99.00\$ Mismatches: 4 Query Match: 69.53\$ Indels: 0  SEQ14-X-AT-28-64-76 (1-400) x BD140153 (1-3111)

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1174 AGEGACGEGEACTICCTCTICAAGCCTGGAGGCACCTCCCCCGCTCTTCTGCACCACATCA 1233
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334 ATGGACGTGAAGGAGGAAGCCTTACCGCTCGCTGACCCGGCGCCGCGACGCCGAGGCGC 393
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                          1 ArglyrThrSerSerSerAla***SerGluGluGlyLysAlaProGlnLysSerTyrSer
                                                            1394 CGCTACACCCAGCTCCTCCGCGGAQGGGAGGAGGCCAAAGCCCCCGCAGAAATCGTACAGC
                                                                                                                   41 SerSerGluThrLeuLysAlaTyrAspGlnAspAlaArgLeuAlaTyrGlySerArgVal
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LKAYDQDALAAYGSRVKDIVEQEAEEFCRTGAMFTLAELGIZEVTPEHGTLYRTDIGL
HCGYSWGAGSDADMEADTLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHB
NTETDHEGGLQNHAARLATPPEPELSHATPNQHHAASINSLNRGNFTPRRNPSRPRTBE
SISGEPPAGGAQEPAHAQENWILNSNIPLETRNIGKOPFLGTLQDNLIEMDILGASRH
GGAYSDGHFKFRGGTSELFCTTSPQFPLTSSTYVSPPPRFBLRSTFARPAFNLKKPS
KYCNNKCAALSLINGSTLFLLAYFVAMHLFGLINWHLQPMEGQMYEITEDTASSWPP
PTDVSLYPSGGTGLETPDRKGKGTTEGKPSSFPPEDSFIDSGEIDVGRRASSWIP
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SLEGTPRQSRGTVPPSSHETGFTQYLDSGIWHLAFYNDGKESBVVSFLTTAIALPPRL
KEMKSQESAGSKLVLRCETSSEYSSLRFKWFKNGELNRKNKFQNIKIQKKPGKSEL
RINKASLADSGEYMCKVISKLGNDSAANITIVESNEIITGMPASTEGAYVSSESPIR
ISVSTEGANTSSSTETGFTGHLVKCARKEKTFCVNGGECFWYKDLSNPSRYLCKCF
NEFTGDRCQNYVMASFYSTFTFELLYRCARKEKTFCVNGGECFWYKDLSNPSRYLCKCF
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                                                                                                                                                                                                                                                                                                                                                                                          Schaefer, G., Fitzpatrick, V.D. and Sliwkowski, M.X. Gamma-heregulin: a novel heregulin isoform that is an autocrine growth factor for the human breast cancer cell line, MDA-MB-175 Oncogene 15 (12), 1385-1394 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chases 1 to 3111)
Schaefer,G., Fitzpatrick,V.D. and Sliwkowski,M.X.
Schaefer,G., Fitzpatrick,V.D. and Sliwkowski,M.X.
Submission-1997) Protein Chemistry, Genentech, Inc., 460
Boint San Bruno Blvd, South San Francisco, CA 94080, USA
Location/Qualifiers
1. 3111
, organism="Homo sapiens"
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Homo sapiens gamma-heregulin mRNA,
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Mammalia; Eutheria; Primates;
1 (bases 1 to 3111)
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Best Local Similarity:
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KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

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MetAspVallysGluArgLysProTyrArgSerLeuThrArgArgArgAspAlaGluArg

(1-3111)

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STABROSTAQUENTHAQDNWILLNSNIPLETRNLGKOPFLGTLQDNLIEMDILSASRH
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10 (sites)
20 (obashi,T., Zhou,X., Feng,K., Richter,B., Moergelin,M., Perez,M.T., Su,W., Chiquet-Ehrismann,R., Rauch,U. and Faessler,R. Mouse Ten-m/Odz is a new family of dimeric type II transmembrane proteins expressed in many tissues
2 (bases I to 8585)
                                                                                  951 Adreacescarriccirricaascriscacescarcriccescricricriscacearca 1010
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ProGlyTyrProLeuThrSerSerThrValTyrSerProProArgProLeuProArg
                                                                                                                                                                                                           1071 AGCACCTTCGCCCGGCCGCCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAG
                                                                                                                                                                                                                                                                                                                        361 ValalametHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyr
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                                                                                                                                                                                      SerThrPheAlaArgProAlaPheAsnLeuLysLysProSerLysTyrCysAsnTrpLys
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AB025413 GI:4760781
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Fax:+81-86-222-7768)
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Mus musculus
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Incyte Genomics, Inc. (US)
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Conservative:
Mismatches:
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REFERENCE AUTHORS

	misc_featu	ORIGIN	Alignment Score Pred. No.:	Score: Percent Similar Best Local Simi	Query Match: DB:	SEQ14-X-AT-28-6	Oy 1	Db 583 #	Oy 21 F	Db 643	Qy 41 8	. 607 da	Qy 61 I	Db 763 I	Oy 81 /	Db 823 (	QY 101 (	Db 883 (	Qy 121	Db 943	Oy 141	Db 1003	Oy 161	Db 1063	Qy 164	Db 1123	Qy 164	Db 1183	Qy 165
Mus musculus (house mouse) Mus musculus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 9722) Wang, X.Z., Kuroda, M., Sok, J., Batchvarova, N., Kimmel, R., Chung, P., Zinszner, H. and Ron, D. Identification of novel stress-induced genes downstream of chop	9631305* 9649432 2 (bases 1 to 9722) Warm Y -7 and Pon D	1998) Skirball Institute, New York	<pre>Medical Center, 550 First Ave., New York, NY 10016, USA 1 0201101/Qualifiers</pre>	/organism="Mus musculus" /mol_type="mRNA" /strain="NIH/Swiss"	/db_xref="taxon:10090" /cell_line="NHH-3T3"	/note="tunicamycin-treated" 19722	e e		/note="similar to Drosophila melanogaster tenm/odz and human gamma-heregulin; type II transmembrane protein"	/codon_start=1 /product="DOC4"	/protein_id="AAC31807.1" /db_xref="G1:3170615"	/translation="MDVKERKPYRSLTRRRDAERRYTSSSADSEEGKGPQKSYSSSET LKAYDQDARLAYGSRVKDMVPQEAEBFCRTGTNFTLRELGLGEMTPPHGTLYRTDIGL	PHCGYSMGASSDADLEADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSKLTLTITIEHE NTETGAPLHCSSASSTPIEQSPSPPSPPANESGRRLLGNGVAQPTPDSDSEEEFVPN	SFLVKSGSASLGVAANDHPSSLQNHPRLKTPPPPFLPHAHTPNQHAASIASLANGNKT PRSNPSPAPTDHGLSGPPAGEPAGEPTHAQDNWYLNSKT PVETRNLGKQPFLGTWQDN	LIEMDIFSASRRDGAYSDGHFFFREGGTSPLFCTTSPGFFLTSSYVSFFRFLFRSI FSRPAFNLKKPSKYCNWKCAALSAILISATLVIILAYFVAMHLFGLNWHLQPMGCQMQ	MYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKKGKGARGKPSLF-PEDSFLDSGEL DVGRRASQKIPPGTFWRSQYFIDHPWHLKFNVSCRAALVGIYGRKGLPPSHTQLDFV	ELLOGRRALTORARSLEGEPOROSRGEVPPSSHETGETOTALSGAMLLAGETNOGAESEV VSETUTAL I BEVUDNOGARGANGTORAGETORA	KCLCHSGWRCASECDWINGTINGTANGASEGALTINGALLICHGALGGGGGGGGGAAACAGGGGGGGGGGGGGGGGGGGGG	HICKADCGGGGCVCVGGICKCEDGWMGAACHQKACGFKCAGGGICKCGCLGICKGGGGCACGCGCCGCGCGCGCGCGCCGCCGCCGCCGCCGCC	CMDPDCCEPLCHVWELCLESFDELDITQETQAFVOQQAIMSETDATAFEVOXESTING I PGENEFEGGHACUTRQQVMTSDCGTPLGVDVITSFRINDEFRGYTISRQDGSFDLVTNGG 1911 BEEDA BETTAGEDTH VIT BORDEFINGHTIVMPHERRITGPRDISUPARPUVGSP	SPLICKFERGETTLY COLLEGE OF THE COLLE	I FFINININANTOEREKKINFARAFELDESTINANTOEREKKINGENOOFSE YESCPDLITHEKKITAVLOGYEIDASKILGGWEITHALINI OSGILHKGNGENOOFSOO DOTTOETMANTOEDESTICHSCHAFTANTOENENTIAVANTOEREKERFEPS	GRUTUILEMGHGKKEGISCLSCLSCHGLANGERKLIGST VALICOSUSGIT GERTALISCS GRUTUILEMGHSPAHKYYLATUDMGSAVFILSDHYRRRVFKVKSTTVVKDLVKNSEVVA	GTGDQCLPPDDTRCGDGGKATEATLINPRGTIVDKGTI Y FVDGTATKK VDGNET 5.1 LLGGNDLTSRPLCGDGSVMEI SOTLEMPTDLTRDMPDDLSLYLDNNVVLQI SENRÇV	RIVAGRPMHCQVPGIDQFLLSKVAHHATLESATALAVSHNGYLI ABTIDEKLINK KQ VTTGGBI IVVAGAPGCDCKNDANCOCFSGDDGVXDAKLNITPSSLAVCADGELVVAD	LGNIRIRETRYNKPFINIONNAMELSKYLDGELIEFIEDISCHLIGERIGGERIAGIE TGDGDITHITDNNAMVNVRRESTGMEDMIVORDGOVYMFGINSAMENVTTGGHEL	AMMITHGNSGLLATKSNENGWITF FETUSFCKLIN VIFF TOUSSSTENDLINGS VILLAY ETSSKDDVIITTHLSGSGAFYTLLODOVRNSYTIGDGSLRLLANGNAL THEFTUSFCKLINGSTENDLINGS	LAGTVNPTVGKRNVTLPIDNGLNI/EWROKREQARGOVI/FGFKLK VHNKNLLSLDFD RVTRTEKIYDDHRKFLXII/YDQGRPSFWDSSSRINGVNVTYSPGGHIAGIQKGIMS RVTRTEKIYDDHRKFLII/I/I/I/I/I/I/I/I/I/I/I/I/I/I/I/I/I/I	ERMEYDQAGK.TISKLYADGKWNSTITLEKSNYLHLISDQKQIIFEFDANDKLUSYLIFFA VARQTLETIRSVGYYRNIYQPPEGNASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKLS KLAETLYDTTKVSFTYDETAGMLKTVNLQNEGFTCTIRYRQIGPLIDRQIFRFTEEGM

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VNAREDXNYDDNSFRYTSMQAVINETPLPIDLYRYDDVSGKTEGFGKFGYIYYDINQII
TTAAMTHSKAIFDAYGRMKBVQYETFRSLMYWMTVQYDNMGRVVKKELKVGPYANTTRY
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SYEVDADGOLGYPYSTRDEGRASHTFREGD
VQYKMDEDGSLRQRGGDVPERNRSAGLILIKAYNRASGWSVRYRYDGIGRRVSSKSSHSH
HLQPFYADLTNFKYTHLYSHSSSEITSLYYDLOGHLFAMELSSGDEFYIACDNIGTP
LAVPSGTGIMIK KOLILYTAYGAIYMDTNNPROFII IGYMGAGLYDDFLTKLYMMRRRDYDVL
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NNAHYLENLHFTIDGVDTHYFVKPGPSBGDLAILGLSGGRRYTDLISVANEDGRRAFALL
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/gene="Doc4"
/note="putative; transmembrane-region site"
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                                             GlnHisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsnPheThrProArgSerAsn
                                                                                                                                                                      GluProAlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsnIleProLeuGluThrArg
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                          GlnAsnHisAlaArgLeuArgThrProProProProLeuSerHisAlaHisThrProAsn
                                                                                                                                                  ProSerProAlaProThrAspHisSerLeuSerGlyGluProProAlaGlyGlyAlaGln
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, R. Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.
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'note="similar to Drosophila melanogaster tenm/odz and Mus GINEL SULFANKARIES SOCIALANDELINE SOURCE AND ALGORITHMENT AND ALGORITHMENT SOURCE AND ALGORITHMENT AND ALGORITH RGVCVRGECHCRVGRGGPGCESPRASCHEQCSGHGSFLADTWTCNCDHNWTGHDCSTE
LCAACCGGHGICVAGSCRCDEGWMGTGCCQPACHPRCSEHGTCKDGYCECSPGWNGEH
LCAACCGGHGICVAGSCRCDEGWMGTGCCQQACHPRCSEHGTCKDGYCECSPGWNGEH
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PLTARAGTCPERGIVVPETOTLQEEVRIPGTUMGEVETOFISCHLSFTRPMTIVLPA
PLTARAGTCPERGIVVPETOTLQEEVRIPGTUMGEVETOFISCHLRITGHTSTI
BESLAKVHLMVARAGTRYRFSAAPNLSYDFWMKTDVSQKVYGLSEAFVSVGFEY
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	308	32 15		349	ASILIA PILI PILI PILI PORTE DE LA CONTROL DE		RESULT 12 AR270936 LOCUS LOCUS DEFINITION Sequence 11 from patent US 6500941.	VERSION AR27035.1 GI:29702178 KEYWORDS . Unknown.	REFERENCE 1 (bases 1 to 2387) AUTHORS Schaefer, G.M. and Sliwkowski, M.	TILLE Gamma-Heregulin JOURNAL Patent: US 6500941-A 11 31-DEC-2002; FEATURES Location/Qualifiers SOURCE 12387	/organism="unknown" /mol_type="genomic_DNA" ORIGIN	: 4.21e-59 Length: 1285.00 Matches: 1206.00 Conservative:			Qy         166 HisProGlyGlyLeuGlnAsnHisAlaArgLeuArgThrProProProProJeuSerHis 185	Oy 186 AlaHisThrProAsnGlnHisHisAlaAserIleAsnSerLeuAsnArgGlyAsnPhe 205	206
Pred. No.:       7.12e-69       Length:       9264         Score       285         Percent Similarity:       69.92	214-X-AT		41 SerSerGluThrLeuLysAlaTyrAspGlnAspAlaArgLeuAlaTyrGlySerArgVal	4.1 IUSASDILe***ProGlnGlualaGluBheCysArgThrGl***AsnPheThrLeu	Qy 81 ArgGluLeuGlyLeuGluValThrProProHisGlyThrLeuTyrArgThrAspIle 100	101 GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp 12	121 ThrvalleuSerProgluHisProValargLeuTrpGlyArgSerThrArgSerGly ::::::	Oy 140 ArgSerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHis 159	Qy         160 GluAsnThrGluThrAspHisPro	167 -	167	923 168	983 TTAGTTAAAACCGGGTCAGGGGAACGTCTGCACTCCGGCCGCTACLGCTAALGAGGGGCGCGCTACLGCTAALGAGGGGCGCGCGCTACLGCTAALGAGGGGCGCGCGCTACLGCTAALGAGGGGCGCGCGCTACLGCTAALGAGGGCGCGCGCTACLGCTAALGAGGGCGCGCGCGCTAALGAGGAGCGCGCGCGCGCGCGCTAALGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	Db 1043 TCGTTCCAGAATCACTCACGGTTGCGAACGCCACCATTACCCCTGTTTCACTCGCACTCC 1102	1103 CCCAGTCAGCACCACCGCCTCCATCGGTTCCCTGAGCCGCACCAACTACACCCAGCGC	Oy 209 SerAsnProSerProAlaProThrAspHisSerLeuSerGlyGluProProAlaGlyGly 228	Qy 229 AlaGluBroAlaHisAlaGluGluAsnTrpLeuleuAsnSerAsnIleProLeuGlu 248       ::: :::

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NUT DYTTENGORGEN TO NORMAN TO NORM
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RVRDGEEGARLWTEGEKRQLLSAGKVQGYDGYYVLSVEQYPELADSANNIQFLRQSEI
GKR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 AGGCGCTATACAAATTCGTCCGCGGACAATGAGGAGTGTAGGCTCCCCACGCAGGAGTCC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 ArgArgTyrThrSerSerSerAla***SerGluGluGlyLysAlaPro---GlnLysSer 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetAspValLysGluArgLysProTyrArgSerLeuThrArg~--ArgArgAspAlaGlu
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Mismatches:
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Best Local Similarity:
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Sohashi, T., Zhou, X., Feng, K., Richter, B., Moergelin, M., Perez, M.T., Su, M., Chiquet-Ehrismann, R., Rauch, U. and Faessler, R.

Su, M., Chiquet-Ehrismann, R., Rauch, U. and Faessler, R.

Mouse Ten-Modz is a mew family of dimeric type II transmembrane proteins expressed in many tissues

M. Cell Biol. (1999) In press

2. (bases 1 to 8964)
Sochashi, T.

Direct Submission

M. Submittered (29-MAR-1999) Toshitaka Ochashi, Okayama University
Medical School. Dept. Mol. Biol. & Biochem.; 2-5-1 Shikata-cho, Okayama, Okayama 700-8252, Japan

(E-mail:ochashi@cc.okayama-u.ac.jp, Tel:+81-86-235-7128, Fax:+81-86-225-7768)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyrGluIleThrGluAsp 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                  GCGGGCGCCCAGGAGCCTGCCCACGCCCAGGAGAACTGGCTGCTCAACAACAACATC
                                                                                                                                                                                                            LeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSerProGlyTyrProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaGlyGlyAlaGluProAlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsnIle
                                                                                                                                                                                                                                                                                                                     IleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAspGlyHisPhe
                                                                                                                                                                                                                                                                                                                                                                                                        ATTGAGATGGACATTCTCGGCGCCTCCCGCCATGATGGGGCTTACAGTGACGGGCACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 ACGTCCAGCACAGTGTACTCTCCTCCGCCCGAACCCCTGCCCCGCAGCACCTTCGCCCGG
                                                                                                                                                              ProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThrLeuGlnAspAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAGTGCGCAGCCCTGAGC
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AB025412.1 GI:4760779
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LOCUS DEFINITION

RESULT 13

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ACCESSION VERSION

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS AUTHORS TITLE JOURNAL

PEATURES

REFERENCE JOURNAL

TITLE

gene

CDS

8964 210 50 91 64

27-JAN-2000

rule

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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151. .>1476
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odd 02.Ten-m gene sequence"
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1 (bases I to 1476)

En-Zur,T., Feige,E., Motro,B. and Wides,R.

The mammalian odz gene family: Homologs of a Drosophila pair of gene with expression implying distinct yet overlapping developmental roles

Dev. Biol. 117, 120 (2000)

2 (bases I to 1476)

Ben-Zur,T., Motro,B. and Wides,R.
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           -GTGCCAACAACACTGTATCGTTACCT 1147
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Conservative:
Mismatches:
                                                                      1476 bp mRNA ODZ3 (ODZ3) mRNA, partial c
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                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (15-OCT-1999) Faculty of
University, Ramat-Gan, Israel
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Ten-m3"
                                                                                     Homo sapiens ODZ3 (ODZ3
AF195420
AF195420.1 GI:6760372
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Homo sapiens
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TITLE
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REFERENCE
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                                                                                                                                        350 GCGGAAATGGGGCTCCCTCACAGAGGTTACTCCATCAGTGCAGGGTCAGATGCGGAATACG
                                                                                                                                                                                                                                                                                                                         -----ThrGluThrAspHisProGlyGlyLeuGlnAsnHisAla
                                                                                                                                                                                                                                                                                                                                                                                         175 ArgleuArgThrProProProProLeuSerHisAlaHisThrProAsnGlnHisHisAla
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                                                                                                                                                                                   ThraspileGlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMet
                                                                                                                                                                                                                                                                        410 GAAAACGAAGCAGTGATGTCCCCTGAGCATGCCATGAGACTTTGGGGCAGGGGGGTCAAA
                                                                                                                                                                                                                                                                                                         SerGlyArgSerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThr
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                 PheThrLeuArgGluLeuGlyLeuGluGluValThrProProHisGlyThrLeuTyrArg
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230 AACAGAGTAAAGGATTTGGTCCACAGAAAGCCGACGAGTATACTAGACAAAGGACAGAAT
TyrSerSerSerGluThrLeuLysAlaTyrAspGlnAsp ---AlaArgLeuAlaTyrGly
                                                            SerArgValLysAspIle***ProGlnGluAlaGluGluPheCysArgThrGly***Asn
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S S	58 SerArgValLysAspIle***ProGlnGluAlaGluGluPheCysArgThrGly***Asn 77 :::	AX662355 LOCUS DERINITION	
oy Dp	78 PheThrLeuArgGluLeuGlyLeuGluUvalThrProProHisGlyThrLeuTyrArg 97 	ACCESSION VERSION KEYWORDS	AX662355.1 GI:29163217
V QU	ThraspileGlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspalaAspMet :::::::	SOURCE ORGANISM	Homo sapiens (human) Homo sapiens (bukar) Eukaryota; Metazoa; Chordat Mammalia; Eutheria; Primate
Q <sub>Y</sub>	alleuSerProGlutisProValArgLeuTrpGlyArgSerThrArg    :::           :::	AUTHORS	Spytek, K.A., Li, L., Wolenc, Malyankar, U., Shimkets, R.A. Gorman, L., Kekuda, R., Patt
Qy Dp		TITLE	Guc, A., Shenoy, S., Kastell Burgess, C.E., Edinger, S., F Millet, I. and Macdougall, J. Proteins and nucleic acids
Qy Db	ThrGluThrAspHisProGlyGlyLeuGlnAsnHisAla :::	υ	Curagen Corporation (US) Location/Qualifier 1. 8645
QY Dp		ORIGIN	/ Organism="none be / mol_type="unassig /db_xref="taxon:96
oy G	A1a 	Alignment S Pred. No.: Score:	
Qy Db		refeur Similarity: Best Local Similarity Query Match: DB:	llarity: 62.41% Similarity: 50.60% .: 6
yy Dp		SEQ14-X-AT-28-64-76 Qy 1 MetAs	28-64-76 (1-400) x AX662355 1 MetAspValLysGluArgLysProT
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& A	30	Db 2	271 TACAGTTCCAGGGACATTGAAAG 58 SerargValLysaspile***Prog
δ	ThrValTyrSer		
셤 ;	9 TCTGTTTATTCA	You and	78 PheThrLeuArgGluLeuGlyLeuG            :::      ::: 391 TTTACCCTAAGGCAGTTAAGGAGTTTA
A G	329 ASTLEULYSTYSFYGSETLYSTYTCYSASTTTPLYSCYSALAALaLeuSetAlaileVal 348 1039 AAATTCAAGAAGTCTTCAAAGTACTGTAGTGAAATGCACTGCACTGTGTGCCGTAGG 1098		
٥y	lleSerAlaThrLeuValIleLeuLeuAlaTyrPheValAlaMetHisLeuPheGlyLeu	da	451 GCGGAAATGGGGCTCCCTCACAGAG
<u>a</u> 8			
qq		Qy 13	138 SerGlyArgSerSerCysLeuSerS
ογ.	386 ThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro 400	Db 5:	571 TCAGGCCGCAGCTCCTGCCTGTCAAC 158 GluHisGluAsnmrGl
0.00	1219 ACCATGCCAACAACACTGTGTCATTACCT 1248		

RESULT 15

PAT 22-MAR-2003 SACAATGAGGGGTACCACACAGAAGTCC 270 330 :::|||||||:::||||||| :AGAGAAGCAGACGAGTTCACTAGACAAGGACAGAAT 390 TGTGAACCAGCAACTCGAAGAGGACTGGCATTTTGT 450 OGLUHISProValArgLeuTrpGlyArgSerThrArg 137 lata, Craniata; Vertebrata; Euteleostomi; tes; Catarrhini; Hominidae; Homo. \*\*\*SerGluGluGlyLysAlaPro---GlnLysSer 38 SAlaTyrAspGlnAsp---AlaArgLeuAlaTyrGly 57 77 GluThrAspHisProGlyGlyLeuGlnAsnHisAla 174 GluGluValThrProProHisGlyThrLeuTyrArg 97 ic, A.R., Vernet, C.A., Eisen, A., Liu, X., A., Tchernev, V.T., Spaderna, S.K., rturajan, M., Gusev, V., Gangolli, B.A., li, L., Casman, S.J., Boldog, F., Ellerman, K., Gunther, E., Smithson, G., oglngluAlaGluGluPheCysArgThrGly\*\*\*Asn SerArgAlaAsnSerAsnLeuThrLeuThrAspThr linear 8645 210 49 92 64 12 ,J.R. ds encoding same 15-AUG-2002; Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: DNA sapiens" signed DNA" :9606" 1645 bp 1 5 (1-8645) g

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349 IleSerAlaThrLeuValIleLeuLeuAlaTyrPheValAlaMetHisLeuPheGlyLeu 368
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                                                                                                                                                                                                                   309 ThrValTyrSerProProProArgProLeuProArgSerThrPheAlaArgProAlaPhe 328
                                                                                                           249
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                                                                                    ArgAsnLeuGlyLysGlnProPheLeuGlyThrLeuGlnAspAsnLeuIleGluMetAsp 269
                                                                                                                                                                                  270 IleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAspGlyHisPheLeuPheLysPro 289
                                                                                                                                                                                              214
175 ArgleuArgThrProProProProLeuSerHisAlaHisThrProAsnGlnHisHisAla 194
                  741
                                                231 ---GluProAlaHisAlaGluAsnTrpLeuLeuAsnSerAsnIleProLeuGluThr
                                   195 AlaserileAsnSerleuAsnArg1yAsnPheThrProArgSerAsnProSerProAla
                                                                      ProThrAspHisSerLeuSerGlyGluProProAlaGlyGlyAlaGln------
                  ----TCCCATAAGCAGCACTCTGCACAGCATCAT---
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                691 ACCTGCAGCCCTTGCCGCCT-
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Search completed: August 14, 2004, 23:48:40 Job time : 5209 secs

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AC120288 Rattus no
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AB025413 Mus muscu
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AJ238613 Gallus ga
AP001141 Homo sapi
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BD270887 Method of
AR270934 Sequence
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-Q=/cgn2_1/USPTO spool/US10029020/runat_06082004_112216_29275/app_query.fasta_1.3519
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-USTABRTA1 - NATRIX-blosum62 -TRANS-bluman40.cdi -LIST-45
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-USTRAT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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                                                                        (without alignments)
2450.585 Million cell updates/sec
                                                             August 13, 2004, 23:35:57; Search time 1255.76 Seconds
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1 TFWRSQVFIDHPVHLKFNVS.....RLLTQBARSLEGTPRQSRGT 71
  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                          nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                          3470272 segs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Homo sapi

Sequence

Sequence

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Method of promoting the proliferation of inner ear hairy cells using ligand of HER2 receptor and/or HER3 receptor. BD270887. I GI:33080655
Homo sapiens (human)
Homo sapiens
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                                                                                  Homo sapiens (human)
JP 2002529425-A/6
10-SEP-2002
28-007-1999 JP 2000580655
WEI QIANG GAO
A61K45/00,A61K38/00,A61K39/395,A61P27/16,C12N5/06/,(C12N5/06,
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 3111)
                                                       853 ACTITCIGGAGAICICAAGIGIICAIAGACCAICCIGIGCAICIGAAAIICAAIGIGICI
                                                                                                                                         41 GlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSer
                               1 ThrPheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                          Method of promoting the proliferation of inner ear hairy cells using ligand of HER2 receptor and/or HER3 receptor Patent: JP 2002529425-A 6 10-SEP-2002; GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism='Homo sapiens (human)'.
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ligand of HER2 receptor and/or HER3 receptor
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    US-10-029-020-14_COPY_450_520 (1-71) x AR270936 (1-2387)
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TITLE
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KEYWORDS
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BD270887
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E 1 (bases 1 to 2387)
S Schaefer,G.M. and Sliwkowski,M.
Gamma-heregulin
AL Parent: US 6500941-A 11 31-DEC-2002;
Location/Qualifiers
2387
"""known"
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Schaefer,G.M. and Sliwkowski,M.
Gamma-heregulin
Patent: US 6500941-A 3 31-DEC-2002;
Location/Qualifiers
1. 1680
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US 6500941.
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GENENTECH COMMENT OS HOMO PO JP 26-M PD 26-M PP 03-F PR 04-F PR PI MARK PC A61K PC COTK PC COTK	ATURES SOURCE SOURCE GIGIN GIGIN GOTE: FORT SIMI ST LOCAL SIMI	QY         1 Threher           Db         1681 ACTTTTN           QY         21 LeuGlyL           Db         1741 CTGGGAA           QY         41 GlnPheA           QY         61 LeuGluG           QY         61 LeuGluG           QY         61 LeuGluG           QY         61 LeuGluG           DB         1861 CTAGAGG           RESULT         AF009227           LOCUS         AF009227           DBETHITION         HOMO SADI           ACCESSION         AF009227           VERGION         AF009227           VERGION
QY         21 LeuGlyLyshlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThr 40           Db         1741 CTGGGAAGGCAGCCTGGTTGGCATTTATGGLAAAGGCTCCTCTTCTTCTTCTTATATATATATATATATAT	AR270934	Alignment Scores:  Score:  Score:  Score:  372.00  Matches: 71  Score: 1.21e-34  Matches: 71  Score: 100.00\$  Matches: 0  Duery Match: 100.00\$  Matches: 0  Duery Match: 100.00\$  Mismatches: 0  Duery Match: 100.00\$  Mismatches: 0  Duery Match: 100.00\$  InherrpargscrdnvalphelleaphisprovalhisleuLysPheasnvalSer 20  InherrpargscrdnvalphelleaphisprovalhisleuLysPheasnvalSer 20  InherrpargscrdnvalphelleaphisprovalhisleuLysPheasnvalSer 20  InherrpargscrdnvalphelleaphisprovalhisleuLysPheasnvalSer 20  InherrpargscrdnvalphelleaphisprovalhisleuLysPheasnvalSer 20  InherrpargscrdnvalphelleaphisprovalhisleuLysPheasnvalSer 20  InherrpargscrdnvalphelleaphisprovalhisleuCorccorccorccorcorcancerist 20  Inherry Match: Db 1741 CTGSGAAAGCCAGCCCTGGTTGGCATTTATGGCAGAGACCACCTCCTCTCATCATACA 1800  Qy

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-FEB-1999 JP 2000530226

-FEB-1999 US 09/020598

RK SLIWKOWSKI, JEFFREY A KERN

IX38/00, AGIK35/12, AGIK39/395, AGIP11/00, AGIP43/00, 7K14/485, 12, AGIK39/395, AGIP11/00, AGIP43/00, 17K14/485, 12N15/09, CI2P21/08, AGIK37/02, CI2N15/00 CC Ition of heregulin as epithelial cell growth factor FH Key Location/Qualifiers
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r.G., Fitzpatrick, V.D. and Sliwkowski, M.X.
factoria a novel heregulin isoform that is an autocrine factor for the human breast cancer cell line, MDA-MB-175 e 15 (12), 1385-1394 (1997)
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H INC,UNIVERSITY OF IOWA RESEARCH FOUNDATION to sapiens (human) 2002509076-A/6
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/organism="Homo sapiens"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Curagen Corporation (US)
Location/Qualifiers
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                   /organism="Homo sapiens"
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Sequence 1 from Patent WO02055704.
AX675551
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NEFTGDRCQNYVMASFYSTSTPFLSLPE"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Polypetides and nucleic acids encoding same
Patent: WO 02057435-A 3 25-UUL-2002;
Curagen Corporation (US)
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cell_type="breast cancer cell"
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                                                                            "map="8p22-p11"
                           db_xref="taxor
chromosome="8"
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1478 CAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGGAGGCGCGCGGAGC 1537
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                      Yue, H., Yao, M.G., Ison, C.H., Lu, Y., Warren, B.A., Elliott, V.S., Baughn, M.R. Ding, L., Xu, Y., Gietzen, K.J., Tang, T.Y., Lal, P.G., Duggan, B.M., Burford, N., Lu, D.A., Richardson, T.W., Tran, U.K., Khare, R. and Walia, M.K.

Proteins associated with cell growth, differentiation, and death Patent: WO 02072830-A 22 19-SEP-2002;

Incyte Genomics, Inc. (US)
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                                                                                                           GlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSer
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                       LeuGluGlyThrProArgGlnSerArgGlyThr
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                             AX600210 8645 bp
Sequence 22 from Patent WO02072830.
AX600210
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ROD 08-MAY-1999

linear

AB025413 8585 bp mRNA Mus musculus mRNA for Ten-m4, complete cds. AB025413

LOCUS DEFINITION ACCESSION

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SVGWGGTNCETPRATCLIDGCSGHGTFLPDTGLCNCDPSWTGHDGSIEICAADGGGHGW
CVGTCREDDGMMGAALDDRACHPRACHGTCRDGKCBCSPGWGEHGTTAHTJRVU
KEGCPGLCNGNGRCTLIDLNGARCHPRACHGTCRDTSMETGGGBGXNNGGPGTTAHTJRVU
KEGCPGLCNGNGRCTLIDLNGAHGTGCDGAPVSQNINPFYDRIKFLVGRDSTHSIPG
PDCCLQPLCNGNGRCTLIDLNGAHGTGCDGAPVSQNINPFYDRIKFLVGRDSTHSIPG
BPRDGGGAPACVIRGQVMTSDGTPLVAVNDERGYTISRQDGSPDLVNGGSISI
ILRFREAPFTTQGHTTAMLPWDRFFYDRIJAGCKNRLSYLSSRTPGYSVSVLRISLTHPTIPF
TSFASSCABKGPIVPEIQALQBEIVIAGCKNRLSYLSSRTPGYKSVLRISLTHPTIPF
TMKVHLMAVAGGRLRKWFAAAPDLGSYYFINNTOVYNGVFGFSBARVSVGYSFSE
CPDLILMEKRTAVLGYSTEIDASCHGARLGANSLDKHALNINGSTLLHKGNGBNQFYSQQPPV
IGSIMGNGRRSISCPSCNGLAADVALLGGSDGSLYVGDFNYIRRIFPSGNV
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DAGYSBOHFLERREGGTSPLFCTYSPORPLASSYVSPPPREDEPRSAFSRENKKRS
KYGNWKCAALASI ISATLVILLAYFYAMHLEGLMWHLOPMEGOMOWYEITEDTRASSW
PVPTDVSLYPSGGIGLETPDRKGKGAABGKRSSLFPEDSFIDSGEIDVGRRASQKIPP
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NCPSNCYGNGDCISGTCHCFLGFLGPDCGRASCPVLCSGNGQYMKGRCLCHSGWKGAE
CDVPTNQCIDVACSSHGTCIMGTCICNPGYKGESCEEVDCMDPTCSSRGVCVRGECHC
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IISTLLGSNDLTSARPLSCDSVMEISQVRLEWPTDLAINPMDNSLYVLDNNVVLQISB
NHQVRIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETTDEKKIN
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PHCGYSMGASSDADLEADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHE
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EEGMVNARFDYNYDNSFRVTSMQAVINETPLFIDLYRYDDVSGKTEQFGKFGVIYYDI
                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (29-MAR-1999) Toshitaka Ochashi, Okayama University
Medical School, Dept. Mol. Biol. & Biochem.; 2-5-1 Shikata-cho,
Okayama, Okayama 700-8252, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (E-mail:oohashi@cc.okayama-u.ac.jp, Tel:+81-86-235-7128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="mRNA"
/strain="Balb/c"
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/tissue_type="brain"
/dev_stage="adult"
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                                                                            Mus musculus (house mouse)
Mus musculus
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GI:4760781
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note="downstream of CHOP 4"

ORIGIN

YDVLAGRWTSPDHELWKRLSSNSIVPFHLYMFKNNNPISNSQDIKCFMTDVNSWLLTF PROCHNVIPOTYRPDTDAMBESYELWHTWKNYDDBWDSKSILGYVCEVOKQLKREVTL BRFDQLYGSTITSCOQAPETKKFASSGSIFGKKVFRALKDGRYTTDIISVANDGRRI AAILNNAHYLENLHFTIDGVDTHYFVKPGPSBGDLAILGLSGGRRTLENGVNVTVSQI SHSHHLQFFYADLTNPTKVTHLYNHSSSEITSLYYDLQGHLFAMELSSGDEFYIACDN IGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRD NTMLSGRTRRYTDIOLOYRALCINTRYGTTVDEEKVIYVELARQRAVRQAWAREQORL REGEEGLRAWTDGEKQOVLNTGRVQGYDGFFVTSVEQYPELSDSANNIHFMRQSEMGR R" 1541 ACGTTCTGGAGATCTCAGGTGTTCATAGACCACCTGTACACCTGAAGTTCAATGTGTCT 1600 ROD 15-AUG-1998 TTRYSYEYDADGGLQTVSINDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDLRDRIT RLGDVQYKMDEDGFLRQRGGDVFEYNSAGLLIKAYNRASGWSVRYRYDGLGRRVSSKS 1 (bases 1 to 9722)
Wang,X.Z., Kuroda,M., Sok,J., Batchvarova,N., Kimmel,R., Chung,P.,
Zinszner,H. and Ron,D. 40 9 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Identification of novel stress-induced genes downstream of chop EMBO J. 17 (13), 3619-3630 (1998)
98315054 1601 CIGGGGAAAGCAGCICIGGIIGGCAFIITAIGGCAGAAAAGGCCIICCICCIICCATACI ThrPheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSer LeuGlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThr GlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSer linear 8585 68 0 2 0 0 complete cds. US-10-029-020-14\_COPY\_450\_520 (1-71) x AB025413 (1-8585) Length:
Matches:
Conservative:
Mismatches:
Indels: mRNA Crecadedrecreacecentalicated LeuGluGlyThrProArgGlnSerArgGly 70 Gaps: 9722 bp Mus musculus DOC4 (Doc4) mRNA, AF059485 Mus musculus (house mouse) AF059485.1 GI:3170614 6.28e-32 353.00 97.14% 97.14% musculus Percent Similarity: Best Local Similarity: Query Match: DB: AF059485 Alignment Scores: Pred. No.: 1721 Н 21 41 61

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YESCPDLILWEKRTAVLQGYBIDASKLGGWSLDKHHALNIQSĞILHKGNGENQFVSQQ
PPVIGSIMGNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFPS
GNYTNILEMƏHSPAHKYYLAYDPMSCAVFLSPTNSRRVFKVKSTTVYKDLVKNSEVVA
GNYTNILEMƏHSPAHKYYLAYDPMSCANAVLSPTNSRRVFKVKSTTVVXDILIST
LLGSNDLIPPDTRCGDGGKATBATLTVAVRGITVDKFGILYFVDGTMIRRYDQNGIIST
LLGSNDLITSARPLSOSVWBISQQVRLEWPTDLAINPMDNSLYVLDNNVYLQISENHQV
RIVAGRPMHCQVPGIDQFLLSKVAIHATLESATALAVSHNGVLYIAETDBKKINRIRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELLDGRRÍLITQEARSLEGPQRQSRGPVPPSSHETGFIQYLDSGIWHLAFYNDGKESEV
VSFLITAIESVDNCPSNCYGNGDCISGTCHCFLGFLGPDCGRASCPVLCSGNGQYMKG
RCLCHSGWKGAECDVPTNQCIDVACSSHGTCIMGTCICNPGYKGESCEEVDCMDPTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTFLPDTGLCNCDPSWTGHDCSI
EICAADCGGHGVCVGGTCRCEDGWMGAACDQRACHPRCAEHGTCRDGKCECTPGWNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCTIEGCPGLCNGNGRCTLDLNGWHCVCQLGRRGTGCDTSMETGCGDGKDNDGDGLVD
CMDPDCCLQPPLCHVNPLCLGSPDPLDIIOETGAPVSQNLNSFYDRIKELVGRDSTHS
IPGENPFDGGHACVIRGGWTSDGTPLVGVNISFINNPLFGYTISRQDGSFDLVTNGG
ISIILKFERAPFITGBHTJWLPWDRFFVWFTIYWRHEENEIPSRDLSNFARPWYSP
SPLTSFASSCAEKGPIVPEIQALQEEIVIAGCKMRLSYLSSRTPGYKSVVRISLTHPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTTSGEISLVÄGAPSGCDCKNDANCDCFSGDDGYAKDAKLNTPSSLAVCADGELYVAD
LGNIRIRFIRKNKPPLNTQNMYBLSSPIDQELYLPDTSGKHLYTQSLPTGDYLYNFTY
TGDGDITHITDNNGNMVNVRRDSTGMPLMLVVPDGQVYWVTMGTNSALRSVTTQGHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETSSKDDVTI TTHLSGSGAFYTLLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHL
LAGTVNPTVGKRNVTLPIDNGLNLVEWRQRKEQARGQVTVFGPRLRVHNRNLLSLDFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARQTLĒTIRSVGYYRNIYQPPBGNASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKLS
KLAETLYDTTKVSFTYDETAGMLKTVNLQNEGFTCTIRYRQIGPLIDRQIFRFTEEGM
                                                                                                                                                                                                                                                          |protein_id="AAC31807.1"
|db_xref="GI:3170615"
|translation="MDVKERKPYRSLTRRRDAERRYTSSSADSEEGKGPQKSYSSSET
                                                                                                                                                                                                                                                                                                                                                                                                                                           PHCGYSMGASSDADLEADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTETCAPLHCSSASSTPIEQSPSPPPSPANESQRRLLGNGVAQPTPDSDSEEEFVPN
SFLVKSGSASLGVAANDHPSSLQNHPRLRTPPPPLPHAHTPNQHHAASINSLNRGNFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSRPAFNLKKPSKYCNWKCAALSAILISATLVILLAYFVAMHLFGLNWHLQPMEGOMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYETTEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGAAEGKPSSLFPEDSFIDSGET
DVGRRASQKIPPGTFWRSQVFIDHPVHLKPNVSLGKAALVGTYGRKGLPPSHTQLDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I PFNLMKVHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFGLSEAFVSVGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVTRTEKIYDDHRKFTLRILYDQAGRPSFWSPSSRLNGVNVTYSPGGHIAGIQRGIMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERMEYDQAGRITSRIFADGKMWSYTYLEKSMVLHLHSQRQYIFEFDKNDRLSSVTMPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNARREDYNYDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQII
TTAVMTHSKHFDAYGRMKEVQYETFRSLMYMMTVQYDNMGRVVKKELKVGPYANTTRY
SYEYDADGQLQTVSINDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDLRDRITRLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRSNPSPAPTDHSLSGEPPAGSAOEPTHAODNWVLNSKI PVETRNLGKOPFLGTWODN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIEMDIFSASRRDGAYSDGHFFFKPGGTSPLFCTTSPGYPLTSSTVYSPPPRPLPRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMMTYHGNSGLLATKSNENGWTTFYEYDSFGRLTNVTFPTGQVSSFRSDTDSSVHVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQYKMDEDGSLRQRGGDVFEYNSAGLLIKAYNRASGWSVRYRYDGLGRRVSSKSSHSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLQPFYADLTNPTKVTHLYSHSSSEITSLYYDLQGHLFAMELSSGDEFYIACDNIGTP
LAVFSGTGLMIKQIIYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HNVI PGYPKPDTDAMEPSYELVHTQMKTQEWDNSKSI LGVQCEVQKQLKAFVTLERFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ritscooapetkkfassgsifgkgvkfalkdgrvttdiišvanedgrriaail
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EGLRAWTDGEKQQVLNTGRVQGYDGFFVTSVEQYPELSDSANN I HFMRQSEMGRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGRWTSPDHELWKRLSSNSIVPFHLYMFKNNNPISNSQDIKCFWTDVNSWLLTFGFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAHYLENLHFTIDGVDTHYFVKPGPSEGDLAILGLSGGRRTLENGVNVTVSQINTML
                                                                                 /note="similar to Drosophila melanogaster tenm/odz and
human gamma-heregulin; type II transmembrane protein"
                                                                                                                                                                                                                                                                                                                                                                                              LKAYDQDARLAYGSRVKDMVPQEAEEFCRTGTNFTLRELGLGEMTPPHGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Doc4"
/note="putative; transmembrane-region site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-029-020-14_COPY_450_520 (1-71) x AF059485 (1-9722)
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Matches:
Conservative:
Mismatches:
Indels:
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347.00
95.71%
93.28%
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Best Local Similarity:
Query Match:
DB:
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CDS
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2 (bases 1 to 9722)
Wang, X.-Z. and Ron, D.
Direct Submission
Submitted (14-Asion
Medical Center, 550 First Ave., New York University
Location/Qualifiers

9649432

MEDLINE PUBMED REFERENCE AUTHORS TITLE

JOURNAL

PEATURES

TITLE JOURNAL

DEFINITION

AF059485

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ACCESSION VERSION

KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS /db xref="taxon:10090"
/ceIl line="NIH-3T3"
/note="tunicamycin-treated"

1. .9722 /gene="Doc4"

gene

organism="Mus musculus"

1. .9722

/mol\_type="mRNA" /strain="NIH/Swiss"

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Alignment Scores:
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SOURCE
ORGANISM
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DEFINITION
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VERSION
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                                      2205
                                                                                                                           2265
                                                                                                                                                                                                    2266 CAGTTAGACTTTGTGGAGGCTCCTGGATGGAAGAAGGCTCCTAACCCAAGAGGGAAGGGC 2325
                                                                                                                                                                                                                                                                                                                                                                                            VRT 05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENTENGPPLHCSSASSSPVDSPYPPSHAANQSQGRLLGNSGAQAGRDSESEDEFGPN
SELVKTGSGNVCTPAATTANGSSPQNHSRLRFPPPLPLEHENBSPSQHTAAIGSLGRSN
YTQRSNPSPAPTDSSAPNGSPTSAQDSSSAQDNWLLNSNVPLETRNIAKQTFLETLQD
NFIEMDILATARRDGAYTDGHFLFKPGGTSPLYCTTSPGYPLTSSTVYSPPRPLFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFSRPAFSLKKPYKHCNWKCAALSAILISVTLVFLLAYFIAMHLFGLNWHLQPVQRQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YQLTEDNTSGLHLPTDLGLPPLGNTGLBFPDRGSRDDGKLDGFFPEDSFIDMGEIDVG
RKVAQLIPPGIFWRSQVFIDHPMYLKFNVSLSKDALVGIYGRRGLPPSHTQFDFVELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGRRILLSQGLPGLDGPPFPAQQRSLVPITSHDTGCIQYMDSGIWHLAVYNDGKETEQV
SFLTTAIDSIDDCPSNCFGNGDCVSGNCHCFPGFRGPDCSRASCPVLCSGNGQYLKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMCHSGWKGSECDVPTNQCIDITCSGHGTCIVGTCICNPSYKGENCEEVDCLDPTCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MEVKERRPYRSLTSRRDTERRYTSSSADSEDGKINPKSYSSSET"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKAFDQDSRLAYGSRVKDLVHHEADBFSRQGPDFSLRDMAFGDPVPPHMGAYRTEMGL
PHRDYSVSVASDADTETDGIMSPEHAVRLWGRSNTKSGRSSCLFSRANSNLTLTDTEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-MAY-1999) Michihiro Mieda, Brain Science Institute, RIERD, Lab. for Developmental Gene Regulation; 2-1 Hirosawa, Wako-shi, Saitama 35-0198, Japan (E-mail:mieda@brain.riken.go.jp, rel:81-48-467-9713, Fax:81-48-467-9714)
Sequence updated (29-Unn-1999).

Logation/Qualifiers
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mieda,M., Kikuchi,Y., Hirate,Y., Aoki,M. and Okamoto,H. Compartmentalized expression of zebrafish ten-m3 and ten-m4, homologues of the Drosophila ten(m)/odd Oz gene, in the central
                    21 LeuGlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThr
                                                                                                               CTGGGGAAAGCAGCTCTGGTCGCCATTTATGGCAGAAAAGGCCTTCCTCCTTCCCATACT
                                                                                                                                                                      GlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSer
ThrPheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSer
                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                     Danio rerio mRNA for ten-m4, complete cds. AB026980
                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                        2326 CTGGAGGGTCCTCAGCGCCAATCACGGGGC 2355
                                                                                                                                                                                                                                                             70
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99425191
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/db_xref="G1:5307785"
                                                                                                                                                                                                                                                             LeuGluGlyThrProArgGlnSerArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
/mol type="mRNA"
/db xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                               9264 bp
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1. .9264
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323. .8797
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Danio rerio
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TGDQCLPYDETRCGDGGKAVEATLTNPRGITVDKYGVIFFVDGTMIRRIDQNGIISTL
LGFNDLTSARPLSCDSVMDISQVRLEWPTDLAVSPMDNSLYVLDNNVVLQISENHQVR
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GRSRRITDIQMQYGTLSLNVRYGSSVDEEKVRVLELARQRAVATAWAHERHRLRQGEE
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LCAADCGGHGICVAGSCRCDEGRMGTGCEQRACHPRCSEHGTCKDGKCECSPGWNGEH
CTIEGCPGLCNGNGRCTLGNNGWYCVCQLGWRGAGCDTSMETACSDGKDNDGDGLTDC
                                                                                                                                                                                                                                                                                                                                                            ESCPDLILWEKRTAVLQGYETTASNLGGWSVDKHHALNIQSGILHKGNGENIFISQQP
PVIGSIMGNGRRRSISCPSCNGLADGNKLLAPVALACGSDGSLYVGDFNYVRRIFTTG
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IYSASDSGCPPTPLHTLFATGTSLFGKGVKVAIREGRVEADI I SLANEDGRRI AAVLD
                                                                                                                                                                                                         AIGLRFERAPFITQEHTLWLPWGRFFVMDTIVMRHEVNDIPSCDLSSFTRPMPIVLPA
                                                                                                                                                                                                                                                    PLTAFAGTCPERGIVVPEIQTLQEEVRIPGTDMRLGYLSSRTSGYKSLLRITLTHSTT
PFSLMKVHLMVAVEGRLFRKWFSAAPNLSYDFVWDKTDVYSQKVYGLSEAFVSVGFEX
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LQFFYADLSSPTRVTHMYNHSSSETTSLYYDLQGHLFAMELSSGDEFYVACDNIGTPL
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GRWTTPDHDIRKRLNSDNIVPFNLYMFKNNNPLSNSQETKCYWTDVNSWLVTFGFQLY
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PAT 22-MAR-2003

linear

DNA

Sequence 39 from Patent WO02062999. AX662357

GI:29163218

AX662357.1

Homo sapiens (human)

Homo sapiens

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Best Local Similarity:
Query Match:
DB:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                             Spytek, K.A., Li, L., Wolenc, A.R., Vernet, C.A., Eisen, A., Liu, X., Malyankar, U., Shimkets, R.A., Tchernev, V.T., Spaderna, S.K., Gorman, L., Kekuda, R., Patturajan, M., Gusev, V., Gangolli, E.A., Guo, X., Shenoy, S., Rastelli, L., Casman, S.J., Boldog, F., Burgess, C.E., Edinger, S., Ellerman, K., Gunther, B., Smithson, G., Miller, I. and Macdougall, J.R.

Miller, I. and Macdougall, J.R.

Proteins and nucleic acids encoding same

Patent: WO 02062299A 39 15-AUG-2002;

Curagen Corporation (US)
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Mismatches:
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Patent: WO 02062999-A 41 15-AUG-2002;
Curagen Corporation (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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Sequence 41 from Patent WO02062999.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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1226 TTCTGGAGATCACAGCTCTTCATTGATCAGCCACAGTTTCTTAAATTCAATATCTCTCTT 1285
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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Proteins and nucleic acids encoding same Proteins and nucleic acids encoding same Corporation (US)
Curagen Corporation (US)
                                                                                                                                                                                                                                                                     22 GlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThrGln
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Matches:
Conservative:
Mismatches:
Indels:
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Indels:
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  Length:
Matches:
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                  Percent Similarity:
Best Local Similarity:
Query Match:
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1477 TATGACTTCGTGGAGCTCCTGGATGGCAGCTGATTGCCAGAGAGCAGCAGAGCTG 1536
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Search completed: August 14, 2004, 11:51:25 Job time: 1270.76 secs

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Sequence 967, App Sequence 1256, Ap Sequence 3735, Ap Sequence 3636, Ap

Seguence Sequence Sequence

Sequence Sequence Sequence

Appli Appli Appli Appli Appli Appli

Sequence 1, Appl Sequence 1, Appl Sequence 66, Appl Sequence 3824, A

Sequence:

Run on:

Searched:

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US-09-252-991A-14186
US-09-566-921-120
US-09-584-568C-3
US-09-584-568C-3
US-09-584-568C-1
US-09-252-991A-31356
US-09-252-991A-31356
US-09-252-991A-31356
US-09-325-991A-31356
US-09-325-991A-31356
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US-09-252-991A-5103
US-09-252-991A-16149
US-08-852-117E-164
US-08-852-117E-164
US-08-852-117E-164
US-09-252-991A-16149
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-13668
US-09-252-991A-7909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08891845; Patent No. 6096873; GENERAL INFORMATION: APPLICANT: Schaefer, Gabriele M. APPLICANT: Sliwkowski, Mark; TITLE OF INVENTION: Gamma-Heregulin NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P1043
TELECOMMUNICATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                              11601
4403765
4411529
309
1284
1293
   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
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TELEX: 910/371-7168
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                              FILING DATE:
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US-08-891-845-3
                                           60.5
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-MODEL=frame+ p2n.model -DEV=xlh
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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11841, A Sequence 11843, A Sequence 11691, A Sequence 11691, A Sequence 14082, A Sequence 14036, A
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Sequence 11, Appl
Sequence 1, Appli
Sequence 1, Appli
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Sequence 3, Appli
                                                                                                                  (without alignments)
1875.793 Million cell updates/sec
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                                                                                                                                                        US-10-029-020-14_COPY_450_520
372
1 TEWRSQVFIDHPVHLKENVS.....RLLTQEARSLEGTPRQSRGT 71
                                                                                                   August 14, 2004, 01:16:21 ; Search time 21.0053 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                     nucleic search, using frame_plus_p2n model
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US-08-891-845-11
US-09-514-573-11
US-08-891-845-11
US-09-514-573-1
US-09-252-991A-11841
US-09-252-991A-11843
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US-09-252-991A-14082
US-09-252-991A-14036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-891-845-3
                                                                                                                                                                                                                                                                                                       682709 segs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                               Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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2304
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118.5
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Perfect score:
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372
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66.5
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Result No.

Sequence 164, App Sequence 15937, A Sequence 16144, A Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli

Sequence 1165, Ap Sequence 13863, A Sequence 13668, A

Sequence 7909, Ap

Sequence 3824, Ap Sequence 4061, Ap Sequence 5103, Ap Sequence 5129, Ap Sequence 5090, Ap Sequence 1, Applii Sequence 5, Applii

Appli

Sequence 3

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1348 ACTITICIGGAGAICICAAGIGITICATAGACCAICCIGIGCAICTGAAAITICAAIGIGICI 1407
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Mismatches:
Indels:
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Matches:
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APPLICANT: Schaefer, Mark
APPLICANT: Sliwkowski, Mark
TITLE OF INVENTION: Gamma Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetiech, Inc.
STRES: South San Francisco
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-891-845-11
; Sequence 11, Application US/08891845
; Patent No. 6096873
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
    ; SEQUENCE CHARACTERISTICS:
; LENGTH: 1680 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLLOGY: Linear
US-09-514-573-3
                                                                                                                                                                                                                                                                                                                                                       1.3e-43
372.00
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2387 base pairs TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1348 ACTITICIGGAGAICICAAGIGITICATAGACCAICCIGIGCAICIGAAATICAAIGIGICI 1407
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Mismatches:
Indels:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LeuGluGlyThrProArgGlnSerArgGlyThr 71
                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/514,573
FILING DATE: 28 FEB 2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/891845
FILING DATE: 10 UULY 1997
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb flop
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APPLICANT: Schaefer, Gabriele M.
APPLICANT: Sliwkowski, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-514-573-3
; Sequence 3, Application US/09514573
; Patent No. 6500941...
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REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P10
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TELEPHONE: 415/255-1994
TELEPA: 415/952-9881
TELERX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1680 base pairs TYPE: Nucleic Acid STRANDEDNESS: Single TOPOLOGY: Linear
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100.00%
100.00%
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Best Local Similarity:
Query Match:
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TOPOLOGY: Linear
TOPOLOGY: Linear
                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                             Alignment Scores:
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US-09-514-573-11
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US-08-891-845-1
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                                                                                                                                                                                                                                                                                                                       853 ACTITCIGGAGAICTCAAGIGITCAIAGACCAICCIGIGCAICTGAAAITCAAIGIGICI
                                                                                                                                                                                                                                                                                               1 ThrPheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSer
                                                                                                                                                                                                                                                                                                                                                                                                             41 GlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSer
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                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LeuGluGlyThrProArgGlnSerArgGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OSCTWARE: Winpatin (Genentech) CURRENT APPLICATION DATA: 08/09/514,573 FILING DATE: 28 FEB 2000 CLASSIFICATION NUMBER: 08/09/514,573 FILING DATE: 10 JULY 1997 APPLICATION NUMBER: 08/891845 FILING DATE: 10 JULY 1997 APPLICATION NUMBER: 60/021640 FILING DATE: 07/12/96 ATTORNEY/AGENT INFORMATION: NAME: Lee, WendY M. REGISTRATION NUMBER: 40,378 REPERENCE/POCKET NUMBER: P1043 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Schaefer, Gabriele M.
APPLICANT: Sliwkowski, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADURESSEE: Genericech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Californi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09514573
Patent No. 6500941
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2387 base pairs
                                                                                                     2.1e-43
372.00
100.00%
100.00%
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COMPUTER READABLE FORM:
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                        Linear
                                                                                                                                            Percent Similarity:
Best Local Similarity:
STRANDEDNESS:
TOPOLOGY: Line
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                                                                                   Alignment Scores:
                                   US-08-891-845-11
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                                                                                                                                                                                          Query Match:
                                                                                                         Pred. No.:
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853 ACTITCIGGAGAICICAAGIGIICATAGACCAICCIGIGCAICCIGAAAIICAAIGIGICI 912
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                                                                                                                                                                                                                                                                                                                                                                                                      41 GlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSer
                                                                                                                                                               US-10-029-020-14_COPY_450_520 (1-71) x US-09-514-573-11 (1-2387)
Length:
Matches:
Conservative:
Mismatches:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                          Indels:
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APPLICANT: Schaefer, Gabriele M.
APPLICANT: Schaefer, Gabriele M.
APPLICANT: Sliwkowski, Mark
: TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET 466 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,845
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTAATION NUMBER: 40,378
REGISTAATION NUMBER: 91043
TELECHONE: 415/952-1994
TELECHONE: 415/952-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08891845
Patent No. 6096873
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
2.1e-43
372.00
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                                                                                                                                                        US-10-029-020-14_COPY_450_520 (1-71) x US-08-891-845-1 (1-3111)
                                                         Conservative:
Mismatches:
Indels:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LeuGluGlyThrProArgGlnSerArgGlyThr 71
                  Length:
Matches:
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SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/514,573
FILING DATE: 28 FEB 2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/891845
FILING DATE: 10 JULY 1997
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: 10437
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INCORMATION:
APPLICANT: Schaefer, Gabriele M.
APPLICANT: Sliwkowski, Mark
TITLE SIIWKOWSKI, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genettech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
CITY: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09514573
Patent No. 6500941
                  3.01e-43
                                   372.00
100.00%
100.00%
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STRANDEDNESS: Single
                                                     Percent Similarity:
Best Local Similarity:
Alignment Scores:
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 107196.136
CURRENT PILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11841
                                                                                                                                                                                                                                                                                                                                                                                                                1801 CAGTITGACTITGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGGAGGCGCGCGGAGC 1860
                                                                                                                                                                                                                                              1681 ACTITCIGGAGAICTCAAGIGITCATAGACCATCCIGGCATCTGAAATTCAATGIGICT 1740
                                                                                                                                                                                                                                                                                                                      961 GCCGACTGTCGGTGTCGTATTTCTGCTCGTAGGTGCTTTCCGAAGCCGAAGTGCTCTT 902
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                                                                                                                                                                                                 1 ThrPheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSer
                                                                                                                                                                                                                                                                                           21 LeuGlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThr
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                                                                                                                                                      US-10-029-020-14_COPY_450_520 (1-71) x US-09-514-573-1 (1-3111)
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28
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30
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Matches:
Conservative:
Mismatches:
                                          Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 GlylleTyrGlyArgLysGlyLeuProPro-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LeuGluGlyThrProArgGlnSerArgGlyThr 71
Length:
Matches:
                                                                                        Indels:
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US-09-252-991A-11841/c
; Sequence 11841, Application US/09252991A
; Patent No. 6551795
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                372.00
100.00%
100.00%
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Percent Similarity:
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Best Local Similarity:
Query Match:
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Sequence 81, Application US/09669751
Sequence 81, Application US/09669751
Sequence 81, Application US/09669751
Setent No. 6551575
GENERAL INFORMATION:
GREENAL INFORMATION:
APPLICANT: Greenspan, Ralph J.
TITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to TITLE OF INVENTION: Balance and the Perception of Gravity
FILE REFERENCE: P. 13864
CURRENT APPLICATION NUMBER: US/09/669,751
CURRENT FILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 261
SOFTWARE: FASTSEQ for Windows Version 4.0
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Mismatches:
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Matches:
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ORGANISM: Drosophila
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Best Local Similarity:
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Query Match:
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Patent No. 6551795
GENERAL INFORMATION:
CESSITORAL INCOMPATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERCGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11691
LENGTH: 2304
                                                                                                                         GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
NUCLEIC AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                       Sequence 11543, Application US/09252991A Patent No. 6551795
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ORGANISM: Pseudomonas aeruginosa
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Query Match:
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Pred. No.:
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Sequence 14186, Application US/09252991A

Sequence 14186, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 1999-02-18

FRIOR APPLICATION NUMBER: US 60/074,788

FRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1243 CAGCGGCGCCAGGGTCACCCGCCGGAT---ACCGCGGCGCCCCAGGTCGAGCAGGACCTT 1299
                                                                    664 CAGCGGCCAGGTCACCCGCCGGTT---ACCGCGCGCCCAGGTCGAGCAGGACCTT 608
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                                     30 TyrGlyArgLysGlyLeuProProSerHisThrGlnPheAspPheValGlu-
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APPLICANT: Tingley, Debora W.
APPLICANT: Tingley, Debora W.
APPLICANT: Tingley, Debora W.
TITLE OF INVENTOR: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFREENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL PROGRAM
SOFTWARE: 13815
LENGTH: 3835
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Mismatches:
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Matches:
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Best Local Similarity:
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US-09-252-991A-14186
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US-09-252-91A-14036/C
; Sequence 14036, Application US/09252991A
; Patent No. 6551795
; Gardence 14036, Application US/09252991A
; Patent No. 6551795
; GARDEAL INFORMATION:
; APPLICANT MARCI J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14036
; LENGTH: 1329
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 14082

LENGTH: 1272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         621 CAGCGGCGCAGGCTCACCCGCCGGAT---ACCGCGGCGCCCAGGTCGAGCAGGACCTT 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 TyrGlyArgLysGlyLeuProProSerHisThrGlnPheAspPheValGlu----Leu 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AspHisProValHisLeuLysPheAsnValSerLeuGlyLysAlaAlaLeuValGlyIle 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-029-020-14_COPY_450_520 (1-71) x US-09-252-991A-14082 (1-1272)
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Matches:
Conservative:
Mismatches:
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ORGANISM: Pseudomonas aeruginosa
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14036
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                           2829 ---CCTACGATTTCCTTCCACATGCCCTTTATTGATCTGGGGTCTGGTAAGTTGATGCTA 2773
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                                                                                                                                                                                                                                                                                                                                                                                                      35 LeuProProSerHisThrGlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeu 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 ProValHisLeuLysPheAsnValSerLeuGlyLysAlaAlaLeuValGlyIleTyrGly 31
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TITLE OF INVENTION: 33167, A NOVEL HUMAN HYDROLASE AND USES THEREFOR FILE REFERENCE: MNI-140

CURRENT APPLICATION NUMBER: US/09/584,568C

CURRENT FILING DATE: 2000-05-31

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

LENGTH: 945
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Matches:
Conservative:
Mismatches:
Indels:
) OTHER INFORMATION: Incyte ID No. 6682888 196545.7;
NAME/KEY: unsure
) LOCATION: 3743-3768

US-09-566-921-120
                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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65.00
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17.47%
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25.33$
17.74$
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; LOCATION: (1)..(945)
US-09-584-568C-3
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US-09-584-568C-3
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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-MODEL=frame+ p2n.model -DEV=xlh
-Og-(cgn2_1/USPTO_spool/MITRA020/runat_06082004_114100_196/app_query.fasta_1.583
-DB=N_Geneseq_29Jan04 - OgMT=fastap_SUPFTX=p2n.rng -MINMATCH=0.1_CODPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-MODE=LOCAL_OTHENT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NORM=MITRA020_@CGN_1_1_40_@runat_06082004_114100_196 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THEAPSIZE=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Aas18526 DNA encod
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Gamma-her
                                                                    August 14, 2004, 02:35:12; Search time 534 Seconds (without alignments) 3182.171 Million cell updates/sec
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OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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ABN85378
ABS78652
AAV19252
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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## ALIGNMENTS

Human, NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; KW cell signal processing; metabolic pathway modulation; metabolic disorder; My cell signal processing; metabolic pathway modulation; metabolic disorder; acne; My Alzheimer's disease; parkinson's disease; neurodegenerative disorder; acne; KW Alzheimer's defect; infertious congenital heart defect; hair growth; KW memory defect; infertility; congenital heart defect; hair growth; KW pigmentation disorder; endocrine disorder; respiratory disease; health; My pigmentation disorder; endocrine disease; allergy; inflammation; My mephrological disorder; urinary system disorder; age-related disorder; My neuropsychiatric disorder; age-related protein; SCUBBI; FRN-M4; KW heta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; KW beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; KW type la membrane sushi-containing domain, butyrophilin; KW ring and adreneration domain containing; SNP; gene; ds; single nucleotide polymorphism. ABS52100 standard; DNA; 8354 (first entry) Human TEN-M4-like gene. 05-NOV-2002 ABS52100; KESULT 1 ABS52100 

Location/Qualifiers replace(117,G) /\*tag= a

variation

Homo sapiens

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The present invention relates to new NOVX polypeptides. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, preferably human. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, the invention are also useful for treating or preventing cirrhosis, capacreatitis, learning and memory defects, infertility, congenital heart defects, acne, hair growth, pigmentation disorders, endocrine diseases, capturedistical diseases, bone marrow transplantation, andocrine diseases, allergy and inflammation, nephrological disorders, urinary system disorders, neuropsychiatric disorders and age-related disorders. The present nucleic acid sequence represents a NOVX gene. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;
Liu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease or
                                                                                                          "Single nucleotide polymorphism (SNP)"
standard_name= "Single nucleotide polymorphism (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BD,
                                                     nucleotide polymorphism
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Shimkets RA, Burgess CE, Zerhusen BI
Boldog FL, Smithson G, Li L, Ji W;
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                                                         "Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 50-52; 318pp; English.
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                  replace(225,C)
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/standard_name=
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20-MAY-2001; 2001US-0288153P.
29-MAY-2001; 2001US-0294075P.
24-JUL-2001; 2001US-0307506P.
10-AUG-2001; 2001US-0311590P.
29-AUG-2001; 2001US-03115617P.
                                                                          replace (260, A)
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2000US-0257314P.
2001US-0288153P.
2001US-0294075P.
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2001US-0322358P.
                                                                                                                                                                                                                       2001WO-US050331
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Stone DJ, Anderson D, S
Spytek KA, Casman SJ, B
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P-PSDB; ABG70388.
                                                                                                                                                  WO200257453-A2
                                                                                                                                                                                                                                                                                                                                                                                                    14-SEP-2001;
                                                                                                                                                                                                                       19-DEC-2001;
                                                                                                                                                                                                                                                           19-DEC-2000;
                                                                                                                                                                                      25-JUL-2002
                          variation
                                                                              variation
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BP; 1968 A; 2437 C; 2271 G; 1678 T; 0 U; 0 Other;
                             8354
397
                                                 0000
                             Length:
Matches:
Conservative:
Mismatches:
                                                                     Indels:
                              6.54e-127
2127.00
99.25%
99.25%
                                                   Percent Similarity:
Best Local Similarity:
   8354
                       Alignment Scores:
    Sequence
                                           Score:
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MetAspVallysGluArgLysProTyrArgSerLeuThrArgArgArgAspAlaGluArg 20 SEQ14-X-AT-28-64-76 (1-400) x ABS52100 (1-8354)

Query Match

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94

1174 1054 360 1114 SerThrPheAlaArgProAlaPheAsnLeuLysLySProSerLysTyrCysAsnTrpLys 340 240 260 300 934 200 754 874 GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp 120 ThrValleuSerProGluHisProValArgLeuTrpGlyArgSerThrArgSerGlyArg 140 160 180 634 694 214 274 100 334 394 454 514 80 9 AGCACCTTCGCCCGGCCGTTTAACCTCAAGAGCCCTCCAAGTACTGTAACTGGAAG GIGGCCAIGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGCAGATGTAT CysAlaAlaLeuSerAlaIleValIleSerAlaThrLeuValIleLeuLeuAlaTyrPhe ValAlaMetHisLeuPheGlyLeuAsnTrPHisLeuGlnProMetGluGlyGlnMetTyr CGCCGCTCTCGCACGCCCAACCCCCAACCACGCGCCTCCATTAACTCCTG AsnArgGlyAsnPheThrProArgSerAsnProSerProAlaProThrAspHisSerLeu SerGlyGluProProAlaGlyGlyAlaGluGluProAlaHisAlaGlnGluAsnTrpLeu LeuGlnAspAsnLeulleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyr SerAspGlyHisPheLeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSer Agricacedecactricerenteaacerecaaceaecerecececerenterecaeaecaeaea ProGlyTyrProLeuThrSerSerThrValTyrSerProProProArgProLeuProArg SerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGlu AsnThrGluThrAspHisProGlyGlyLeuGlnAsnHisAlaArgLeuArgThrProPro LeuAsnSerAsnIleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThr ProProLeuSerHisAlaHisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeu LysAspile\*\*\*ProGlnGluAlaGluGluPheCysArgThrGly\*\*\*AsnPheThrLeu ArgGluLeuGlyLeuGluGluValThrProProHisGlyThrLeuTyrArgThrAspIle cessascressecresaasaastaaceccccrcacesacccresaccacacarr ArgTyrThrSerSerSerAla\*\*\*SerGluGluGluGlybysAlaProGlnLysSerTyrSer SerSerGluThrLeuLysAlaTyrAspGlnAspAlaArgLeuAlaTyrGlySerArgVal 361 695 1055 1115 201 935 995 341 161 515 181 575 635 221 241 755 261 815 281 875 301 321 61 275 335 395 141 455 155 215 81 101 121 95 21 41 g d 임 à g g g à 8 ò à g ð à g ò à a 유 g ð 셤 à g ò d ð 셤 à d  $\delta$ ò ð

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This nucleic acid molecule codes for human gamma-heregulin (gamma-HRG) (see AAW44817), a novel member of the heregulin superfamily, that has a unique N-rerminal domain not present in previously identified heregulins. Gamma-HRG is secreted by human breast cancer MDA-MB-175 calls. It leads to the formation of a constitutive active receptor complex and stimulates to the growth of these cells in an autocrine manner. The nucleic acid was isolated by screening a MDA-MB-175 with a probe corresponding to the EGF-like domain and part of the N-terminal sequences of HRG-beta-3. It can be used for the recombinant production of gamma-HRG, or for in vivo or exvivo gene therapy. A claimed nucleic acid, which is complementary to the nucleic acid sequence encoding the N-terminal domain of gamma-HRG, is blue to reduce production of gamma-HRG by MDA-MB-175 cells. The invention provides claimed methods for activating an ErbB receptor and for enhancing proliferation, differentiation or survival of a cell by contacting the cell (preferably a glial or muscle cell) with gamma-HRG
Gamma-heregulin; gamma-HRG; human; autocrine growth factor;
breast cancer; MDA-MB-175 cell; diagnosis; gene therapy; BrbB receptor;
cell proliferation; cell differentiation; cell survival;
neurological disorder; muscular disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activate ErbB receptor and or survival of a cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding gamma-heregulin - used to enhance proliferation, differentiation
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534. .2645
/*tag= a
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                                                                                                     CDNA; 3111
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                                                                                                                                                                                                       Human gamma-heregulin cDNA
                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
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                                                                                                     AAV19251 standard;
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                                                                                                                                     AAV19251;
                                                                   RESULT 2
AAV19251
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3111 396 0 4

> Mismatches: Indels: Gaps:

SEQ14-X-AT-28-64-76 (1-400) x AAV19251 (1-3111)

Length: Matches: Conservative:

4.42e-127 2122.00 99.00% 99.53%

Best Local Similarity:

Query Match: DB:

Percent Similarity:

Pred. No.:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the nucleotide sequence of cDNA coding for gamma-heregulin (gamma-HRG, see AAY06639). The invention provides HRG ligands, including gamma-HRG, that have affinity for and stimulate HERZ, HER3 and/or HERR4 receptors in autophosphorylation. A new method of treating respiratory distress syndrome in humans uses HERZ, HER3 and/or HER4 receptor ligands as epithelial growth factors. A novel method of inducing epithelial cell growth and/or proliferation comprises contacting a normal epithelial cell which expresses HERZ, HER3 and/or HER4 receptors with an isolated ligand which activates HERZ, HER3 and/or HER4 receptors or their combination. Also claimed are methods of increasing lung surfactant protein A, or of treating chronic obstructive pulmonary disease, respiratory distress or emphysema, by administering an effective amount of an isolated HER ligand to a patient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heregulin ligands can be used to induce epithelial cell growth, and promote repair and healing of tissue damage or injury.
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The patent discloses a method for inducing hair cell generation, or inner ear-supporting cell growth, regeneration, and/or proliferation, by heregulins (HRG), the ligand for HRR2/HER3 dimeric receptors. Heregulin proteins function as activators of HRR-2 oncogene and result from alternate splicing of a single gene mapped to chromosome Bp. The two major types, alpha and beta HRG's are based on two variant BGF-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting calsease states associated with tissue damage, e.g. ofcotoxic injury, acoustic assault, degenerative hearing loss, balance impairments, damage associated with surgery or physical injury and inner ear disorders related to hair cell dysfunction. The present sequence is the human heregulin variant, gamma-HRG protein encoding cDNA, isolated from a native HRG source, such as human MDA-MB-175 cells. It has atleast one biological property as the native sequence
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                                                                                                                                                                                                                                                                                                                                      activator; HER2 receptor; HER3 receptor; HER-2 oncogene; chromosome 8p; hair cell related hearing disorder; octoxic injury; tissue damage; acoustic assault; degenerative hearing loss; balance impairment; treatment; hair cell; surgical injury; physical injury; inner ear disorder; ss.
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                                                                   GlulleThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Method for inducing hair cell generation and inner-ear-supporting ogrowth regeneration and proliferation, useful for treating hearing disorders.
                                                                                                                                                                                                                                                                                                                     Heregulin; variant; gamma-HRG; human; inner-ear-supporting cell;
                                                                                                                                                                                                                                                                                    Human Heregulin variant, gamma-HRG encoding cDNA
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                                                                                                                                                                                 400
                                                                                                                                                                                                                                                                                                                                                                                                Human; heregulin; antiasthmatic; antiinflammatory; vulnerary; antiulcer; epithelial cell growth; HBR2; HBR4; HR6; HBR4; HR0; lung cell; asthma; lung surfactant protein A; respiratory distress; emphysema; pneumonitis; chronic obstructive pulmonary disease; COPD; chronic bronchtis; ulcer; neonatal pulmonary disease; neonatal respiratory distress syndrome; empenital diaphragmatic hernia; lesion; acute lung injury; cystic fibrosis; surgical wound; resection; growth factor; smoke inhalation; gamma-HRG; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Human heregulin, gamma-HRG"
                                                                                                                                                                                                                                                                                                                                                                      gamma-HRG.
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treatment of respiratory
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constant pulmonary diseases including neonatal respiratory diseases including neonatal respiratory diseases including neonatal respiratory diseases syndrome, meconium aspiration syndrome, chronic lung disease of the neonate, congenital diaphragmatic hernia and acute lung injuries including smoke or chemical inhalactor, penemonitis due to aspiration, rediation, near drowning, cystic fibrosis and other epithelial cell crauma diseases including injuries associated with surgical wounds and resections, ulcers, leaions and tissue tears as normal epithelial cell growth factors. For treating infants/neonates with respiratory distress cas well as youth and adult with poor lung function due to lung injury or damage. The HRG binds with varying and very high affinity to the HER2, HER3 and/or HER4 receptors. The method stimulates growth and cells and/or HER4 receptors. The method stimulates growth and cells and allowing the affected tissue to develop comman physiological functions more quickly. Hence the method improves organs and allowing the affected tissue to develop cormal physiological functions more quickly. Hence the method improves organization and speeds of the development of a barrier to infection while treating lung cells that are damaged by inhalation of smoke resulting in cemphysema. It also facilitates regeneration of epithelial cells. The emphysema. It also facilitates regeneration of epithelial cells. The emphysemal procession and procession and procession and procession and procession and procession of epithelial cells. The
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                                                                                 LeuAsnSerAsnIleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThr
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The present sequence is a coding sequence for a NOV protein. The NOV proteins and coding sequences are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma, AIDA mephropathy, cirthosis, arthritis, Alzheimer's disease, infections [e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. Novi is a TEN-M4 like protein and the NoVI gene is localised to chromosome 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
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                                                                                                                                                Padigaru M, Li L, Zerhusen BD, Casman SJ, Shenoy S, Spytek Zhong M, Gangolli EA, Burgess CB, Patturajan M, Vernet CAM, Taylor S, Tchernev VT, Miller CB, Guo X, Boldog FL, Grosse Alsobrook JP, Gerlach V, Galinger S, Rothenberg ME, Ellerman Macdougall J, Malyankar U, Millet I, Peyman J, Smithson G;
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            09-JAN-2001; 2001US-0260417P.
10-JAN-2001; 2001US-0260831P.
28-FEB-2001; 2001US-0272338P.
09-MAR-2001; 2001US-024476P.
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                                    SerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGlu
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                                                                                                        AACACTGAGACTGATCATCCGGGCGGCCTGCAGAACCACGCGCGGCGGCTCCGGACGCCGCCG
                                                                                                                               ProproLeuSerHisAlaHisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeu
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The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to CGDD, a biologically active cord sequence at least 90% identical to CGDD, a biologically active crispens or an immunogenic fragment. Also included are the polymucleotides encoding CGDD-12, a recombinant polymucleotide comprising a promoter sequence operably linked to the CGDD comprising a promoter sequence operably linked to the CGDD polymucleotides, a cell transformed with the recombinant polymucleotide, an anticartive cordination of CGDD polymucleotide microarray. The polypeptides, polymucleotide and a cGDD polymucleotide microarray. The polypeptides, polymucleotide and a gonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of CGDD, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, cirnosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia cycla, polycitaemia, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, cirnosis, primary thromobocytopaenia or cancer), developmental disorders (e.g. Alzheimer disease, Parkinson's disease or enurological disorders (e.g. Alzheimer disease, Parkinson's disease or collection and products, contact dermatitis, crohn's disorders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. Alzheimer disease, alabetes mellitus, crohrat dermatitis, crohn's disease, matemia or mental retardation, osteoporosis, pancreatitis, rheumatoid arthritis, contact dermatitis, crohn's disease, matemia or mental retardation, osteoporosis, pancreatitis, rheumatoid arthritis, crohrat dermatitis, trohn's disease, matemia or mental retardation of concert dermatitis, trohn's disease, matemia or mental retardation, osteoporosis, pancreatitis, prover with a sessessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid a compa
            neurological disorder; Alzheimer disease; Parkinson's disease; asthma, reproductive disorder; infertility; autoimmune disorder; gout; allergy; inflammatory disorder; acquired immunodeficiency syndrome; uveitis; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; diabetes mallitus; glomerulonephritis; irritable bowel syndrome; multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baughn MR;
Burford N;
acidosis; anaemia; mental retardation; epilepsy; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human proteins associated with cell growth, differentiation death, useful for diagnosing, treating or preventing autoimmune inflammatory disorders (e.g. AIDS, allergy or anemia), cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8645 BP; 2060 A; 2494 C; 2319 G; 1771 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ao MG, Ison CH, Lu Y, Warren BA, Elliott VS,
Xu Y, Gietzen KJ, Tang TY, Lal PG, Duggan BM,
Richardson TW, Tran UK, Khare R, Walia NK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 175-178; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-2001; 2001US-0268111B.
23-FEB-2001; 2001US-0271175P.
08-MAR-2001; 2001US-0274503P.
09-MAR-2001; 2001US-0274552P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                     rheumatoid arthritis.
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Lu DAM,
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Length: Matches:

5.67e-123 2066.00

Alignment Scores: Pred. No.: Score:

Human; ss; gene; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thromobocytopaenia; developmental disorder;

Human cDNA encoding CGDD10, INCYTE 7488573CB1.

(first entry)

16-DEC-2002

1244

380

1304

400

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AGCACCTTCGCCCGGCCGGTTTAACCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAG 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone 20 encodes an N-terminally truncated isoform (see AAW44818) of human gamma-heregulin (gamma-HRG) (see also AAW44817), a novel member of the heregulin superfamily. It was isolated from a MDA-MB-175 human breast cancer cell library after screening with an EGF-like domain. Compared to gamma-HRG cDNA (see AAV19251), clone 20 contains a 78 base insert between codons 560 and 561, and lacks the 5' end. The truncated gamma-HRG was insoluble when expressed as a thioredoxin fusion protein in Escherichia coli cells. Gamma-HRG nucleic acid and polypeptide are claimed, together with their uses e.g. for enhancing the proliferation, differentiation or survival of glial or muscle cells
                                                                                                                                                                                                                                                                                                 Gamma-heregulin; gamma-HRG; human; autocrine growth factor;
breast cancer; MDA-MB-175 cell; diagnosis; gene therapy; BrbB receptor;
cell proliferation; cell differentiation; cell survival;
neurological disorder; muscular disorder; ss.
                                              1245 GAGATCACGGAGGACACCAGCAGTGGCCTGTGCCAACCGACGTCTCCCTATACCCC
                                CysAlaAlaLeuSerAlaIleValIleSerAlaThrLeuValIleLeuLeuAlaTyrPhe
                                                                               ValAlaMetHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyr
                                                                                                                              GlulleThrGluAspThrAlaSerSerTrpProValProThrAspValSerLeuTyrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activate ErbB receptor or survival of a cell.
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enhance proliferation, differentiation
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                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                           Human gamma-heregulin cDNA clone
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Pred. No.:
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     0 4 4 4
     Conservative:
Mismatches:
                                                               (1-8645)
                          Indels:
                                                        SEQ14-X-AT-28-64-76 (1-400) x ABS78652
  97.50%
97.50%
96.90%
Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                   The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions, and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present DNA sequence represents a gene of the
                                                                                                                                                                                                                                                              New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
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Drmanac RT,
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Weng G, Zhou P,
Boyle BJ;
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Ghosh M, Xue AJ, Wehrman T, 1
Ma Y, Wang D, Chen R, Xu C,
                                                      2001US-0339453P
2002US-0365091P
2002US-0372384P
2002US-0372384P
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12-APR-2002; 2
22-APR-2002; 2
24-APR-2002;
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11-DEC-2001; 2
14-MAR-2002; 2
14-MAR-2002; 3
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Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide;

encoding cDNA SEQ ID NO:37.

17-DEC-2002 Human NOV15b

(first entry)

BP

ABQ82344 standard; cDNA; 8645

RESULT 10 ABQ82344 ABQ82344;

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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, notitopic, cardiovascular, antidiabetic, antidinflammatory, antithematic, antiabacterial, curucide, immunosuppressive, antidialergic, antidanaemic, antibacterial, fundicide, composition and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibadies can be used in the manufacture of a medicament for treating a syndrome associated with a composition of a medicament for treating a syndrome associated with a composition of a leasant of a medicament for treating a syndrome associated with a composition of a cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alisteimer's disease or pick's disease, disorders of vesicular transport (e.g. cystic fibrosis, diabetes mellitus, Grave's disease, or goitre, y gastriointestinal companies aucoimmune diseases (e.g. ulocrative colitis, or gastric and duodenal disorders), aucoimmune haemolytic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic
                cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy;
stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy;
                                                    Pick's disease, vesicular transport disease, cystic fibrosis, goitre, diabetes mellitus, Grave's disease, gastrointestinal disorder, vaccine, ulcerative colitis, gastric disorder, duodenal disorder, infection, autoimmune disease, allergic reaction, autoimmune haemolytic anaemia,
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usev V, Gangolli EA, Guo X, Shenoy S;
ldog F, Burgess CE, Edinger S, Ellerman K;
llet I, Macdougall JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
           gene therapy;
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   antibacterial; protozoacide; antihelminthic;
                                                                                                                              arthritis; gene; chromosome 4; ss.
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                                                                                                                                                                                                     Location/Qualifiers
151. .8316
                                                                                                                                                                                                                                                          /product= "NOV15b"
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2001US-0259785P.
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2001US-0279832P.
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2001US-0283889P.
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2001US-0286683P.
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18-APR-2001;
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29-MAY-2001;
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09-MAR-2001;
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04-JAN-2001;
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17-SEP-2001;
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                                                                                                                               rheumatoid
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385

---IleThrGluAsp

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AACTGGCAGCTACAGCAGACTGAAAATGACACATTTGAGAATGGAAAAGTGAATTCTGAT 1218
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                                                                                                                                                                                                           1039 AAATTCAAGAAGTCTTCAAAGTACTGTAGCTGGAAATGCACTGCACTGTGTGCGCTAGGG
                                                                                                                                                                                                                                                      Gly---GlyThrSerProLeuPheCysThrThrSerProGlyTyrProLeuThrSerSer
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                                                                                                                                             329 AsnLeulyslysProSerlysTyrCysAsnTrpLysCysAlaAlaAlaLeuSerAlaIleVal
                                                                                                                                                                                                                                     IleSeralaThrLeuValIleLeuLeuAlaTyrPheValAlaMetHisLeuPheGlyLeu
                   270 IleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAspGlyHisPheLeuPheLysPro
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02-JAN-2001; 2001US-0259415P.
04-JAN-2001; 2001US-0259785P.
20-FEB-2001; 2001US-0269814P.
09-MAR-2001; 2001US-0279863P.
29-MAR-2001; 2001US-0279832P.
29-MAR-2001; 2001US-0279833P.
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210
49
92
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Matches:
Conservative:
Mismatches:
Indels:
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975.00
62.41%
50.60%
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Best Local Similarity:
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                                                                                                                               Alignment Scores:
Pred. No.:
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kets RA, Tchernev VT, Spaderna SK, Gorman L;
jan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
no SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
on G, Millet I, Macdougall JR;
                                                                                        Spytek KA, Li L, Wolenc AR, Vern
Malyankar U, Shimkets RA, Tcherne
Kekuda R, Patturajan M, Gusev V,
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2001US-0313325P.
  2001US-0283889P.
                                               17-SEP-2001; 2001US-0322699P
26-NOV-2001; 2001US-0333350P
                                                                          (CURA-) CURAGEN CORP.
                                                                                                                                            WPI; 2002-732706/79.
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                       29-MAY-2001; 2
16-AUG-2001; 17-AUG-2001; 5
        18-APR-2001;
25-APR-2001;
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New NOVX polypeptides and polymucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune

Claim 8; Page 110-112; 444pp; English

manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers care, it is that and uterus), neurological disorders (e.g. epilepsy, stroke, ischamic cerebrovascular disease, Alzheimer's disease or picks disease, disorders of vesicular transport (e.g. cystic fibrosis, disease), disorders of vesicular transport (e.g. cystic fibrosis, disease), disorders of vesicular transport (e.g. cystic fibrosis, disorders of vesicular transport (e.g. cystic fibrosis, disorders (e.g. ulcrative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helmithic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helmithic conditions and as vaccines. The NoVX nucleotide sequences may be used in chromosome mapping, identifying individuals from minute biological samples (tissue typing), and in forensic identification of a biological sample. The present sequence encodes human NoVISa, which is The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, antidiabetic, antiinflammatory, antirhemmatic, antiarthritic, virucide, immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a

Sequence 8675 BP; 2362 A; 2067 C; 2201 G; 2041 T; 0 U; 4 Other;

1 MetAspVallysGluArgLysProTyrArgSerLeuThrArg---ArgArgAspAlaGlu 19 210 49 92 64 Length:
Matches:
Conservative:
Mismatches: SEQ14-X-AT-28-64-76 (1-400) x ABQ82343 (1-8675) Indels: 7.55e-53 975.00 62.41% 50.60% 45.73% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Score: ò g

20 ArgArgTyrThrSerSerBla\*\*\*SerGluGluGlyLysAlaPro---GlnLysSer 38

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> TyrSerSerSerGluThrLeuLysAlaTyrAspGlnAsp---AlaArgLeuAlaTyrGly 39

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271	TACAGTICCAGCGAGACATIGAAAGCTITIGAICAIGAITCCTCGCGGCTGCTTTACGGC 330
58 331	SerArgvallysAspIle***ProGlnGluAlaGluGluPheCysArgThrGly***Asn 77 :::
78	OHİSGİYTAKLEUTYKAKG 9'     AAGAGGACTGGCATTTTGT 4
98	ThraspileGlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMet 117
118	13
138	SerGlyArgSerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThr 157 
158	
175	ArgleuArgThrProProProDeuSerHisAlaHisThrProAsnGlnHisHisAla 194     :: 
195	AlaSerIleAsnSerLeuAsnArgGlyAsnPheThrProArgSerAsnProSerProAla 214
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231	GlubroAlaHisAlaGluGluAsnTrpLeuLeuAsnSerAsnIleProLeuGluThr 249 
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270 3	
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309 T :	ThrValTyrSerProProProArgProLeuProArgSerThrPheAlaArgProAlaPhe 328 :::
329 A	ysprosellystyrcysasntrplyscysalaala: 
349 I : 1099 G	eValAlaMetHisLeuP  :::           TATAGCAATGCATCTCT
369 A	9 ASTITPHISLEUGInProMetGluGlyGlnMetTyrGluIleThrGluAsp 385
386 T     1219 A	hrAlaSerSerTrpProValProThrAspValSerLeuTyrPro 400 

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AGGCCCCCGCCCCGCTGCTGCCAGGAATACTTTCTCCAGGAAGGCTTTCAAGCTGAAG 1319
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Human; FCTEX; myelogenous leukaemia; carcinoma; melanoma; glioma; ds; astrocytoma; congenital neonatal alloimmune thrombocytopaenia; infection; meurological disorder; neurodegenerative disorder; nerve trauma; wellodysplastic syndrome; Charcot-Marie-Tooth neuropathy; amilial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy; kw mental health condition; immunological disorder; allergy; infertility; worthial asthma; Avellino type eosinophila; lung disease; deafness; kw reproductive disorder; reproductive disorder; parceatic disorder; glycoprotein Ia deficiency; kw desmoid disease; turcot syndrome; liver cirrhosis; hepatitis C; virucide; kw gastric disorders; pancreatic disease; Schistosoma mansoni infection; kw gastric disorders; pancreatic disease; Schistosoma mansoni infection; kw gastric disorders; plasmodium falciparum parasitaemia; diabetes; kw keis-Bucklers corneal dystrophy; cytostatic; immunosuppressive; antialergic; antiasthmatic; antiinfertility; immunosuppressive; kw gynaecological; antiinfertility; immunostimulant; auditory; haemostatic; kw gene therapy; FCTR3a; neurestin-like protein; FCTR3f.
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The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the nucleic acids encoding them. These sequences are useful for the treatment or prevention of numerous disorders including myelogenous leukaemia, carcinomas, melanomas, gliomas, astrocytomas, congenital neonatal

Novel polypeptides designated as FCTRX polypeptides, useful in detection, prevention and treatment of a broad range of pathological states.

WPI; 2001-596837/67. P-PSDB; AAU08681 Claim 9; Page 37-39; 215pp; English.

Majumder K;

Herrmann J, Rastelli L;

Shimkets R, Mezes PS,

Fernandes E, J, Mishra V,

Macdougall J,

ϋ

Vermet

RASTELLI L.

(MAJU/) (MACD/) (MISH/) (MEZE/) (RAST/)

2003-625633/59.

WPI; 2003-625633, P-PSDB; ADB32029

VERMET C. FERNANDES E. SHIMKETS R. HERRMANN J. MAJUMDER K. MACHOUGALL J. MISHRA V. MEZES P S.

(VERM/) (SHIM/) (HERR/)

05-MAR-2001; 2001US-00800198 03-MAR-2000; 2000US-0186592P

08-MAY-2003

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170 LeuGlnAsnHis-----AlaArgLeuArgThrProProProProLeuSerHisAla 186
                      924 CCTCCGAACCACCACCAGTCGACTCTGAGGCCCCTCTCCCACCC---CCTCACAAC 980
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                                                                                                                                                                                                                                                                                                           263 AspAsnLeuIleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAsp
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The invention relates to FCTRX polypeptides and the polynuclectides canceding them. The sequences of the invention are useful for the encoding them. The sequences of the invention are useful for the encoding them. The sequences of the invention are useful for the case cancer of a medicament for diagnosing and treating disorders associated with the FCTRX polypeptide, such as colorectal cancer, adenomatous polyposis coli, myelogencus leukaemia, congenital neonatal adenomatous polyposis coli, myelogencus leukaemia, congenital neonatal cumours, mammary tumours, human gliomas, astrocytomas, renal cell autoinmum, breast adenocarionoma, ovarian carcinoma, melanomas, clear carcinoma, breast adenocarinomas, neurological disorders, cell and granular cell carcinomas, neurological disorders, control familial myelodysplastic syndrome, Charcot-Marie-Tooth neuropathy, Gardner syndrome, mental health conditions, immunological disorders, allergy and infection, methal lung conditions, immunological disorders, allergy and infection, sethma sthma, lung deficiency, desmoid tumour, turcot syndrome, liver cirrhosis, hepatitis conditions, spinocrebellar ataxia, plasmodium falciparum infection, groencuw's corneal dystrophy and lattice corneal dystrophy. This sequence creates cDNA encoding an FCTRX polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                          New FCTRX polypeptide and encoding polynucleotide, useful for preventing or treating FCTRX-related disorders, such as cancer, autoimmune, neurodegenerative, gastrointestinal, reproductive and inflammatory
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US2003087816-A1

Homo sapiens

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carcinomas, melanomas, gliomas, astrocytomas, ongenital neonatal alloimmune thrombooytopaenia, neurological disorders, neurodegenerative disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Marie-Tooth neuropathy, demyelinating Gardner syndrome, familial myelodysplastic syndrome, mental health conditions, immunological disorders, allergy and infection, bronchial asthma, Avellino type cosinophilia, lung diseases, reproductive disorders, infertility, male and female reproductive disorders, glycoprotein Ia deficiency, desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric disorders, panacreatic diseases such as diabetes, Schistosoma mansoni infection Spinocerebellar ataxia, Plasmodium falciparum parasitaemia, corneal dystrophy-Greonouw type I, Corneal dystrophy-Jatio BNA encoding FCTR3b, a neurestin-like protein
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invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and their acids encoding them. These sequences are useful for the treat prevention of numerous disorders including myelogenous leukaemia,
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breast cancer; MDA-MB-175 cell; diagnosis; gene therapy; BrbB receptor;
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-Q=/CQm121/USDPTO_spool/USD10029020/runat_06082004_112215_29265/app_query.fasta_1.3519
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MARS=100
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                                                                                                                                         Clone 20 encodes an N-terminally truncated isoform (see AAW44818) of human gamma-hRc9 (see also AAW44817), a novel member of the heregulin (seegalin (see also AAW44817), a novel member of cancer cell library after screening with an EGF-like domain. Compared to gamma-HRG cDNA (see AAV1921), clone 20 contains a 78 base insert between insoluble when expressed as a thioredoxin fusion protein in Escherichia codons 560 and 561, and lacks the 5' end. The truncated gamma-HRG was insoluble when expressed as a thioredoxin fusion protein in Escherichia with their uses e.g. for enhancing the proliferation, differentiation or survival of glial or muscle cells
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breast cancer; MDA-MB-175 cell; diagnosis; gene therapy; ErbB receptor;
cell proliferation; cell differentiation; cell survival;
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                                                                               DNA encoding gamma-heregulin - used to activate ErbB receptor enhance proliferation, differentiation or survival of a cell.
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                                            WPI; 1998-110589/10.
P-PSDB; AAW44818.
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This nucleic acid molecule codes for human gamma-heregulin (gamma-HRG)

(Gee ANM44817), a novel member of the heregulin superfamily, that has a

unique N-terminal domain not present in previously identified heregulins.

C damma-HRG is secreted by human breast cancer MDA-MB-175 calls. It leads

C damma-HRG is secreted by human breast cancer MDA-MB-175 calls. It leads

C to the formation of a constitutive active receptor complex and stimulates

C to the formation of a constitutive active receptor complex and stimulates

C to the growth of these calls in an autocrine manner. The nucleic acid was

C isolated by screening a MDA-MB-175 with a probe corresponding to the EGF-

CI like domain and part of the N-terminal sequences of HRG-beta-3. It can be

CC used for the recombinant production of gamma-HRG, or for in vivo or ex

C vivo gene therapy. A claimed nucleic acid, which is complementary to the

CC nucleic acid sequence encoding the N-terminal domain of gamma-HRG, is

CD to reduce production of gamma-HRG by MDA-MB-175 cells. The invention

C provides claimed methods for activating an ErbB receptor and for

C contacting the cell (preferably a glial or muscle cell) with gamma-HRG
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                                                                                                                                                                                                                                                                                                                   DNA encoding gamma-heregulin - used to enhance proliferation, differentiation
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  97WO-US011841.
                                                        96US-0021640P
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                                                                                                                                                                      Sliwkowski M;
                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                            WPI; 1998-110589/10.
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Best Local Similarity:
                                                                                                                                                                                                                                                          P-PSDB; AAW44817
                                                                                                                                                                      Schaefer GM,
08-JUL-1997;
                                                        12-JUL-1996;
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9

Gamma-heregulin cDNA.

WO9802541-A1

Heregulin; variant; gamma-HRG; human; inner-ear-supporting cell; activator; HER2 receptor; HER3 receptor; HER-2 oncogene; chromosome 8p; hair cell related hearing disorder; ototoxic injury; tissue damage; acoustic assault; degenerative hearing loss; balance impairment;

Human Heregulin variant, gamma-HRG encoding cDNA.

(first entry)

21-SEP-2000 AAD00791;

AAD00791 standard; cDNA; 3111 BP

AAD00791

RESULT

treatment; hair cell; surgical injury; physical injury; inner ear disorder; ss.

/product= "Human Heregulin variant, gamma-HRG protein"

99WO-US025744. 98US-0107522P.

28-OCT-1999; 07-NOV-1998; (GETH ) GENENTECH INC

WPI; 2000-376313/32.

Gao W;

P-PSDB; AAY71176.

Location/Qualifiers 334. .2640

Homo sapiens.

/\*tag=

WO200027426-A1.

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This is the nucleotide sequence of cDNA coding for gamma-heregulin (gamma-HRG, see AAY06339). The invention provides HRG ligands, including gamma-HRG, that have affinity for and stimulate HER2, HER3 and/or HER4 receptors in autophosphorylation. A new method of treating respiratory distress syndrome in humans uses HER2, HER3 and/or HER4 receptor ligands as epithelial growth factors. A novel method of inducing epithelial growth and/or proliferation comprises contacting a normal epithelial cell which expresses HER2, HER3 and/or HER4 receptors with an isolated ligand which activates, HER2, HER3 and/or HER4 receptors or their combination. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claimed are methods of increasing lung surfactant protein A, or of treating chronic obstructive pulmonary disease, respiratory distress or emphysema, by administering an effective amount of an isolated HBR ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to
Gamma-heregulin; HRG-alpha; human; ligand; HER2; HER3; HER4; receptor;
lung surfactant; respiratory distress syndrome; emphysema;
epithelial growth factor; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heregulin ligands can be used to induce epithelial cell growth, and promote repair and healing of tissue damage or injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3111 BP; 799 A; 873 C; 777 G; 662 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 111-116; 120pp; English.
                                                                                                       Location/Qualifiers
334. .2640
/*tag= a
                                                                                                                                                                                                                                                             99WO-US002390.
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                                                                                                                                                                                                                                                                                                                                                                                        Kern JA;
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-494213/41.
P-PSDB; AAY06639.
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                                                                                                                                                                                                                                                                                                 04-FEB-1998;
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                                                                             Homo sapiens
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The patent discloses a method for inducing hair cell generation, or inner cear-supporting cell growth, regeneration, and/or proliferation, by heregulins (HRG), the ligand for HERZ-19BR3 dimeric receptors. Heregulin proteins function as activators of HER-2 oncogene and result from alternate splicing of a single gene mapped to chromosome 8p. The two major types, alpha and beta HRG's are based on two variant EGF-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting cells and for treatment of hair cell related hearing disorders and accoustic associated with tissue damage, e.g. ototoxic injury, acoustic assault, degenerative hearing loss, balance impairments, damage associated with surgery or physical injury and inner ear disorders crelated to hair cell dysfunction. The present sequence is the human heregulin variant, gamma-HRG protein encoding CDNA, isolated from a native HRG source, such as human MDA-MB-175 cells. It has atleast one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3111 BP; 799 A; 873 C; 777 G; 662 T; 0 U; 0 Other;
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Mismatches:
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Query Match:
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CTGGGAAAGGCCCTGGTTGGCATTTATGGCAGAAAAGGCCTCCCTTCACATACA 1800
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Mismatches:
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Best Local Similarity: Percent Similarity:

Query Match: DB:

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 $US-10-029-020-14\_COPY\_450\_520$  (1-71) x AAD00791 (1-3111)

or inner by

Method for inducing hair cell generation and inner-ear-supporting ogrowth regeneration and proliferation, useful for treating hearing disorders.

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1801 CAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGGAGGCGCGCGGAGC 1860
                                                                                       The invention relates to inducing epithelial cell growth and/or proliferation comprising contacting a normal spithelial cell, which expresses HER2, HER3 and/or HER4 (preferably HER2/HER3, HER2/HER4, HER3 or HER4) receptors with an isolated ligand such as HER3/HER4, HER3 or HER4 receptors with an isolated ligand such as mergalin (HRG) which activates HER2, HER3 and/or HER4 receptors. The method is used for inducing epithelial cell (preferably lung cell) growth and/or proliferation, for increasing lung surfactant protein A and for
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                                                                                                                                                                                                                                                                                                                                                                                                                         Human; heregulin; antiasthmatic; antiinflammatory; vulnerary; antiulcer; epithelial cell growth; HER2; HER3; HER4; HRG; lung cell; asthma; lung surfactant protein A; respiratory distress; emphysema; pneumonitis; chronic obstructive pulmonary disease; COPD; chronic bronchtis; ulcer; menental pulmonary disease; neonatal respiratory distress syndrome; meconium aspiration syndrome; congenital diaphragmatic hernia; lesion; acute lung injury; cystic fibrosis; surgical wound; resection; growth factor; smoke inhalation; gamma-HRG; ss.
                                                                                                                              GlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducing epithelial cell growth and/or proliferation, useful in the treatment of respiratory disease, comprises use of heregulin ligand as
                                                                 LeuGlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThr
 ThrPheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSer
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/product= "Human heregulin, gamma-HRG"
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                                                                                                                                                                                              LeuGluGlyThrProArgGlnSerArgGlyThr
                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding human heregulin, gamma-HRG.
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334. .2640
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                                                                                                                                                                                                                                                                                              AAS18526 standard; cDNA; 3111 BP
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99US-00243198.
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
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02-FEB-1999;
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growth factor.
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treating respiratory distress or emphysema, for treating chronic obstructive pulmonary disease (COPD) e.g. chronic bronchitis, asthma, neonatal pulmonary diseases including neonatal respiratory distress syndrome, meconium aspiration syndrome, otherwise including sease including neonates, congenital diaphragmatic hernia and acute lung disease of the neonate, congenital diaphragmatic hernia and acute lung injuries including smoke or chemical inhalation, pneumonitis due to aspiration, radiation, near drowning, cystic fibrosis and other epithelial cell resections, ulcers, lesions and tissue tears as normal epithelial cell growth factors. For treating infants/neonates with respiratory distress conswell as youth and adult with poor lung function due to lung injury or damage. The HRG binds with varying and very high affinity to the HBR2, HBR3 and/or HBR4 receptors. The method simulates growth and profile the epithelial cells, repairing and re-establishing the cellular barriers of organs and allowing the affected tissue to develop comman physiological functions more quickly. Hence the method improves convening and speeds of the development of a barrier to infection while
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1681 ACTITCIGGAGAICTCAAGIGITCAIAGACCAICCIGIGCAICIGAAAITCAAIGIGICT 1740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating lung cells that are damaged by inhalation of smoke resulting in emphysema. It also facilitates regeneration of epithelial cells. The present sequence represents the coding sequence of human heregulin gamma-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuGlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThr 40
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                à
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Mismatches:

Best Local Similarity:

/standard\_name= "Single nucleotide polymorphism (SNP)" replace(225,C)

Location/Qualifiers

replace (117, G)

\*tag= c standard\_name= "Single nucleotide polymorphism (SNP)"

"Single nucleotide polymorphism (SNP)"

/standard\_name=

\*tag=

replace (260, A)

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Useful for treating or preventing a NOVX-associated disorder such as useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, or preferably human. The invention is also useful for treating metabolic of disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, pancreatitis, learning and memory defects, infertility, congenital heart defects, acne, hair growth, pigmentation disorders, endocrine disorders, neurological disease, bone marrow transplantation, endocrine diseases, allory and inflammation, nephrological disorders, urinary system conservation callory and inflammation, nephrological disorders, urinary system conservation callored disorders. The present nucleic acid sequence represents a NOVX gene. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8354 BP; 1968 A; 2437 C; 2271 G; 1678 T; 0 U; 0 Other;
type la membrane sushi-containing domain; butyrophilin;
type la membrane-sushi domain containing; SNP; gene; ds;
single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present nucleic acid sequence represents
encodes a NOVX protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 50-52; 318pp; English.
                                                                                                                                                                                                                                                                                                                                                                        2000US-0257314P.
2001US-0288153P.
2001US-0294075P.
2001US-0311590P.
2001US-0311590P.
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Anderson D, Shir
Casman SJ, Bolo
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P-PSDB; ABG70388.
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24-JUL-2001;
10-AUG-2001;
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29-AUG-2001;
                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                          19-DEC-2001;
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02-MAY-2001;
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                                                                                                         variation
                                                                                                                                                      variation
                                                                                                                                                                                                    variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene Therapy, Nov, cancer; heart disease; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; asthma; IgA nephropathy; cirhosis; arthritis; Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy; wasting disorder; TEN-M4 like protein; chromosome 11; gene; ds.
                                                                                                                                                                                    ThrPheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSer
                                                                                                                                                                                                                                  1382 ACTTICTGGAGATCTCAAGTGTTCATAGACCATCCTGTGCATCTGAAATTCAATGTGTCT
                                                                                                                                                                                                                                                                                                            21 LeuGlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThr
                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSer
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K;
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Zhong M, Gangolli EA, Burgess CE, Patturajan M, Vernet CAM;
Taylor S, Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse l
Alsobrook JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman I
Macdougall J, Malyankar U, Millet I, Peyman J, Smithson G;
Gunther E, Stone DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trans_except= (pos: 1138. .1147,aa:Met)
/product= "NOV1 protein"
                                                                                                                       US-10-029-020-14_COPY_450_520 (1-71) x ABS52100 (1-8354)
      000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LeuGluGlyThrProArgGlnSerArgGlyThr
                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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10-JAN-2001; 2001US-0260811P.
28-FEB-2001; 2001US-027338P.
09-MAR-2001; 2001US-0284704P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN85378 standard; DNA; 8438
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100.00%
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P-PSDB; ABB98401.
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                                   Query Match:
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R; Liu X;

r UM, Kekuda R Zerhusen BD, i L, Ji W;

N, Vernet CAM, Malyankar UM, Shimkets RA, Burgess CE, Zerhu Boldog FL, Smithson G, Li L,

Length: Matches: Conservative:

7.59e-42 372.00 100.00\$

Percent Similarity:

Alignment Scores:

19-SEP-2002

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The present sequence is a coding sequence for a NOV protein. The NOV proteins and coding sequences are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obseity, asthma, igA nephropathy, orithosis, arthritis, AIDS diabetes, obseity, asthma, e.g. bacterial, viral, parasitie), atroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. NOV1 is a
                      useful for preventing or
                                                                                                                                                                                                                                                                                                                                                                                                                                   TEN-M4 like protein and the NOV1 gene is localised to chromosome
                   NOVX polypeptides and encoding polynucleotides, useful for prever treating NOVX-associated disorders e.g. cancer, inflammation, or Alzheimer's disease, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8438 BP; 2001 A; 2434 C; 2268 G; 1735 T; 0 U; 0 Other;
                                                                                                                                                           Claim 9; Page 8-9; 358pp; English.
                                                                                                           pharmacogenomics
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US-10-029-020-14\_COPY\_450\_520 (1-71) x ABN85378 (1-8438) Conservative: Mismatches: Length: Matches: Indels: 372.00 100.00% 100.00% 100.00% 7.7e-42 Percent Similarity: Best Local Similarity: Aliqnment Scores: Query Match: Pred. No.:

40 9 ThrPheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSer LeuGlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThr 41 GlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSer CTAGAGGGACCCCGCGCCAGTCTCGGGGAACT 1570 LeuGluGlyThrProArqGlnSerArqGlyThr 71 1418 61 1538 Н 21 à g à du à Ωþ à q

ABS78652 standard; cDNA; 8645 BP (first entry) 16-DEC-2002 ABS78652; ABS78652 RESULT 

Human cDNA encoding CGDD10, INCYTE 7488573CB1.

Human; ss; gene; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; polirhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thromobocytopaenia; developmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS; neurological disorder; Alzheimer disease; parkinson's disease; asthma; reproductive disorder; infertlity; autoimmune disorder; gout; allergy; inflammatory disorder; acquired immunodeficiency syndrome; uveitis; diabetes mellitus; glomerulonephritis; cohn's disease; infection; multiple sclerosis; osteoarthritis; csteoporosis; pancreatitis; arthritis. rheumatoid

Homo sapiens

WO200272830-A2.

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The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to CGDD, a biologically active caid sequence at least 90% identical to CGDD, a biologically active fragment or an immunogenic fragment. Also included are the polymuclectides encoding CGDD1-12, a recombinant polymuclectide comprising a promoter sequence operably linked to the CGDD oplymuclectides, a cell transformed with the recombinant polymuclectide, an anti-cGDD polymuclectides, a cell transformed with the recombinant polymuclectide, an anti-cGDD polymuclectide in compounds which bind to/modulate or are atomitized of CGDD or alter the expression of CGDD polymuclectide and acceptants and antagonists are useful for diagnosing, treating or cGDD polymuclectide with abservant expression of CGDD, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, proveysmal nocturnal haemoglobinuria, polycythaemia or articularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, primary thromobocytopaenia or cancer), developmental disorders (e.g. renal tubular acidosis, an amendal retardation), neurological disorders (e.g. Alzheimer disease, parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. Alzheimer CC (acquired immunodeficiency syndrome) allergies asthma, autoimmune thyroiditis, contact dermatitis, parcasitic, processing context dermatitis, parcasitic, processing context dermatitis, parcasitic, processing to the effects of infections. They are also useful in the assessment of the effects of exceptences of proceins associated with CGDD. The present sequence encodes congounds on the expression of nucleic acid and amino acid sequences of proceins associated with CGDD. The present sequence encodes
                                                                                                                                                                                                                                                     Baughn MR;
Burford N;
                                                                                                                                                                                                                                                                                                                                                                                                                  New human proteins associated with cell growth, differentiation and death, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8645 BP; 2060 A; 2494 C; 2319 G; 1771 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                        , Lu Y, Warren BA, Elliott VS,
KJ, Tang TY, Lal PG, Duggan BM,
Tran UK, Khare R, Walia NK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 175-178; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atherosclerosis or hepatitis.
                                                                                      09-FEB-2001; 2001US-0268111P.
23-FEB-2001; 2001US-0271175P.
08-MAR-2001; 2001US-0274503P.
09-MAR-2001; 2001US-0274552P.
                                               08-FEB-2002; 2002WO-US003715.
                                                                                                                                                                                                                                                             Yao MG, Ison CH, L
Xu Y, Gietzen KJ,
                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                         Richardson TW,
                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-723356/78.
                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABG97359
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Lu DAM,
                                                                                                                                                                                                                                                          Yue H,
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8645 71 0 0 0 Conservative: Mismatches: Indels: Length: Matches: 7.95e-42 372.00 100.00% 100.00% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match:

US-10-029-020-14\_COPY\_450\_520 (1-71) x ABS78652 (1-8645)

1452 ACTITICIGGAGALCICAAGIGITCATAGACCAICCIGIGCAICIGAAATICAAIGIGICI 1511 1 ThrPheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSer

> ò g à

40 LeuGlyLysAlaAlaLeuValGly11eTyrGlyArgLySGlyLeuProProSerHisThr 21

associated disorders,

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Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antinflammatory; fungicide; antirheumatic; antiarthrift; immunosuppressive; antiallergic; virucide; antianaemic; antibacterial; procrozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy; diabetes mellikus; Grave's disease; cystic fibrosis; goitre; diabetes mellikus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia;
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                          GlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSer
                                                                                                      CTAGAGGGGACCCCGCCCAGTCTCGGGGAACT 1664
                                                                              LeuGluGlyThrProArgGlnSerArgGlyThr 71
                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; gene; chromosome 4; ss.
                                                                                                                                                                                                                                        Human NOV15c encoding cDNA SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
258. .8144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "NOV15c"
                                                                                                                                                          ABQ82345 standard; cDNA; 8473 BP
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2001US-0286683P
2001US-0294080P
2001US-0312915P
2001US-0313325P
2001US-0333350P
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2001US-0279832P.
2001US-0279833P.
2001US-0283889P.
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2001US-0259785P.
2001US-0269814P.
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Patturajan M, Gu
                                                                                                                                                                                                              (first entry)
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Rastelli L,
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29-MAR-2001;
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29-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-2001;
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                                                                                                      1632
                                                                                                                                                                                    ABQ82345;
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                                                                                                                                RESULT 9
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New NOVX polypeptides and polynucleotides useful for treating NOVX-

WPI; 2002-732706/79. P-PSDB; ABP53588

Gunther E,

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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, noctropic, cardiovascular, antidiabetic, antiinflammatory, antirheumatic, antiarthritic, virucide, immunosuppressive, antiallergic, antianeamic, antiarthritic, virucide, immunosuppressive, antiallergic, antianeamic, antiarthritic, virucide, therapy. The NOVX proteins, nucleotides or antibodies can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the human disease selected from NOVX-associated disorder. Such as cancers convary, testis and uterus), neurological disorder. Such as cancers (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or Pick's disease, alzheimer's disease or Pick's disease, or goitre), gastrointestinal confiscative collitis, or gastric and duodenal disorders), autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be biological samples (tissue typing), and in forense indentification of a hinhorical sammle whe present sequences may be biological samples (tissue typing), and in forense indentification of a hinhorical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1245 CAGAAGGATGCATTGATTGGAGTATATGGCCGGAAAGGCTTACCGCCTTCCCATACTCAG 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sociated disorders, such as cancers, neurological disorders, disorders
Vesicular transport, gastrointestinal disorders, and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; noctropic; antidiabetic; antiinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antialpergic; virucide; antianaemic; antiahacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 GlylysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThrGln 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 PheaspPhevalGluLeuLeuaspGlyArgArgLeuLeuThrGlnGluAlaArgSerLeu 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes human NOVISc, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheTrpArgSerGlnValPhelleAspHisProValHisLeuLysPheAsnValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8473 BP; 2301 A; 2017 C; 2145 G; 2006 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113
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Conservative:
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                                                                                      Claim 8; Page 119-121; 444pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1365 CTTGAGACGGAGAGCCGGCCG 1388
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80.88%
70.59%
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                                            diseases,
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stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy;
     Pick's disease, vesicular transport disease, cystic fibrosis; goitre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.
                                                                  Location/Qualifiers
299. .8140
/*tag= a
                                                                                             /product= "NOV15d"
                                                                                                                                                                                         2001US-0279863P.
2001US-0279832P.
2001US-0279833P.
2001US-0283889P.
                                                                                                                                                                                                                         2001US-0284447P.
2001US-0286683P.
2001US-0294080P.
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2001US-0313325P.
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                                                                                                                                             31-DEC-2001; 2001WO-US049976
                                                                                                              WO200262999-A2
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02-JAN-2001;
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25-APR-2001;
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13-APR-2001;
                                                                                                                                                                                                                                                 16-AUG-2001;
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                                                                                                                                                                                                                                                                         26-NOV-2001;
                                                         Homo sapiens
                                                                                                                                                                                                                                                                 17-SEP-2001
                                                                                                                              15-AUG-2002
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## (CURA-) CURAGEN CORP.

Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;
U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;
Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
Casman SJ, Burgess CE, Edinger S, Ellerman K;
Smithson G, Millet I, Macdougall JR; Malyankar U, Kekuda R, Pat Rastelli L, C Gunther E, Spytek KA,

WPI; 2002-732706/79. P-PSDB; ABP53589 New NOVX polypeptides and polymucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune diseases

Claim 8; Page 123-125; 444pp; English.

The present invention describes novel human proteins designated NOVX,
where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective,
cytostatic, anticonvulsant, cerebroprotective, nootropic, candiovascular,
cytostatic, anticonvulsant, cerebroprotective, notropic, candiovascular,
contidiabetic, anticonvulsant, cerebroprotective, antiarthritic, virucide,
immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide,
immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide,
controzoacide and antihelminthic activities, and can be used in gene
therapy. The NOVX proteins, nucleotides or antibodies can be used in the
control a medicament for treating a syndrome associated with a
human disease selected from NOVX-associated disorder. such as cancers
(e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle,
covary, testis and uterus), neurological disorders (e.g. epilepsy, stroke,
ischaemic cerebrovascular disease, Alzheimer's disease or pick's
disease, disorders of vesicular transport (e.g. cystic fibrosis,
disorders (e.g. ulcerative colitis, or gastric and duodenal disorders),
autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic
antoimmune diseases (e.g. allergic reactions, autoimmune haemolytic
and protozoal infections. The NOVX proteins can be used as immunogens to
produce antibodies and as vaccines. The NOVX nucleotide sequences may be

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1226 TICTGGAGATCACAGCTCTTCATHGATCAGCCACAGTTTCTTAAATTCAATATCTCTCTT 1285
                                                                                                                                                                                                                                                                                                                                                                1286 cagaaggardcarrdaarragagrarararggccggaaaggcrraccgccrrcccaracrcag 1345
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; noctropic; antidiabetic; antiinflammatory; fungicide; antithematic; antiallergic; virucide; antithematic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; prick; disease; vesicular transport disease; Alzheimer's disease; allergy; pick's disease; vesicular transport disease; cystic fibrosis; goltre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative collitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune baemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.
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                   ಹ
used in chromosome mapping, identifying individuals from minute
biological samples (tissue typing), and in forensic identification of a
biological sample. The present sequence encodes human NOV15d, which is
                                                                                                                                                                                                                                                                     PheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSerLeu
                                                                                                                                                                                                                                                                                                                                    22 GlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThrGln
                                                                                                                                                                                                                                                                                                                                                                                                 42 PheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSerLeu
                                                                               Sequence 8487 BP; 2306 A; 2029 C; 2148 G; 2001 T; 0 U; 3 Other;
                                                                                                                              8487
48
7
113
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                                                                                                                                                              Conservative:
Mismatches:
                                                                                                                                Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 GluGlyThrProArgGlnSerArg 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
151. .8316
/*tag= a
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2001US-0259785P.
2001US-0269814P.
2001US-0279863P.
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254.00
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                                                      located on chromosome 4
                                                                                                                                                                                Similarity:
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04-JAN-2001; 2
20-FEB-2001; 2
09-MAR-2001;
                                                                                                                                                                 Percent Similarity:
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                                                                                                                   Alignment Scores:
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                                                                                                                                     No.:
                                                                                                                                                                                 Local
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42 PheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSerLeu 61

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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, cardiovascular, antidiabetic, antidinflammatory, antidianematic, antidarcerial, fundicide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a contrapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a contrapy. The NOVX measociated disorder selected from NOVX-associated disorder, such as cancers (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or Pick's disbetes mellitus, Grave's disease, or goitre), gastrointestinal disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), candenia, or rheumatoid arrhritis), viral, bacterial, fungal, helminthic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX proteins can be used as immunogens to used in chromosome mapping, identifying individuals from minute cological samples (tissue typing), and in forensic identification of a biological sample (the present sequence encodes human NOVISD, which is
                                                                                                                                                                                                                                                                                         Wolenc AR, Vernet CAM, Eisen A, Liu X, kets RA, Tchernev VT, Spaderna SK, Gorman L; jan M, Gusev V, Gangolli EA, Guo X, Shenoy S; SJ, BOJGOSF, Burgess CE, Edinger S, Ellerman K; on G, Millet I, Macdougall JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
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U, Shimkets RA, Tone...
Patturajan M, Gusev V, Gr
Casman SU, Boldog F, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 114-117; 444pp; English.
                                            13-APR-2001; 2001US-0283889P.
18-APR-2001; 2001US-0284447P.
25-APR-2001; 2001US-0286683P.
                                                                                                               29-MAY-2001; 2001US-0294080P.
16-AUG-2001; 2001US-0312915P.
    2001US-0279832P.
2001US-0279833P.
                                                                                                                                                            2001US-0313325P.
                                                                                                                                                                                 2001US-0322699P.
                                                                                                                                                                                                      26-NOV-2001; 2001US-0333350P.
                                                                                                                                                                                                                                                                     Spytek KA, Li L,
Malyankar U, Shimkets L.,
Kekuda R, Patturajan M, G
Rastelli L, Casman SU,
R. Smithson G, P
                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
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                                                                                                                                    16-AUG-2001;
17-AUG-2001;
                                                                                                                                                                                 17-SEP-2001;
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Conservative: Length: Matches: 5.52e-25 Similarity: Percent Similarity: Best Local Similari Alignment Scores: Pred. No.:

PheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSerLeu 8645 48 7 13 0 US-10-029-020-14\_COPY\_450\_520 (1-71) x ABQ82344 (1-8645) Mismatches: Indels: 254.00 80.88% 70.59% 68.28% Query Match: ð 셤 ð

New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders

WPI; 2002-732706/79.

P-PSDB; ABP53586

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1477 TATGACTICGTGGAGCTCCTGGATGGCAGCTGATTGCCAGAGAGCAGCGGAGCCTG 1536
                                                                                                                                                                                                                                  Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide; antianemic; antibacterial; protezoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy; diabetes mellitus; Grave's disease; cystic fibrosis; goitze; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; vaccine; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             et CAM, Eisen A, Liu X;
v VT, Spaderna SK, Gorman L;
Gangolli EA, Guo X, Shenoy S;
Burgess CE, Edinger S, Ellerman K;
Macdougall JR;
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                                                                                                                                                                                                           Human NOV15a encoding cDNA SEQ ID NO:35.
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                                                            1537 CTTGAGACGGAGAGACCGGGCGG 1560
                                   69
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/product= "NOV15a"
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Casman SJ, Boldog F,
Smithson G, Millet I,
                              62 GluGlyThrProArgGlnSerArg
                                                                                                                         BP.
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02-JAN-2001; 2001US-0259415P.
04-JAN-2001; 2001US-0259415P.
20-FEB-2001; 2001US-0259814P.
09-MAR-2001; 2001US-0279832P.
29-MAR-2001; 2001US-0279832P.
29-MAR-2001; 2001US-0279833P.
13-APR-2001; 2001US-0284444P.
25-APR-2001; 2001US-0286683P.
25-APR-2001; 2001US-0286683P.
16-AUG-2001; 2001US-0286683P.
17-AUG-2001; 2001US-03869P.
17-SEP-2001; 2001US-0313355P.
17-SEP-2001; 2001US-0333350P.
                                                                                                                      ABQ82343 standard; cDNA; 8675
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                                                                                                                                                                              (first entry)
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Kekuda R, Pattura,...
Rastelli L, Casman SJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                               17-DEC-2002
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                                                                                                                                                   ABQ82343;
                                                                                          RESULT 12
                                                                                                       ABQ82343
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Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                                                                                                                                                                                                                                                                                             Gish KC, Mack DH, Wilson KE,
                                                                                                                                                                                                                                     06-APR-2001; 2001US-0281922P.
24-APR-2001; 2001US-0286214P.
30-APR-2001; 2001US-00847046.
04-MAY-2001; 2001US-0288589P.
                                                                                                                                                                                                                                                                                                                                                    (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                08-DEC-2000; 2000US-00733742.
24-JAN-2001; 2001US-0263957P.
16-MAR-2001; 2001US-0276791P.
16-MAR-2001; 2001US-0276888P.
                                                           12-OCT-2001; 2001WO-US032045
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-471335/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ABG61913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate tissue
                                                                                                                                08-DEC-2000;
08-DEC-2000;
                  18-APR-2002.
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                                                                                                           The present invention describes novel human proteins designated NoVX, where X is 1 to 20 e.g. NoVI. NoVX sequences can have neuroprotective, cycostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, articlabetic, anticonvulsant cycle anticonvulsant. Antipleumatic, antibatchitic, virucide, immunosuppressive, antihalengic, antipacterial, fungicide, protozoacide and antihelminitic activities, and can be used in gene therapy. The NoVX proteins, nuclectides or antibacterial, fungicide, protozoacide and antihelminitic activities, and can be used in gene manufacture of a medicament for treating a syndrome associated with a manufacture of a medicament for treating a syndrome associated with a convary, testis and uterus), neurological disorders (e.g. plukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Albheimer's disease or pick's disease, disease, or goitre), gastrointestinal disorders (e.g. utcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. allergic reactions, autoimune haemolytic and protozoal infections. The NoVX proteins can be used as immunogens to produce antibodies and as vaccines. The NoVX nuclectide sequences may be used in chromosome mapping, identifying individuals from minute con concast con chromosome mapping), and in forensic identification of a concast con chromosome protoses the present sequence encodes human NoVISa, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1477 ICCICCCCCAGIAIGACTICCIGGAGCICCIGGAIGGCAGCAGCAGCAGTAITGCCAGAGAG 1536
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    of vesicular transport, gastrointestinal disorders, and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8675 BP; 2362 A; 2067 C; 2201 G; 2041 T; 0 U; 4 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaArgSerLeuGluGlyThrProArgGlnSerArg 69
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Indels:
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Matches:
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                                                                       Claim 8; Page 110-112; 444pp; English.
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75.00%
65.28%
62.90%
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Hevezi P;

Afar D,

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The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancerasociated polynuclectides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancerassociated polynuclectide sequences are differentially prostate cancerassociated polynuclectide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing or treating prostate cancer associated genes are useful for diagnosing or treating prostate cancer is associated genes are useful for diagnosing or treating prostate cancer or associated genes are useful for diagnosing or treating prostate cancer or as well as for identifying modulators of prostate cancer or agents that in the prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABK92115-ABK92263 represent prostate cancer ansociated polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12879 BP; 3852 A; 2674 C; 2768 G; 3585 T; 0 U; 0 Other;
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36
18
14
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Matches:
Conservative:
Mismatches:
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Claim 22; Page 394-397; 436pp; English.
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79.41%
52.94%
59.14%
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Best Local Similarity:
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Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

gene therapy; gene; ds.

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ð 셤 ð a à d WO200230268-A2

Mammalia

Prostate cancer-associated DNA sequence #116.

gene therapy;

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The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asundi V, Zhou P, Xu C, Cao Y;
J, Zhang J, Ren F, Chen R, Wang ZW;
Goodrich R;
                                                                                                                                                                                                       vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                                                                                           cell proliferation; cell differentiation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1414-1426; 6221pp; English.
1493 GATGATACACAGCACTCCCTCGG 1516
                                                                                                                                                           Human polynucleotide SEQ ID NO 373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Drmanac RT, Asur
wang D, Wang J,
                                                               AAK51828 standard; cDNA; 13202
                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-00560875.
2000US-00598075.
2000US-00620325.
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2000US-00663561.
2000US-00693325.
2000US-00728422.
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Yang Y, Wejhrman T,
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                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                           cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAM78695
                                                                                                                                                                                                                                                                                                     WO200157190-A2
                                                                                                                                                                                                                                                                         sapiens.
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20-OCT-2000;
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Xue AJ,
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13202 36 18 14 0

Matches: Conservative: Mismatches: Length:

6.91e-20 220.00 79.41% 52.94% 59.14%

Similarity:

Query Match: OB:

Percent Similarity:

Indels:

US-10-029-020-14\_COPY\_450\_520 (1-71) x AAK51828 (1-13202)

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1639 TTCTGGCGTTTCCAGATTACTATCCACCATCCAATATATCTGAAGTTCAATATTTCTTTA 1698
                                                                                                1699 GCCAAGGACTCTCTGCTGGGAATTTATGGCAGAAGAACATTCCACCTACATACTCAG 1758
                                                                                                                                                          41
                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                typing; cancer; breast cancer; colon cancer; lung cancer; sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              pancreatic cancer; uterine cancer; organ transplantation disorder; ds; cardiovascular disease; melanoma; atherosclerosis, diabetes mellitus; ischaemic heart disease; haemorrhage; peripheral vascular disease; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a new isolated NOV4 nucleic acid. The nucleic acid is useful for identifying a compound that binds the nucleic acid. The nucleic acid is useful in gene therapy, in screening assays, in detection assays e.g. chromosomal mapping, cell and tissue typing and forensic biology, predictive medicine e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics and methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALS; peripheral neuropathy; nervous system tumour; neurotoxin; tremor; neuropathy; acute brain injury; peripheral nerve trauma; human; NOVX; gene therapy; epilepsy; breast tumour associated protein 47.
                                                                                                                                   PheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSerLeu
PheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSerLeu
                                                                 Human breast tumour associated protein 47-like polypeptide NOV11 DNA.
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                                                                                                                                                                                                       62 GluGlyThrProArgGlnSerArg
                                                                                                                                                                                                                                                                                                              BP.
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2000US-0191158P.
2000US-0193086P.
2000US-0201388P.
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P-PSDB; ABO23243.
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16-MAR-2000;
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30-MAR-2000;
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treatment including therapeutic and prophylactic. The nucleic acid is also useful cor useful for expressing NoVX protein. The nucleic acid is also useful to provide polynuclectide reagents e.g. labelled probes that are useful con an in situ hybridisation technique, for identifying a specific tissue (for example brain tissue) and for use in forensic science. The nucleic acid is also useful for mapping genes on a chromosome and thus locating come regions associated with genetic disease, identifying an individual from a minute biological sample and to aid in forensic identification of biological sample. The nucleic acid is also useful for treating cancer, especially cancers of the breast, colon, lung, pancreas or uterus, or a melanoma or sarcoma. The nucleic acid is also useful for treating cancer, atheroscalerosis, ischemic heart disease, haemorrhage, disbetes mellitus, corputating haematopois, hypertension and systemic lupus erythematosus. NOVX protein encoded by the nucleic acid is useful for regeneration and systemic lupus crythematosus. NOVX protein encoded by the nucleic acid is also useful for treating infections, corputating haematopoisis, for regeneration of bone, cartilage, tendon ligament and/or nerve tissue growth or regeneration and for wound corputation are acid is also useful for treating infections, corputating haematopoises, Alphaimer's disease, Hunting ton's disease, nucliple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral corputation and injury, peripheral nerve trauma or injury and other neuropathies, brain injury, peripheral nerve trauma or injury and other neuropathies, bunn injury, peripheral nerve trauma or injury and other neuropathies, bunnan breast tumour associated protein 47-like polypeptide
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2 PheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSerLeu US-10-029-020-14\_COPY\_450\_520 (1-71) x ACD40264 (1-1429) Conservative: Mismatches: Indels: Length: Matches: 1.12e-17 195.50 70.59% 55.88% 52.55 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Pred. No.: à

944 GGGAAGGACGCTCTCTTTGGTCTTTACATAAGAAGAGGACTTCCACCATCTCATGCCCAG 1003 ----GAGNAGIGGAGIGIG 1048 42 PheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGluGluAlaArgSerLeu 61 GlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThrGln 41 :::||||||||::: 1004 TATGACTTCATGGAACGTCTGGACGGGAAG 22 d  $\delta$ g 8 q

ò 셤 Search completed: August 14, 2004, 02:28:55 Job time : 135.435 secs

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AX662357 Sequence
AX662355 Sequence
AX662353 Sequence
AR026980 Danio rer
AR155869 Homo sapi
AR155869 Homo sapi
AR026410 Mus muscu
AR026410 Mus muscu
AR026410 Punio rer
AR086610 Rattus no
AR086610 Rattus no
AR032953 Homo sapi
AX250008 Sequence
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AX250068 Sequence
BX648178 Homo sapi
AX250067 Sequence
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AXX50063 Sequence
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AJ238613 Gallus ga
AF086608 Rattus no
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AC073599 Mus muscu
X68794 Drosophila
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AP002412 Homo sapi
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AC103323 Rattus no
AF008228 Drosophil
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   GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Rattus no Rattus no

Homo sapi

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

AX556500

LOCUS

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obashi,T., Zhou,X., Feng,K., Richter,B., Moergelin,M., Perez,M.T., Su,W., Chiquet-Ehrismann,R., Rauch,U. and Faessler,R.
Mouse Ten-m/Odz is a new family of dimeric type II transmembrane proteins expressed in many tissues
J. Cell Biol. (1999) In press
Obassi to 8585)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
Duggan, B.M., Burford, N., Lu, D.A., Richardson, T.W., Tran, U.K., Khare, R. and Walia, N.K. Proteins associated with cell growth, differentiation, and death Patent: WO 02072830-A 22 19-SEP-2002; Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-MAR-1999) Toshitaka Oohashi, Okayama University Medical School, Dept. Mol. Biol. & Biochem.; 2-5-1 Shikata-cho, Okayama, Okayama 700-8252, Japan
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Fax:+81-86-222-7768)
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Mus musculus mRNA for Ten-m4, complete cds.
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Conservative:
Mismatches:
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                              Gangolli, E.A., Patturajan, M., Vernet, C.A., Malyankar, U.M., Kekuda, R., Stone, D.J., Anderson, D., Shimkets, R.A., Burgess, C.E., Zerhusen, B.D., Liu, X., Spytek, K.A., Casman, S.J., Boldog, F.L., Solypetides, and Ji, W. Polypetides and nucleic acids encoding same patent: WO 02057453-A 13 25-JUL-2002; Curagen Corporation (US)
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Baughn, M.R., Ding, L., Xu, Y., Gietzen, K.J., Tang, T.Y., Lal, P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGlyAlaGly
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Sequence 22 from Patent WO02072830.
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ARSILEGPPROGYET TIDHVHLKFNVSLGKAALVGTYGKRGLEPSTGFDFVELLDGRRLLTQE

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NCPSNCYGNODCI SGTCHCFLGFLGPDGGASCPVLCSGNGQYMKGRCLCHSGWKGAE

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KEGCPGLCNCNNNRCCTLDLNGWHCVCQLGWRGTGCDTSMETGCGGGCNDGDGLUDCMD
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PHCGYSMGASSDADLEADTVLSPEHPVRLMGRSTRSGRSSCLSSRANSNLTLTDTEHB
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BEGWNVAREDYNYDNSFRYTGMQAVINETPLPIDILRYKDDVGGKTEQFGKFGVIYYDI
NQIITTANWTHTKHFDAYGRMEVQYETFRSLMYWMYVQYDNMGRVYKKELKVGEYAN
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RLGDVQYKMDEDGFLRQRGDVFEYNSAGLLIKAYNRASGMSVRXRYDGLGRRYOSKS
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DGAYSDGHFLFKPGGTSPLFCTTSPGYPLTSSTVYSPPPRPLPRSTFSRPAFNLKKPS
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GIMSERMEYDQAGRITSRIFADGKMWSYTYLEKSMVLHIASQRQYIFEPPKNDRLSSV
TMPNVARQTLETIRSVGYYRNIYQPPEGNASVIQDFTEDGHLLHTFYLGTGRRVIYKY
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NTMLSGRTRRYTDIQLQYRALCLNTRYGTTVDEEKVRVLELARQRAVRQAWAREQORL
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8585 98 0 3 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

55e-42

Alignment Scores:

ORIGIN

Pred. No.:

Score:

605.00 97.03% 97.03% 98.06%

> Percent Similarity: Best Local Similarity: Query Match: DB:

Gaps:

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                    2441 TGGATGGGGGCCCCATGCGACCAACGGCCTGCCACCCACGCTGTGCAGAACACGGGACC
                                                                                                                                           2501 TGCCGGGACGGCAAGTGCGAATGCAGCCCCGGCTGGAATGGAGAGACACTGCACCATCGCT
                                                                                                                                                                                            41 HisTyrLeuAspArgValVallysGluGlyCysProGlyLeuCysAsnGlyArg
                                                                                                                                                                                                                              2561 CACTATCTGGATAGGGTAGTTAAAGAGGGCTGTCCTGGCTTGTGCAATGGAATGGCAGA
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                                      1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr
                                                                                                                 21 CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrIleAla
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US-10-029-020-14_COPY_750_850 (1-101) x AB025413 (1-8585)
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Mismatches:
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Location/Qualifiers
1. 8438
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/mol_type="unassigned DNA"
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Matches:
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Sequence 1 from Patent WO02055704.
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SOURCE
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2309 TGCCGCGACGGCAAGTGCGAGTGCAGCCCTGGCAATGGCGAACACTGCACCATCTCC 2368
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                                                                           ---AlaHisTyrLeuAspArgValValLys-----GluGlyCysProGlyLeuCysAsn
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                                                                                                                                                                                                                                                                GlyAsnGlyArgCysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrp
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/tissue type="brain"
/dev stage="adult"
1. .8964
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Mus musculus
Eukaryota; Metazoa; Chordat
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50. .8197
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AB025412.1 GI:4760779
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Direct Submission
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AB025412
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TITLE

PITYSSPESSPENGETINGTHERM THERMY THE THE THEOTOCHER THEOLOGY THE SERVACE AND THE THEOTOCHERS THEORY THEOTOCHER SRRVI-EKYRRQTRLSBILYDSTRVSFTYDETAGVLKTVNLQSDGFICTIRYRQIGPLI DRQIFRFSEDGMVNARPDYSYDNSFRYTSMGGVINETPLPIDLYQFDDISGKVEGPGK GRGIVYVDIDQIISTAVMYTYKHFDAHGRIKEIOYEIFRSLMYMITJQYDNMGRVTKRB IKIGFPRANTTKYAREYDVDGQLQTYVLNEKIWMRYNYDLNGMIHLANBSSSAALITPLR YDLRDRITRLGDVQYRLDEDGFLRQRGTEIFEYSSKGLLTRVYSKGSGWTVIXRYDGI QSTIVVNGRITRRFADVEMQEGALALHVRYGMILDEBKARILEQARQRALARAWAREQQ RVRDGEBGARLWIEGEKRQLLSAGKVQGYDGYYVLSVEQYPBLADSANNIQFLRQSEI GKR" LSLGKMAEVQVSRRKAGAEQSWLWFATVKSLIGKGVMLAVSQGRVQTNVLNIANEDCI KVAAVLNNAFYLENLHFFIEGKDTHYFIKTTTPESDLGTLRTTSGRKALENGINVTVS GRRVSSKTSLGQHLQFFYADLTYPTRITHVYNHSSSBITSLYYDLQGHLFAMEISSGD LIHFGERDYDILAGRWTTPDIEIWKRIGKDPAPFNLYMFRNNNPASKIHDVKDYITDV nswlvtfgfhlhnaipgfpvpkfdltepsyelvksqqwedvpp1fgvqqqvarqakaf

8964 85 7 9 0 Conservative: Mismatches: Indels: Length: Matches: Gaps: 1.95e-36 541.00 91.09% 84.16% 87.68% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: .. 0N ORIGIN Score:

US-10-029-020-14\_COPY\_750\_850 (1-101) x AB025412 (1-8964)

ζŏ	1 Trj	TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr 20
Db	2153 TGC	TGGACCGGCCGGCGTGTAATCAGAGAGCTTGCCACCCTCGCTGTGCTGAGCACGGGACG
Š	21 CY	CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrlleAla 40
QQ	2213 TG	TGCAAGGACGGCAAGTGCGACGCCAAGGATGGAACGGAGAGCACTGCACAATTGCT 2272
δ	41 Hi	41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg 60
qq	2273 CA	CACTATTTGGGATAAGATAGTTAAAGAGGGTTGCCCCGGCTTGTGCAACAGCAATGGGAA 2332
٥٧	61 CY	61 CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGlyAlaGly 80
qq	2333 TG	TGCACACTGGACCAAAACGGCTGGCACTGCGTTTGCCAGGCAGG
ò	81 CY	81 CysAspThrSerMetGluThrAlaCysGlyAspSerLysAspAsnAspGlyAspGlyLeu 100
qq	 2393 TG	:::

ROD 15-AUG-1998

linear

mRNA

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AF059485

AF059485 RESULT 6

LOCUS

::: 2453 ATT 2455 101 Val 101

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RCLCHSGWKGAECDVPTNQCIDVACSSHGTCIMGTCICNPGYKGESCEEVDCMDPTCS
SRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTELPDTGLCNCDPSWTGHDCSI
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HCTIEGCPGLCNGNGRCTLDLNGWHCVCQLGWRGTGCDTSMETGCGDGKDNDGDGLVD
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IPFNIMKVHLMVAVGGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFGLSBAFVSVGYB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAC31807.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHCGYSMGASSDADLEADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTETGAPLHCSSASSTPIEQSPSPPPSPPANESQRRLLGNGVAQPTPDSDSEEEFVPN
SFLVKSGSASLGVAANDHPSSLQNHPRLRTPPPPLPHAHTPNQHHAASINSLNRGNFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRSNPSPAPTDHSLSGEPPAGSAQEPTHAQDNWYLNSKIPVETRULGKOPFLGTWQDN
LIEMDIFSASRRDGAYSDGHFFFKPGGTSPLFCTTSPGYPLTSSTVYSPPPRPLPRST
FSRPAFNLKKPSKYCNWKCAALSAILISATLVILLAYFVAMHLFGLNWHLQPMEGGWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CMDPDCCLQPLCHVNPLCLGSPDPLDIIQETQAPVSQQNLNSFYDRIKFLVGRDSTHS
IPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFINNPLFGYTISRQDGSFDLVTNGG
ISIILRFERAPFITQEHTLMLPWDRFFVMETIVMRHEENEIPSRDLSNFARPNPVVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETSSKDDVTITTHLSGSGAFYTLLQDQVRNSYYIGADGSLRLLLLANGWEVALQTEPHL
LAGTVNPTVGKRNYTLPIDNGLNLVEWRQRKEQARGQVTVFGPRLRYHNRNLLSLDFD
RVTRTEKIYDDHRKFTLRILYDQAGRPSFWSPSSRLNGVNVTYSPGGHIAGIQRGIMS
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 9722)
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VORRAASQKITERGTFWRSQVPTDHPWHIKTNVSLGKAALVGIVGRKGLEPSHTOLDFV
BLLDGRRLLTYGRARELEGPQRGSRGPVPPSSHETGIOYLDSGIWHLAFYNDGKESEV
VSFLTTALESVDNCPSNCYGNGDCISGTCHCFLGFLGFDGPDCGRASCPVLCSGNAQYMKG
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VTTSGEISLVAGAPSGCDCKNDANCDCFSGDDGYAKDAKLNTPSSLAVCADGELYVAD
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                                                                                                                                                                                                                                                                                                   Wang, X.Z., Kuroda, M., Sok, J., Batchvarova, N., Kimmel, R., Chung, P., Zinszner, H. and Ron, D. Identification of novel stress-induced genes downstream of chop EMBO J. 17 (13), 3619-3630 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 9722)
Wang,X.-Z. and Ron,D.
Direct Submission
Submitted (14-APR-1998) Skirball Institute, New York University
Medical Center, 550 First Ave., New York, NY 10016, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to Drosophila melanogaster tenm/odz and
human gamma-heregulin; type II transmembrane protein"
   musculus DOC4 (Doc4) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/cell_line="NIH-3T3"
/note="tunicamycin-treated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="downstream of CHOP
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/strain="NIH/Swiss"
                                                                                                                                Mus musculus (house mouse)
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                                                                  AF059485.1 GI:3170614
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CDS

FATURES

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TTAVWTHSKHFDAYGRMKEVQYETFRSLMYMTVQYDNMGRVVKKELKYGPYAMTTRY
SYEYDADGOLQTVSINDKPIMRYSYDLNGNLHLLSPGNSARLTPLRYDLRDRITRLGD
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NNAHYLENLHFTIDGVDTHYFVKFGPSEGDLALGLSGGRRTLENGVNVTVSQINTML
                                                                                                                                                                                                                                  SGRTRRYTDI QLQYRALCLNTRYGTTVDEEKVRVLELARQRAVRQAWAREQQĒLREGE
EGLRAWTDGEKQQVLNTGRVQGYDGFFVTSVEQYPELSDSANNIHFMRQSEMGRR"
KLAETLYDTTKVSFTYDETAGMLKTVNLQNEGFTCTIRYRQIGPLIDRQIFRFTEEGM
                 VNARFDYNYDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3046 TGGATGGGGCCGCATGCGACCAACCGGCCTGCCACCCACGCTGTGCAGAACACGGGACC 3105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3259 TGCGACACATCCATGGAAACGGGCTGTGGAGACGGCAAGGACAACGACGGAGATGGCTTG 3318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThr1leAla 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spytek, K.A., Li, L., Wolenc, A.R., Vernet, C.A., Eisen, A., Liu, X., Malyankar, U., Shimkets, R.A., Tchernev, V.T., Spaderna, S.K., Gorman, L., Kekuda, R., Patturajan, M., Gusev, V., Gangolli, E.A., Guo, X., Shenoy, S., Raelli, L., Casman, S.J., Boldog, F., Burgess, C.E., Edinger, S., Ellerman, K., Gunther, E., Smithson, G., Millet, I. and Macdougall, J.R.
Proteins and nucleic acids encoding same
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/gene="Doc4"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2266 TGGACGGGCCCAGCCTGTAATCAGAGAGCCTGCCACCCCGCTGTGCCGAGCACGGGCC
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Sequence 35 from Patent WO02062999.
AX662353
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Matches:
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Proteins and nucleic acids encoding same
Patent: WO 02062999-A.37 15-AUG-2002;
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Sequence 37 from Patent W002062999.
AX662355.1 GI:29163217
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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ENTEKGPPLHCSSASSSPVDSPYSPPSHAANOSGRLLGNSGAQAGRDSESEDEFGPN
SFLVKTGSGNVCTPAAATANGSFQNNISRLRTPBPLPLFHSFSCHHTASIGSLSRSN
YTQRSNPSPAPTDSSARNBGSFQNISSRAQDINKLLNSNVPLETRNIAKGTELETLQD
NFIEMDILATARRDGAYTDGHFLFKFQGTSPLYCTTSPGYPLISSTVYSPPPRPLPRN
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LKAFDQDSRLAYGSRVKDLVHHEADEFSRQGPDFSLRDMAFGDPVPPHMGAYRTEMGL
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Sequence updated (29-Jun-1999).
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
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CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrIleAla
                                                                                                  CysAsnGlyAsnGlyArgCysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeu
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/protein_id="BAA81893.1"
/db_xref="G1:5307785"
                                                                                                                                                                                                                                                                                                                                  2566 AATGAAGGGATGGACTCATT 2586
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musculus Doc4"
                                                                              HisTyrLeuAspArgValVal---
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/gene="ten-m4"
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CTIEGCPGLCNGNGRCTLGNNGWYCVOQLGRRGAGCDTSMETACSDGKDNDGDGLTDC MDPDCCLQASCHTTSLCVGSPDPLDIIQETQISSSLSTLQSFYQRIHFLVGRDSTHVI PDVNPFDGIHACVIRGQVVYNSDGTPLVGVNISFINKPAYGYTITRQDGSFDLVSNGGV AIGLRFRAPPITQEHTVMLPWGRFFVWDTIVWRHBVNDIPSCDLSSFTRPMPIVLPS PLTAFRGTCPFRGIVVPEIQTLQEEVRIPGTDMRLGYLSSRTSGYKSLLRITLHSTI ESCPDLILWEKRTAVLOGYETTASNIGGWSYDKHHALNIOSGILHKGNGENIFISQOP PVIGSIMGNGRRRSISCPSCNGLADGNKLLAPVALACGSDGSLYVGDFNYVRIFFTG NVTSVLELSNSPAHKXYLATSPVSGWLYLSDTSSRKVFKVKSLYAVKDVAKNLELVAG TEDQCLEYDETRCGDGGKAVEATLTNERGITVDKYGVIFFVDGTMIRRIDDNGIISTL
IGFNDLTSARPLSCDSVMDISQVRLEWPTDLAVSPMDNSLYVLDNNVVLQISSNHQVR
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GRGDLSSITDKNKNRVSIRRDSTGLPLMLMGPDGQTFWFTWGLTYNFTYS CMCHSGWKGSECDVPTNQCIDITCSGHGTCIVGTCICNPSYKGENCEEVDCLDPTCSG LCAADCGGHGICVAGSCRCDEGWMGTGCEQRACHPRCSEHGTCKDGKCECSPGWNGEH WITHGSSGLLATKSNEDGWSTFYEYDNYGRLINVTYPFGRVSSYRTDSDSTYRVOTE
GSNKEDITYTNLSASGTFYTLMQDQVRNSYYIGLDGSLRIVLANGWEVSLHTEPHLL
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RMEYDQNGRITSKIFADGKSWSYTYLEKSWYLLLYSQRQYIFEFDKNDRLSSVTMPNV RGVCVRGECHCFVGWGGPGCESPRASCMEQCSGHGSFLADTNTCNCDHNWTGHDCSTE PFSLMKVHLMVAVEGRLFRKWFSAAPNLSYDFVWDKTDVYSQKVYGLSEAFVSVGFEY ARQTLĒTTRSIGYYRNTYRPEGNATVLQDYSEDGLĪLĢTIHGTGRRVIYKYGKLSR LLEILYDTRIAFSYDGSAGMLKTVGLGSEGFACTIRYRQIGPLIDRQIFRFSEEGMV NARPIYNYSRVTSMQAVINETPLPIDIXKYDDVSGKTEQFGKFGVIYYDINQIIT TAVMTHTKHPDAYGRVKEVQYEIFRSIMYMMVQFDMGKRVVAKELKYGFYANTTRYA YEYDADGOLQVVSINDKFLMRYSYDLMGNILHLLSPGNSARLTPLRYDIRDRITRLGDV QYRLDEDGFLRQRGNDFFEYNSAGLLVKTYNKVNGWTIKYRYDGLGRRVSSRSTQGHH LQFFYADLSSPTRVTHMYNHSSSEITSLYYDLQGHLFAMFLSSGDEFYVACDNIGTPL AVFSGAGLMIKQILHTAFGEVYLDSNPSFOLVĪGYOGGLYEBLTKLVHMGRRDYDVLA GRWTTPDHDIRKRLNSDNIVPFNLYMFKNNNPLSNSQETKCYMTDVNSMLVTFGFQLY NVIPGYRKFVTDAMEPSYELVHTQIKTQEWDSTKSVLGVQCEVQRQLKSFVRLERFGQ KASYLQDLHFTIAGLDTHYFVKSGLVEGDLSLLGMTVCQRTLETGVNVTVSQVMWLG GRSRRITDIQMQYGTLSLNVRYGSSVDEEKVRVLELARQRAVATAWAHERHRLRQGEE IYSASDSGCPPTPLHTLFATGTSLFGKGVKVAIREGRVEADIISLANEDGRRIAAVLD GSRAWIDGERQQLLSSGRVQGYEGFYIVSVDQFPELTDNINNVHFWRQTEMGRR"

Conservative: Mismatches: Length: Matches: Indels: 3.16e-33 503.50 85.00% 81.00% Percent Similarity: Best Local Similarity: Alignment Scores: Best Local S Query Match: Pred. No.: Score:

ORIGIN

US-10-029-020-14\_COPY\_750\_850 (1-101) x AB026980 (1-9264)

1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr 20	2783 TGGATGGGCACCGGGTGCGAGCAACGGGCTTGTCACCCTCGCTGCAGCAAAGACACGGGACC 2842	21 CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrlleAla 40	2843 TGCAAGGACGAAAGTGCGAATGCAGCCCGGGATGGAATGGAGAACACTGCACTATC 2899	41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg 60	
TrpMetG1	TGGATGGG	CysArgAs	TGCAAGGA	HisTyrLe	!
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CysAspThrSerMetGluThrAlaCysGlyAspSerLysAspAsnAspGlyAspGlyLeu 100 81 g à

CysThrieuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGlyAlaGly

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2996 TGCGACACATCAATGGAGACGGCCTGCAGTGACGGCAAAGGACAATGATGGAGATGGGTTG 3055

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ITSNISSIDSFYTMVODQLRNSYQIGYDGSLRIFYASGLDSHYQTEPHVLAGTANPTV
AKRNMTLPGENGONLVEWRFRKEQAQGKVNVFGRKLRVNGRNLLSVDFDRTTKTEKIY
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/db_xref="GI:6760369"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                    AF195418
AF195418.1 GI:6760368
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S Isogai, T. and Yamamoto, J.

E Isogai, T. and Yamamoto, J.

Direct Submission

Direct Submission

Submitted (15-07).

Exarusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

(Email:genomicsobri.or.jp, Tel:18-438-52-3976, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA inbrary construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5.- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

RAB; annotation: HRI and RAB.
               HOMOS SADIENS CDNA FLJ43881 fis, clone TESTI4009028, highly similar LO Mus musculus odd Oz/ten-m homolog 3 (Drosophila) (Odz3).
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                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="testis"
/clone_lib="TESTI4"
/note="cloning vector: pME18SFL3"
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Matches:
Conservative:
                                                                                                                       AK125869.1 GI:34532128
Oligo capping; fis (full insert sequence)
Chomo sapiens (human)
Homo sapiens
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Gaps:
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/db_xref="taxon:9606"
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VPPGIFWRSQLFIDQPQFLKFNISLQKDALIGVYGRKGLPPSHTQYDFVBLLDGSRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROD 27-JAN-2000
                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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/note="similar to the Drosophila melanogaster pair rule
CysAspThrSerMetGluThrAlaCysGlyAspSerLysAspAsnAspGlyAspGlyLeu
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S Ben-Zur,T., Feige,E., Motro,B. and Wides,R.
The mammalian odz gene family: Homologs of a Drosophila pair rr
gene with expression implying distinct yet overlapping
developmental roles

L Dev. Biol. 117, 107-120 (2000)

E 2 (bases 1 to 7816)
S Ben-Zur,T., Motro,B. and Wides,R.
Direct Submission

L Submitted (15-Or1-1999) Faculty of Life Sciences, Bar-Ilan
University, Ramat-Gan, Israel
University, Ramat-Gan, Israel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF195418 7816 bp mRNA
Mus musculus ODZ3 (Odz3) mRNA, partial cds.
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/codon start=2
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DNSFRVTSETAGVLKKVNLOSDGFICTIRYROIGPLIDROIR PRESDGMVNARPDYSY
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ALALHYRYGMTLDERGRALLDGARQRALARWAREQRYNDGEGGRIUMTEGERRQLL
SAGKVQGYDGYYVLSVUSYPELABSANNIQFIRQSEIGKR,"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1259 TGTGACGTAGCCCTTGTGTACAGACAGCAACAACAAGAAGAAGAAGAAGGACTC 1318
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGlyAlaGly
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Conservative:
Mismatches:
Indels:
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483.50
82.18%
77.23%
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Best Local Similarity:
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SOURCE
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TGTGACGTAGCCATGGAGACTCTTTGCACAGATAGCAAGGACAATGAAGGAGATGGACTC 2395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Obhashi, T. Zhou, X., Feng, K., Richter, B., Moergelin, M., Perez, M.T., Su, W., Chiquet-Ehrismann, R., Rauch, U. and Faessler, R.
Mouse Ten-m/Odz is a new family of dimeric type II transmembrane proteins expressed in many tissues
2. (Dases 1 to 8373)
                                                                                                                                                                                                                                                                                               21 CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThr1leAla 40
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Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (29-MR-1999) Toshitaka Oohashi, Okayama University
Medical School, Dept. Mol. Biol. & Blochem.; 2-5-1 Shikata-cho,
Okayama, Okayama 700-8252, Japan
(E-mail:oohashi@cc.okayama-u.ac.jp, Tel:+81-86-235-7128,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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77
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Mus musculus mRNA for Ten-m1, complete cds.
                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                                      Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa, Chordata,
Mammalla, Eutheria, Rodentia;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB025410
AB025410.1 GI:4760775
                                                                                                   3.94e-31
478.50
81.19%
76.24%
77.55%
.8487
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Best Local Similarity:
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2396 ATT 2398
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                                                                                     Alignment Scores:
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DB:
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ORGANISM
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AB025410
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AUTHORS
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JOURNAL
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80

2358 CACTACTTAGAT --- GCTGTTCGAGATGGATGTCCAGGGCTCTGCTTTGGAAATGGACGA

HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg

41

ò a à 셤 à

61

PRI 30-NOV-1999

AF100772 8297 bp mRNA linear Homo sapiens tenascin-M1 (TNM1) mRNA, complete cds. AF100772

AF100772.1 GI:6165844

Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

LOCUS

RESULT 15 AF100772

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Brandau,O., Schuster,V., Weiss,M., Hellebrand,H., Fink,F.M.,
Kreczy,A., Friedrich,W., Strahm,B., Niemeyer,C., Belohradsky,B.H.
and Meindl,A.

(bases 1 to 8297)

REFERENCE AUTHORS Epstein-Barr virus-negative boys with non-Hodgkin lymphoma are mutated in the SH2D1A gene, as are patients with X-linked lymphoproliferative disease (XLP) Hum. Mol. Genet. 8 (13), 2407-2413 (1999)

Tosses 1 to 8297)

The standau(), Ooblashi,T., Faessler,R. and Meindl,A.

Direct Submissel.

Submitted (22-OCT-1998) Medizinische Genetik, LMU-Muenchen,
Goethestr. 29, Muenchen 80336, Germany
Location Qualifiers

10556288

MEDLINE PUBMED

JOURNAL

TITLE

TITLE JOURNAL

FEATURES

AUTHORS

REFERENCE

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/map="Xq24-q25" 1. .8297

gene="TNM1" /gene="TNM1"

gene

CDS

. .8242

81 ÇysAspThrSerMetGluThrAlaCysGlyAspSerLysAspAsnAspQlyAspGlyLeu 100

gene CDS

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DVSGRTRQTGPLIGGGRRVLYKTWRHYKHTKI FNANQOVINETPLFLDLYRYV
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HGNSARLTPLRYDLRDRITRLGEIOYKMDEDGFLRQRGNDIEPRYNSUCLLQKAYNKVS
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FHGGLYDFLTKLVHLGQRDYDVVAGRWTTPNHHIWKQLNLLFKFNLYSFENNYPVGK
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MARQRAVAQAWTQEQRRLQEGEEGTRVWTEGEKQQLLGTGRVQGYDGYFVLSVEQYLE
LSDSANNIHPMRQSEIGRR"
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                                                                                                                                                                                                                                                                                                                                                                                            AYVIAVHLEGLTWOLOPVGOIYANGISNGNPCTESMDTTYSPIGGRVSDKSEKKVFOK
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2238 TGGGTAGGACCAACATGTGAGGAACGTTCCTGTCACTCTCACTGTGCTGAGCATGCCCAA 2297
                                                                                                                                                                           TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr 20
                                                                                                                                             US-10-029-020-14_COPY_750_850 (1-101) x AB025410 (1-8373)
                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                        3.37e-30
467.50
83.00%
72.00%
                                                                      Percent Similarity:
Best Local Similarity:
                           Alignment Scores:
Pred. No.:
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                                                                                                      Query Match:
ORIGIN
                                                            Score:
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21 CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrlleAla 40

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RSMTTRSQPSPAAPPTSTQDSVHLHNSWYLNSNIPLETHHSLFKHGSGSSAIFSAA
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ANYIAVHLFGITWQLQPVGELYANGVSKGNKGTESMOTTYSPIGGKVSBKKVFC
KGRAIDTGSVDIGAQVWQTIPPGLFWRFQTITHHPYYLKFNISAKOSKSEKKVFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSTHTOFDEWILDOWCKOLWKODSKGSDDTQHSPRNILLTSIQETGFTEYMDGOPWYLA PYNDGKKMEQVFVLTTAIEIMDCSTNCNCHGECISGHCHCPFGFLGPDCARDSCPVL CGCNGBYEKAHCVCRHGWKOPECDYPEGCISGHCTCHGHCTCLWGVCICVPGFLCBEICE EEDCLDDPDSNGSIGICYCKGFTCTGHGTCIMGVCICVPGFLCBFCCFTCHGTCIMGVCICVPGFLCATCHGTCTGHGTFLLDAGVCSCD KWTGSDCSTFELCTWECGSHGVCSRGICCCEGGWVGPTCEERSCHSTTEHGGCKDGK
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MEMLCGDNLDNDGDGLTDCVDPDCCQQSNCYISPLCQGSPDPLDLIQQSQTLFSQHTS
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Function="putative receptor molecule"

PROCOINET SPNPTVLPESTERMILENSE FEREALLINE INVECTOR VERY VEAL STARS
PROCOINET SPNPTVLPESTERMINET SPNPTVLPERGESCHERTTORWEPALINLYYTEANNYTET
YGWYWGLAEALLVYYTET INVGMINYHLTVANDGRITORWEPALINLYYTEANNYTDI
YGWYWGLAEALLVYYTET INVGMINYHLTVANDGRITORWEPALINLYYTEANNYTDI
YGWYWGLAEALLVYYTET INVGMINYHLTVANDGRITORWEPALANGHEINP
OSGITHKGMIGENMET EPSGNSVS ILEIGISTSPAHKYYTAMDFWISELYLSDTWIRKYDI
IKSIVETROLSKNFEVVAGTGOCLPPOGOGRASEASLINSPRGITVDRHGETY
KYGLDMINKL DENAVITTYGSNGLYSTORGESCHOOTHEYNSKOALHSPINSE
GLLFTAETDERKVNRIQOTTWGSNGLYSTORGENOSTORTHYNDMIYETISSARALSVSHS
GLLFTAETDERKVNRIQOTTWGRITYTSROCHTUNDMIYETISSPARALSVSHS
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HAHTLMITTRDYYNFTYNSEGGLGATTSROCHTUNDMIYETISSPARALSVSH
HAHTLMITTRDYYNFTYNSEGGLGATTSROCHNUM GEVSSEHSDLEKLTKVELDTSNRENVLAGTNLTATSTTYLLKGENTGSTYRVNEDGSL RVTFASGMEIGLSSEPHILAGAVNPTLGKCNISLPGEHNANLIEWRQRKEQNKGNVSA RERRLARANNILSIDPDHITRYGKIYDDHRKFTLRILYDGYGRPILMSPVSRYNBVN ITYSPSGLVTFIQRGWNEKMEYDGSGKIISRTWADGKIWSYTYLEKSVMLLHSQRR YIFBYDQSDCLLGSVTWPSMVRHSLQYMLSVGYYRNIYTPPDSSTSFIQDYSRDGRLLQ TLHLGTGRRVLYKYTKQARLSEVLYDTTQVTLTYEESSGVIKTIHLMHDGFICTIRYR YYDGLGRRVASKSSLGQHLQFFVDATANPIRVTHLYNHTSSEITSLYYDLQGHLJAMB LSSGEEYYVACDNTGTPLAVFSSRGQVIKEILYTPYGDIYHDTYPDFQVIGFHGGLY DFLTKLVHLGQRDYDVVAGRWTTAYHHIWKQLNLLFKPFNLYSFENNYPVGKIQDVAK ELOKOLENPETEDET GETTEN FOR FATE DEBLALED I BLIMALOZIO, ALOEMONE DE LOKOLENPETEDEN GETTEN BENDEN I LIGOLOGI ALOEMONE DE LOKOLENPETEN GETTEN BENDEN BEN QTGPLIGRQIFRESEEGLVURRFDYSYNNFRYTSMQAVINETBLPIDLYRYVDVSGRT EQFGKFSVINYDLNQVITTTVMKHTKIFSANGQVIEVQYSILKALAYMMTIQYDBVVGR HGNMCIRVGVDANITRYFYBYDADGQLQTVSVNDKTQWRYSYDLNGDINLLSHGKSAR TISSNGVLKRVSAQGYNPALMTYPGNTGLLATKSNENGWTTVYEYDPEGHLTNÄTFPT YTTDIRSWLELFGFQLHNVLPGFPKPELENLELTYELLRLQTKTQEWDPGKTILGIQC LTPLRYDLRDRİTRLGEIQYKMDEDGFLRQRGNDIFEYNSNGLLQKAYNKASGWTVQY

Length:
Matches:
Conservative:
Mismatches:
Indels: 6.02e-30 464.50 82.00\$ 71.00\$ Similarity: Percent Similarity: Alignment Scores: Pred. No.: Best Local S Query Match: Score: NIBINC

US-10-029-020-14\_COPY\_750\_850 (1-101) x AF100772 (1-8297)

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2329 40 09 1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr 20 21 ÇysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrlleAla 2270 TGCAAAGATGAAAATGTGAGTGTAGCCCTGGATGGGAGGGCGACCACTGCACAATTGCT g ð d ð

2386 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg 2330 CACTACTTAGAT --- GCTGTCCGAGATGCCTGCCCAGGGCTCTGCTTTGGAAATGGACGA 41

> g δ П ð

81

Search completed: August 14, 2004, 11:51:47 Job time : 1808.37 secs

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AR025413 Mus muscu
AK67551 Sequence
AK60210 Sequence
AK6059485 Mus muscu
AJ279031 Gallus ga
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AX125869 Homo sapi
AB040888 Homo sapi
AX662357 Sequence
AX662355 Sequence
AX662355 Sequence
AX622513 Mus muscu
AB025412 Mus muscu
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AJ238613 Gallus ga
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AP000116 Homo sapi
AP01141 Homo sapi
AP02412 Homo sapi
AP02768 Homo sapi
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AX250063 Sequence
AX250066 Sequence
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AB026980 Danio rer
AX921803 Sequence
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AB032953 Homo sapi
AX250013 Sequence
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AC103323 Rattus no
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AL807754 Zebrafish
AL023878 Human DNA
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AX250067 Sequence
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-UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGN=15 - MODE=LOCAL
-OUTPWT=pto - NORM==crt - HEARSTIXE=500 - MINLEN=0 - MAXLEN=200000000
-USRE=US10029020 @CGN 1 1.19065 @TUNDAT - LOOPCH02 20275 - NCPU=6 - ICPU=3
-NO MMAP - LARGEQUERY - NEG SCORES=0 - WAIT - DSPBLOCK=100 - LONGLOG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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1 YIRRIFPSGNVTNILELRNK.....LLGSNDLTSARPLSCDSVMD 151
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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                  27-NOV-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          Gangolli, E.A., Patturajan, M., Vernet, C.A., Malyankar, U.M., Kekuda, R., Stone, D.J., Anderson, D., Shimkets, R.A., Burgess, C.E., Zerhusen, B.D., Liu, X., Spytek, K.A., Casman, S.J., Boldog, F.L., Smithson, G., Li, L. and Ji, W.
Polypetides and nucleic acids encoding same
Patent: WO 02057455-A 13 25-JUL-2002;
Curagen Corporation (US)
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Matches:
Conservative:
Mismatches:
Indels:
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               8354 bp 1
Sequence 13 from Patent WO02057453.
AX556500
AX556500.1 GI:25899736
                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity:
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GIMSBRMEYDQAGRITSRIFADGKMMSYTYLEKSMVLHLHSQRQYIFEFDKNDFLSSV
TMPNVARQTLETIRSVGYYRNIYQPPEGNASVIQDFTEDGHLLHTFYLGTGRRVIYKY
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SLSGBPPAGSAQEPTHAQDNWLLNSNIPLETRNLGKQPFLGTLQDNLIBMDILSASRH
DGAYSDGHFLFKPGGTSPLFCTTSPGYPLTSSTVYSPPPRPLPRSTFSRPAFNLKKPS
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GHELAMMTXHGNSGLLATKSNENGWTTFYEXDSFGRLTNVTFPTGQVSSFRSDTDSSV
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EPHLLAGTVNPTVGKRNVTLPIDNGLNLVEWRQRKEQARGQVTVFGRRLRVHNRNLLS
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EEGMYNARFDYNYDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDI
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PHCGYSMGASSDADLEADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHE
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                                                                                                                                                                                                                                     Moergelin, M., Perez, M.T.,
                                                                                                                                         Sciurognathi; Muridae; Murinae; Mus.
                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                          Ochashi,T., Zhou,X., Feng,K., Richter,B., Moergelin,M., Perez,M.T
Su,W., Chiquet-Ehrismann,R., Rauch,U. and Faessler,R.
Mouse Ten-m/Odz is a new family of dimeric type II transmembrane
proteins expressed in many tissues
J. Cell Biol. (1999) In press
2 (bases 1 to 8585)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission Submission Submitted (29-MAR-1999) Toshitaka Oohashi, Okayama University Medical School, Dept. Mol. Biol. & Blochem.; 2-5-1 Shikata-cho, Okayama, Okayama 700-8252, Japan (E-mail:oohashi@cc.okayama-u.ac.jp, Tel:+81-86-235-7128,
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/db_xref="GI:4760782"
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                                                                                                     Chordata;
                                                                                                                                                   Rodentia;
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Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="Balb/c"
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Mammalia; Eutheria;
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Best Local Similarity:
Query Match:
       Stone, D.J.
                                                                                                                                               Scores:
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Spytek,K.A., Zhong,M., Gangolli,E.A., Burgess,C.E., Patturajan,M.,
Vernet,C.A., Taylor,S., Tchernev,V.T., Miller,C.E., Guo,X.,
Boldog,F.L., Grosse,W.M., Alsobrook,J.P., Gerlach,V.,
Edingermark,S., Rothenberg,M.E., Ellerman,K., Macdougall,J.,
Malyankar,U., Millet,I., Peyman,J., Smithson,G., Gunther,E. and
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                Length:
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Sequence 1 from Patent WO02055704.
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                                                                                                                                                              2.41e-77
767.00
99.34%
96.03%
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                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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DB:
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AX67551
LOCUS
DEFINITION
                                                                                                                                                             Pred. No.:
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VERSION
KEYWORDS
SOURCE
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      using the
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yue, H., Yao, M.G., Ison, C.H., Iu, Y., Warren, B.A., Elliott, V.S., Baughn, M.R., Ding, L., Xu, Y., Gietzen, K.J., Tang, T.Y., Lal, P.G., Duggan, B.M., Burford, N., Lu, D.A., Richardson, T.W., Tran, U.K., Khare, R. and Walla, N.K., Proteins associated with cell growth, differentiation, and death Patent: WO 02072810-A 22 19-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3764 TACATTAGAAGGATCTTCCCCTCTGGAAATGTCACCAACATCCTAGAGGGTCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                 3884 ATGAGTGGGCCGTCTTCTGACAGCAACAGCCGGCGGGTCTTTAAAATCAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrValValValuysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetSerGlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSer
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     methods of
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151
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     and
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Matches:
Conservative:
Mismatches:
Proteins, polynucleotides encoding them
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          same
Patent: WO 02055704-A 1 18-JUL-2002;
Curagen Corporation (US)
Location/Qualifiers
                                                                             1. .8438
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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WO02072830.
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Sequence 22 from Patent
AX600210
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759.50
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SPLTSFASSCAEKGP VPEIQALQEEIVIAGCKMKLGYLSSRYPGYKSVVRISLTHPT
IPFNLMKVHLMYAVEGRLFRKWFAAADDLSYYFIWDKTDVYNQKVFGLSEAFVSVGYE
YESCPDLILWEKRTAYLQGYEIDASKLGGWSLDKHTALNIOGGILHKGNGEBORFVSQQ
PPVIGSIMGORRESISCYSCNGLADGNKLLAPALTCGSDGSLYVGDFNYIRLIFPS
GNVTNILEMSHSPAHKYYLATDPMSQAYFLSDTNSRRYFKVKSTTVYKDLVKNSEVYA
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LLGSNDLJTSARPLSCDSVMEISQVRLEWPTDLAINPMONSLYVLDNNNVLQISENHQV
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SGRTRRYTDIQLQYRALCLNTRYGTTVDEEKVRVLELARQRAVRQAMAREQORLREGE
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PHCGYSMGASDADLEADTVLSPEHFYRLMGRSTRSGRSSCLSSRANSNLTLTDTBHE
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SFLYKSGSASLGVAANDHPSSLQNHPRLRTPPPPLPHTPNOHHAASINSLRRGNFT
PRSNPSPATDHSLSGEPPAGSAQEPTHAQDNWVLNSKIPVTRNCHFYDD
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DVGRRASQKIPPGTFWRSQVFIDHPVHLKFNVSLGKAALVGTYGRKGLPPSHTQLDFV
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VSFLTTALESVDNCPSNCYGNGDCISGTCHCFLGFLGPDCGRASCPVLCSGNGQYMKG
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SRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTFLPDTGLCNCDPSWTGHDCSI
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IPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFINNPLFGYTISRQDGSFDLVTNGG
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VTTGGEISLVAGAPGGCDCKNDANCDCFSGDDGYAKDAKLNTPSSLAVCADGELYVAD
LGNIRIRFIRKNKPFLNTQNMYELSSPIDQELYLFDTSGKHLYTQSLPTGDYLYNFTY
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ETSSKODYTITTHLSGSGAFYTLLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHL
LAGTVNPTVGKRNYTLPIDNGLNLVEWRQRKEQARGQVTVFGFRLRVHNRNLLSLDFD
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ERMEYDQAGRITSRIFADGROMSYTYLEKSWYLHLHSQRQYIFEFDKNDRLSSVTMPN
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VNARFDYNYDNSFRVTSMQAVINETFLPIDLYRYDDVSGKTEQFGKFGVIYYDINQII
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VOYKADEDGSLRORGGDVFEYNSAGLLIKAYNRASGASVRYRYDGLGRRVSSKSSHSH
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ECAADGGGGGGCOTCKCCECGEOGWIGAACDGAACHPROATSHETGCGDGKDNDGDGLVD
HCTIEGCPGLCNGNGRCTLDLNGWHCVCQLGWRGTGCDTSMETGCGDGKDNDGDGLVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MDVKERKPYRSLTRRRDAERRYTSSSADSEEGKGPQKSYSSSET"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to Drosophila melanogaster tenm/odz and
human gamma-heregulin; type II transmembrane protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1813. .1881
/gene="Doc4"
/note="putative; transmembrane-region site"
                                                                                                                                                                                                                                                                                                            /gene="Doc4"
/note="downstream of CHOP 4"
                                                                                                                                                                                                       /cell_line="NIH-3T3"
/note="tunicamycin-treated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAC31807.1"
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/mol_type="mRNA"
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'ceIl_line="NIH-3T3"
Location/Qualifiers
                                                                                                                                      strain="NIH/Swiss"
                                                                                                                                                                                                                                                                                                                                                                                                                         gene="Doc4"
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                                           source
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       FEATURES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 9722)
Wang, X. Z., Kuroda, M., Sok, J., Batchvarova, N., Kimmel, R., Chung, P., Zinszner, H. and Ron, D.
Zinszner, H. and Ron, D.
Enentification of novel stress-induced genes downstream of chop BMBO J. 17 (13), 3619-3630 (1998)
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Wang,X.-Z. and Ron,D.
Direct Submission
Submission
Submitted (14-APR-1998) Skirball Institute, New York University
Medical Center, 550 First Ave., New York, NY 10016, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValValLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 GlyalavalPheLeuSeraspSerasnSerargargvalPheLysileLysSerThrval
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144
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AF059485.1 GI:3170614
                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                   /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="incyte ID No: 7488573CB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 AlaArgProLeuSerCysAspSerValMetAsp 151
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       Location/Qualifiers
1. .8645
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AUTHORS
TITLE
JOURNAL
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SOURCE
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THENCL BEBGLANDAMES HOLT GROTTGTETDGCPDICARGRECTLGQUSMQ
CVCOTGWRGEDCHVANDETS CADNKONEGDGLVDCLOCDGCTCQUSILGRGSRDPL
DIQOSHSGSPAVKSFYDRIKLLVGKOSTHIL REGENEPNSSLYSLIRGQVVTTDGTPL
VGVNVSEYVKPFKOTTTRODGMFDLVANGGSSLTLHFERAPFMSGETVWLPWNSFY
AMDTLVWKTEENSI PSCDLSGFVRPDPV1 ISSPLAFERAPFMSGETVWLPWNSFY
AMDTLVWKTEENSI PSCDLSGFVRPDPV1 ISSPLAFERAPFMSGETVWLPWNSFY
AMDTLVWKTEENSI PSCDLSGFVRPDPV1 ISSPLAFFSDAPGRAPTVGFFLDFSNL
GGWSLDKHVLNVKSGILHKGNGFROPTTOGPSLILWEKRTALLGGFFLDPSNL
GGWSLDKHVLNVKSGILHKGNGFROPTTOGPSLTAMGNRRRSTSCPSCNGLAEG
NKLLAPVALATGIDGSLFVGDPVI IRR IFFSRNVTSI LELANKEFFHSNNPAHKY YLA
VDPVSGSLYVSDTNSRRIYKVKSLTGTKDLAGNSEVVAGTGEQCLPPDEARCGDGGRA
VDATLARS RGATAVDPWDNSTIRN IFFSRNVTSI LELANKEFFHSNNPAHKY YLA
VDATLARS RGATAVDPWDNSTIRN IFFSRNVTSI LIANDARDETGCNSWD
VSQYRLEWPTDLAVDPWDNSLYVLENNVILN ITAHLGNPUNGTGLAGASDCDCKN
DVNCKYCSGDDGFATDAILNSPSSLAVAPDCTI Y TADLGNIR IRAVSKNRP ILINS FNQ
YEAAS PGEGELYVFRADGILLNSFSSLAVAPDCTI Y TADLGNIR IRAVSKNRP ILINS FNQ
YEAAS PGEGELYVFRADGILLNSFSSLAVAPDCTI Y TADLGNIR IRAVSKNRP ILINS SVERS
TTFYDYDHGGRLTNVTRP TGVVT SLHREMEKS IT TID IENSKNDDDVTVI TNLSSVERS
TTFYDYDHGGRLTNVTRP TGVVT SLHREMEKS IT TID IENSKNDDDVTVI TNLSSVERS
TTFYDYDHGRRLTNVTRP TGVVT SLHREMEKS IT TID IENSKNDDDVTVI TNLSSVERS
TTFYDYDHGRRLTNVTRP TGVVT SCHREMEKS IT TID IENSKNDDDVTVI TNLSSVERS
TTFYDYDHGRLTNVTRP TGVVT SCHREMEKS IT TID IENSKNDDDVTVI TNLSSVERS
TTFYDYDHGRLTNVTRP TGVVT SCHREMEKS IT TID IENSKNEDDGKN
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AGABDGAAAPPAGRGWWTRNSSIDSGETEWGRKWTQEVPEOVFWRSQIHISQPQFLK
FNI SIGKDALFGYYIRGLPPSHAQYDFWERLDGKEKWSVUESPRERRSIQTILVQNEA
VFVQYLDVGLAHLAFATNBGKOKEWYSFSTVILDSVQDCPRNCHGNGECVGWYGFPPF
VFVQYLDVGLAHLAFACPVLCSGNGOYSKGTCLCVSGWRGPRCDVPISQCTDG
NCVCSIGYKGRNCEVCDPTCSNHGWVWGPECLCSGPWGGTNGELDRAGQCDQCSG
HGTYLSDTGLCSCDPWWGPDCSVEWCSVDGTHGWCIGGARCEGWTGYACDQRVC
HPRCTFHGTCKDGKCECREGWNGHCTIGRQTTGTFTDGCDDLCNGNGRCTLGQNSWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                    NKSDEENDFHTHLSEKLKDROTSWOOLABTKNSLIRRPIPPTSSSSLLPSAQLPSSHN
PPPVSCQMPLLDSNTSHQIMDTNPDBEBFSPNSYLLRACSGPQQASSSGPSNHHSQSTL
RPPLPPHNHSLSHHHSSANSLNRNSLTNRRNQIHAPAPAPNDLATTPESVQLQDSWV
LNSNVPLETRHFLFKTSSGTTPLFSSSSPGYPLTSGTVYTPPPRLLFRNTFSRNAFKL
                                                                                                                                                                                                                                                                                                                                                              translation="MDIKDRRHRSLTRGRCGKECRYTSSSLDSEDCRVPAQKSYSSSE
                                                                                                                                                                                                                                                                                                                                                                                    TLKAYGHDTRMHYGNRVSDLVHRESDEFPRQGTNFTLAELGICEPSPHRSGYCSDIGI
                                                                                                                                                                                                                                                                                                                                                                                                              LHQGYSLSTGSDADSDTEGGMSPEHAIRLWGRGIKSSRSSGLSSRENSALTLTDSDNE
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GVLKMVNLQSGGFSCTIRYRKIGPLVDKQIYRFSEEGMVNARRPYTHDNSFRTASIK
PIISETPLPVDLYRYDEISGKVEHFGKFGVIYYDINQIITTAVMTLSKHFDTHGRIKE
VQYEMFRSLMYMMTVQYDSMGRVTKRELKLGPYANTIKYTYDYDGDGQLQSVAVNDRP
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GKGIMFAVKKGRVTTGISSIATDDSRKIASVLNSAHYLEKMHYSIEGKDTHYFVYKIGS
ADSDLVTLAMTSGRKVLDSGVNVTVSQPTLLINGRTRRFTNIEFQYSTLLINIRYGLT
ADTLDEEKARVLDQARQRALGSAWAKEQQKARDGREGSRVWTDGEKQQLLNTGRVQGY
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NHSNSEITSLYYDLQGHLFAMESSSGERYYVASDNTGTPLAVFSINGLMIKQLQYTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEIYYDSNPDFQLVIGFHGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTWWKNIGREP
APFNLYMFKSNNPLSNELDLKNYVTDVKSWLVMFGFQLSNIIPGFPRAKMYFVSPPYE
                             /db xref="taxon:9031"
/tissue lib="11 day and 14 day embryonic brain; 11 day
beryonic retina"
                                                                                                                                                                                                           function="pattern formation and neuronal development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8409
113
23
15
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                         /protein_id="CAC09416.1"
/db_xref="GI:10241574"
                                                                                                                                                                                                                                   codon_start=1
evidence=experimental
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'evidence=experimental
                                                                                                                                                                                                                                                                                         product="teneurin-2"
                                                                                                                             gene="TEN2"
                                                                                                                                                                                gene="TEN2"
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625.00
90.07%
74.83%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                              4569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProArgGly1leThrValAspLysPheGlyLeulleTyrPheValAspGlyThrMetlle 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGA279031
Gallus gallus partial mRNA for teneurin-2 (TEN2 gene), long splice
variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ArgArglleAspGlnAsnGlyIleIleSerThrLeuLeuGlySerAsnAspLeuThrSer 140
                                                                                                                                                                                                                                                           TyrileArgArgilePheProSerGlyAsnValThrAsnileLeuGluLeuArgAsnLys 20
                                                                                                                                                                                                                                                                                                                                                                              40
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae;
Phasianinae, Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tucker,R.P., Chiquet-Ehrismann,R., Chevron,M.P., Martin,D., Hall,R.J. and Rubin,B.P. Teneurin-2 is expressed in tissues that regulate limb and somite pattern formation and is induced in vitro and in situ by FGF8 Dev. Dyn. 220 (1), 27-39 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 8409)
Chiquet-Ehrismann, R.
Direct Submission
Submitted (13-SEP-2000) Chiquet-Ehrismann R., Cell Biology,
Friedrich Miescher Institute, Maulbeerstrasse 66, CH-4058 Basel,
SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 GlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThrVal
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/organism="Gallus gallus"
/mol_type="mRNA"
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                       GlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThrVal
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/db_xref="taxon:9031"
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WO0166747.
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1 TyrileArgArgIlePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLys  $20\,$ 

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Isogai,T. and Yamamoto,J.

Direct Submission

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Razusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Razusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Razusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Razusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Remail:genomics8hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Beconowy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5' = 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Byaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GPFANTTKYAYEYDVDGQLQTVYLNEKIMWRYNYDLNGNLHLLNPSNSARLTPLRYDL
RDRITRLGDVQYRLDEDGFLRQRGTEIFEYSSKGLLTRVYSKGSGWTVIYRYDGLGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YEYESCLDLTLWEKRTAILQGYELDASNMGGWTLDKHHVLDVQNGILYKGNGENQFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSSKTSLGQHLQFFYADLTYPTRITHYYNHSSSEITSLYYDLGGHLFAMEISSGDEFY
IASDNTGTPLAVFSSNGLMLKQIQYTAYGEIYFDSNIDFQLVIGFHGGLYDPLTKLIH
FGERDYDILAGRWTTPDIEIWKRIGKDPAPFNLYMFRNNNPASKIHDVKDYITDVNSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVTFGFHLHNAIPGFPVPKFDLTEBSYELVKSQQWDDIPPIFGVQQQVARQAKALLGU
GKMAEVQVSRRRAGGAQSWLWFATVKSLIGKGVMLAVSQGRVQTNVLNIANEDCIKVA
AVLNNAFYLENLHFTIEGKDTHYFIKTTTPESDLGTLRLTSGR"
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                     Tel:81-438-52-3913,
                                                                                                                                                                                                                                                                                                                                                       /note="Start codon is not identified."
/codon_start=3
/product="KIAA1455 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-029-020-14_COPY_1250_1400 (1-151) x AB040888 (1-5309)
                                                                                                                                                                                                                   clone_lib="pBluescriptII SK plus"
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Matches:
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Gaps:
                URL:http://www.kazusa.or.jp/huge,
                                                                                                                     organism="Homo sapiens"
                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fh16070"
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                              gene="KIAA1455"
                                                                                                                                                                                                                                                                                                      :1. .>5309
'gene="KIAA1455"
                                        Fax:81-438-52-3914)
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Direct Submission
Submitted (04-APR-2000) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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DNA Res. 7 (2), 143-150 (2000)
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Homo sapiens mRNA for KIAA1455 protein, partial cds.
AB040888
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25
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                     tissue type="testis"
/clone_lib="TESTI4"
/note="cloning vector: pME18SFL3"
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Mismatches:
Indels:
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Matches:
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clone="TESTI4009028"
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AB040888
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                                                                                                                                               3960 AGGAAAGTIGACCAAAAIGGAAICAIATCAACICIICIGGGCICIAACGAITIGACIICA 4019
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                        3840 CCGTTTGACGAGGCGAGATGTGGAGGGAAGGCCGTGGAAGCCACTCATGAGT 3899
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Miller, I. and Macdougall, J.R.
Proteins and nucleic acids encoding same Patent: WO 02062999A 41 15-AUG-2002;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 GlyAlaValPheLeuSerAspSerAspSerArgArgValPheLys1leLysSerThrVal
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    ProArgGly1leThrValAspLysPheGlyLeuileTyrPheValAspGlyThrMetile
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Indels:
                                                                                                                                                                                             Length:
Matches:
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                           AX662359 8487 bp
Sequence 41 from Patent WO02062999.
AX662359
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                            PropheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn
                                                                                101 proArgGlylleThrvalAspLysPheGlyLeuileTyrPheValAspGlyThrMetile
                                                                                                                                                                                      ArgarglleAspGlnAsnGlyllelleSerThrLeuLeuGlySerAsnAspLeuThrSer
61 ValVallysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu
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                                                                                                                                                                                                                                                                                                                                             Sequence 39 from Patent WO02062999.
AX662357
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Location/Qualifiers
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Best Local Similarity:
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Pred. No.:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           121 ArgArglleAspGlnAsnGlyIleIleSerThrLeuLeuGlySerAsnAspLeuThrSer
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Proteins and nucleic acids encoding same
Patent: WO 02062999-A 35 15-AUG-2002;
Curagen Corporation (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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1. 8675
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                                                    3836 CCGTTTGACGAGGCGAGATGTGGGGGATGGAGGCCCGTGGAAGCCACACACTCATGAGT 3895
                                                                                                 PAT 22-MAR-2003
                                 ProArgGlyIleThrValAspLysPheGlyLeulleTyrPheValAspGlyThrMetile 120
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3892 GGAGATCTGTACGTTCTGACACAACACCGGAGAATTTATGGCCCAAAGTCACTTACG 3951
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Proteins and nucleic acids encoding same Patent: WO 0206299A. 37 15-AUG-2002;
Curagen Corporation (US)
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Matches:
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Indels:
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                                                                                                                                                                   141 AlaArgProLeuSerCysAspSerValMet 150
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1. 8645
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Pred. No.:
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Nakajima, D., Kikuno, R., Ohara, R., Inamoto, S., Aizawa, H., Yuasa, S., Nakajima, D., Nagase, T., Ohara, O. and Koga, H.

Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse
KIAA-homologues complete nucleotide sequences of 400 mouse
KIAA-homologues conflicted by screening of terminal sequences of conflicted conflicted by screening of terminal sequences of conflicted conflicted partial sampled from size-fractionated libraries

M. Dasses 1 to 5804)

Direct Submission

N. Kikuno, R., Nagase, T., Ohara, O. and Koga, H.

Sobacatch, N., Kikuno, R., Nagase, T., Ohara, O. and Koga, H.

Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mail:mouse@kazusa.or.ip, Tel:al91-38-52-3918)

The CREATE program supported by Japan science and technology

corporation; cDNA full insert sequencing: Kazusa DNA Research

Institute; CDNA library construction, clone selection and 5'- &
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/gene="mKTAA1455"
/note="color in predicted by in silico analysis. Start codon is not identified."
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GNSGLLATKSDETGWTTFFDYDSEGRLTNVTFPTGVVTNLHGDMDKAITVDIESSSRB
EDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGSLRIFYASGLDSHYQTEPHVLAGTA
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                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/tissue Lype="brain"
/dev stage="adult"
/note="vector:modified pBC SK+"
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Mus musculus mRNA for mKIAA1455 protein.
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/gene="mKIAA1455"
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FLI_CDNA.
Mus_musculus (house mouse)
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DSQGRIVSRVPADGKTWSYTYLEKSMVLLLHSQRQYIFEYDMMDRLSAITMPSYARHT
MQTIRSIGYYRNIXNPPESNASIITDYNEEGLLLQTAFLGTSRRVLFKYRRQTRLSEI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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EHENRSDSESEQPSNNPGQPTLQPLPPSHKQHPAGHHPSITSLNRNSLTNRRNQSPAP
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SYXSPPTRPLPRNTLSRSAFKFKKSSKYCSWRCTALCAVGYSYLLAILLSYFTAMHLF
GLMWHLQOTENDTFRNGKYNSDTVPTNTVSLPSGDNGKLGGFTHENNTIDSGELDIGR
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GLDSHYQTEBHVLAGTANPTVAKRNWTLPGENGQNLVEWRFRKEQAGGKVNVFGRKLR
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GQLASIQRGTTSEKVDYDSQGRIVSRVFRADGKTWSYTYLEKSWYLLHSGORYFEYD
MWDRLSAITWESVARHTMOTIRSIGYYRNIYNPPESNASIITDVNEEGLLLQTAFELG
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Oohashi, T., Zhou, X., Feng, K., Richter, B., Moergelin, M., Perez, M., Su, W., Chiquet-Ehrismann, R., Rauch, U. and Faessler, R.
Mouse Ten-m/Odz is a new family of dimeric type II transmembrane proteins expressed in many tissues
J. Cell Biol. (1999) In press
(bases 1 to 8964)
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-MAR-1999) Toshitaka Oohashi, Okayama University
Medical School, Dept. Mol. Biol. & Biochem.; 2-5-1 Shikata-cho,
Okayama, Okayama 700-8252, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (E-mail:oohashi@cc.okayama-u.ac.jp, Tel:+81-86-235-7128,
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/dev_stage="adult"
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/strain="Balb/c"
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IKIGPFANTTKYAYEYDVDGQLQTVYLNEKIMĀRYNYDLNGNLHLLĀPSSSARLTPLR YDLADRITRLGDVQYRLDEDGFLRQRGTEIFEYSSKGLLTRVYSKGSGWTVIYRYDGL GRRVSSKTSTGQHLQFFYRADLTYPTRITHVYNHSSSETTSLYYDLQGHLFAMEISSGD EFYTASDNTGTPLAVESSNGLMLKOTQYTAYGEIYFDSNVDFQLVIGHFGGLYDPLTK LIHFGERDYDILAGFWTTPDIEIWKRIGKDPAPFNLYMFRNNNPASKIHDVKDYITDV NSWLVTFGFHLHNAIPGFPVPKFDLTEPSYELVKSQQWEDVPPTFGVQQQVARQAKE LISGGRMAEVQVSRRKAGAEQSWLMFATVKSLIGKGVWLAVSQQRVQTNVLNIANEDCI

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AP001141 Homo sapi
AP002412 Homo sapi
AP002489 Danio rer
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1 KINRIRQVTTSGEISLVAGA......SSKDDVTITTNLSASGAFYT 261
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                   - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                3470272 seqs, 21671516995 residues
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
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Sequence Sequence

Homo sapi

Sequence

Db 5042 TTGGCCATGATGACATACCATGGCAATTCCGGCCTTCTGGCAAACCAAAAGCAATGAAAAC 5101  Qy 201 GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAshValThrPhePro 220		Doldog, F. L., Grose, W. M., Alsobok, J. B., Gerlach, V., Boldog, F. L., Grose, W. M., Alsobok, J. B., Gerlach, V., Edingermark, S., Rothenberg, M. E., Ellerman, K., Macdougall, J., Malyankar, U., Millet, I., Peyman, J., Smithson, G., Gunther, E. and Stone, D.J.  TITLE Proteins, polynucleotides encoding them and methods of using the same JOURNAL Patent: WO 02055704-A 1 18-JUL-2002;  Curagen Corporation (US)	rce 18438 /organism="Homo sapiens" /nol_type="unassigned DNA" /do_xref="taxon:9606" t Scores: 2.96e-128 Length:	Score:     Percent Similarity: 100.00% Conservative: 0     Best Local Similarity: 100.00% Mismatches: 0     Query Match: 6 Gaps: 0     Obs. 0     Cars Copy_1490_1750 (1-261) x AX675551 (1-8438)	Oy 1 LysileAsnArgileArgGinValThrThrSerGlyGluileSerLeuValAlaGlyAla 20	TyralalysAspalalysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu 60
AX556500  AX556500  BS54 bp  DNA linear PAT 27-NOV-2002  DEFINITION AX56500  VERSION AX56500. GI:25899736  WERYMORDS  SOURCE  ORGANISM Homo sapiens (human) AX556500.1 GI:25899736  Homo sapiens (human) ORGANISM Homo sapiens (human)  REFERENCE  AUTHORS  REFERENCE  AUTHORS  A	Alignment Scores: Pred. No.: Score: Score: Score: Score: Score: Score: Score: Score: Score: Score: 1384.00 Matches: Conservative: Dest Local Similarity: 100.00\$ Mismatches: Ouery Match: 6 Gaps: 0	-10-029		81 LeuAsnThrGlnAsnMetTyrGluLeuSerSerProlleAspGlnGluLeuTyrLeuPhe	4802 GATACCACGGCAAGCACTGTACACCCAAAGCCTGCCACAGGAGACTACCTGTACAAC 121 PheThrTyThrGlyAspGlyAspIleThrLeuIleThrAspAsnAsnGlyAsnMetVal	DD 4922 AATGTCCGCCGAGACTCTACTGGGATGCCCCTCTGGCTGG

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differentially spliced"
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                                      4928 AATGICCGCCGAGACTCTACTGGGATGCCCCTCTGGCTGGTGGTCCCAGATGGCCAGGTG 4987
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Homo sapiens mRNA; cDNA DKFZp686K11107 (from clone DKFZp686K11107).
BX640737
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 8993)
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s. Wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
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Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
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The German Human cDNA Consortium
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Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                   US-10-029-020-14_COPY_1490_1750 (1-261) x AX600210
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Proteins associated with cell growth, differentiation, and death Patent: WO 02072880-A 22 19-SEP-2002; Inc. (US)
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|mol_type="unassigned DNA"
|do xref="taxon:9666"
|noTe="Incyte ID No: 7488573CB1"
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SLSGEPPAGSAQEPTHAQDNWLLNSNIPLETRNLGKQPFLGTLQDNLIEMDILSASRH
DGAYSDGHFLFKPGGTSPLFCTTSPGYPLTSSTVYSPPPRPLPRSTFSRPAFNLKKPS
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GHELAMMTHGNSGLLATKSNENGWTFFYEVDSFGRLINVTFPTGGVSFRSDTDSSV
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GIMBERMEYDQAGRITSKI FADGKUMSYYTLEKSNULHLHSQROYIFBEDKNDRLSSY
TMRNVARQTLETIR SYGYYRNIYQPPEGNAS VIQDFTBGHLLHFSCROYIGRENYYK
GKLSKLABTLYDTTKVSFTYDBTAGMLKTVNLQNEGFTCTIRYRQIGPLIDRQIFRFT
                        Cohashi,T., Zhou,X., Feng,K., Richter,B., Moergelin,M., Perez,M.T., Su,W., Chiquet-Ehrismann,R., Rauch,U. and Faessler,R.
Mouse Ten-m/Odz new family of dimeric type II transmembrane profesins expressed in many tissues
J. Cell Biol. (1999) In press
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PHCGYSMGASSDADLEADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHE
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EVVAGTGDQCLPFDDTRCGDGGKATEATLINPRGITVDKFGLIYFVDGTMIRRVDQNG
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NHQVRIVAGRPMHCQVPGIDHPLLSKVAIHATLESATALAVSHNGVLYIAETDEKKIN
RIRQVTISGEISLVAGAPSGCDCKNDANCDCFSGDDGYAKDAKLNTPSSLAVCADGEL
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SHSHHLQFFYADLINPTKVTHLYNHSSSEITSLYYDLQGHLFAMELSSGDEFYIACDN
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YDVLAGRWTSPDHELWKRLSSNSIVPPHLYMFKNNNPISNSQDIKCFMTDVNSWLLFF
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                                                                                                                                                                                                                                                                                  Submitted (29-MAR-1999) Toshitaka Oohashi, Okayama University Medical School, Dept. Mol. Biol. & Biochem.; 2-5-1 Shikata-cho, Okayama, Okayama 700-8252, Japan (E-mail:ochashi@cc.okayama-u.ac.jp, Tel:+81-86-235-7128, Fax:+81-86-222-7768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
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/tissue_type="brain"
/dev_stage="adult"
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GPQLHNVI PGYPKPDTDAMEPSYELVHTQMKTQEWDNSKSILGVQCEVQKQLKAFVTL
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                                                                                                                                                                                                                                                                                                 4721 CCCAGTGGCTGTGACTGTAAAATGATGCCAACTGTGACTGCTTCTCTGGAGATGATGGT
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Mismatches:
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SOURCE

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BICAADOCGGGGGTCRCEDGGWAGAACDQRACHPRCAEHGTCRDGKCECTPGWGGE
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TGDGDITHIIDNNGNMVNNYREDSTGMELMLVVDDGQVYWVIMGTNSALRSVTTGGHEL
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                                                                                        ROD 15-AUG-1998
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Zinszner,H. and Ron,D. Zinszner,H. and Ron,D. Identification of novel stress-induced genes downstream of chop 98315054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vanisher 1 to 9722)
Wang, X.-Z. and Ron, D.
Direct Submission
Submitted (14-APR-1998) Skirball Institute, New York University
Medical Center, 550 First Ave., New York, NY 10016, USA
Location/Qualifiers
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human gamma-heregulin; type II transmembrane protein"
                                                                                             linear
                                                                                                                            Mus musculus DOC4 (Doc4) mRNA, complete cds.
AF059485
AF059485.1 GI:3170614
                                                                                                  mRNA
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="NIH/Swiss"
/db_xref="taxon:10090"
/cell_line="NIH-3T3"
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                                                                                                  9722 bp
                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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LAGTVNPTVGKRNYTLPIDNGLNLVEWRQRKEQARGQVTVFGPRLRVHNRNLLSLDFD
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/gene="Doc4"
/note="putative; transmembrane-region site"
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Qy 2 Db 58 Qy 2			
	5878 ACTEGECCAGGTGAGGTTTCCGAAGCGATACAGACAGCTCAGTGCACGTGCAGGTGAGG 5937		
Qy 2 Db 59	241 ThrSerSerLysAspAspValThr1leThrThrAsnLeuSerAlaSerGlyAlaPheTyr 260 	ORIGIN	55.
Qy 2 Db 59		Alignment Pred. No. Score: Percent S:	Alignment Scores: Pred. No.: Score: Percent Similarity
RESULT 7 AB037723 LOCUS		Best Local Query Match DB:	Best Local Similar Query Match: DB:
DEFINITION ACCESSION VERSION	2 protein, partial cds.	US-10-	US-10-029-020-14_C
KEYWORDS SOURCE	·. iens	8 8	
ORGANISM	Sapiens Vota: Metazoa: Chordata: Cramiata: Varteheata.	<b>a</b> (	
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	à t	
AUTHORS TITLE	Nagase, T., Kikuno, R., Ishikawa, K.I., Hirosawa, M. and Chara, O. Prediction of the coding sequences of unidentified human genes.	g ò	63 TTAA 67 GlvA
JOURNAL	AVI. The Complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro DNA Res. 7 (1). 65-73 (2000)	qq	
MEDLINE PUBMED	20181126 10718198	ò	87 TyrG
REFERENCE AUTHORS	2 (12) 2 (12) Obara, O., Naqase, T. and Kikumo, R	qo	 183 TATG
TITLE	omission	à	107 LeuT
	oummitted (31-0AN-2000) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdminfoskazusa or in	qq	243 CTGT
	URL:http://www.kzzusa.or.jp/huge/, Tel:+81-438-52-3913, Fax:+81-438-52-3914)	ζŎ	127 GlyA
COMMENT FEATURES	On May 9, 2002 this sequence version replaced gi:7242958. Location/Qualifiers	දි	303 GGCG
source	18624 /organism≃"Homo saviens"	ò	147 ThrG
		qa	363 ACTG
	/clone="bf00104" /tissue_type="brain"	δ	167 ThrA:
	KPGW"	qu	423 ACCA
gene	cDNA sequence for KIAA1302."	λ	187 HisG
CDS	/gene="KIAA1302" <5903850	qq	483 CATG
	/gene="KIAA1302" /note="Start codon is not identified."	ζ	207 Glu-
	/codon_start=1 /product="KIAA1302 protein"	QQ	543 GA-C
	/protein_id="BAA92540.2" /db_xref="G1:20521828"	ò	208
	/translation="STERLDNKPETTRYDSFGRLTNVTFPTGQVSSFRSDTDSSVHVO VETSSKDDVTITTNLSASGAFYTLLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPH	QO	602 TTAG
	LIAGTVNPTVGKRNVTLPIDNGLNLVEWRQRKEQARGQVTVFGRRLRVHNRNLLSLDF DRVTTEKT YDDRKFKTRILYDQAGESEMSPSEMSRENMGVNVTYSPGGYIAGIQRGIM CDDMCVOAAATTERT TENEVERSENESSESSENMGVNVTYSPGGYIAGIQRGIM	δλ	
	SERVE LUÇAGKI ISKIFALGKI MATIYLEKSMULLLHSQRQYIFFEFDKNDRLSSVTMP NVARQILETIRSVGYYRNIYQPPEGNASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKL	qq	662 Trccc
	SKLAETLYDTIKVSFTYDETÄGMIKTINIQNEGFTCTIRYRQIGPLIDRQIFRFTEEG MVNARFDYVINDSFRYTSMQAVINETPLPIDLYRYDVSGKTERGFGKFGTYYDINQI ITTAVMIHTKHPDAYGRMKEVOYFEEG INVAMMYONDINGKTER VANDAVARIANDA	8	
	IIIONETTITUTTUTTUTTORIORENĀITETKRPIMINĀINMEKAAKKRPIKĀRĀKĀRĀKĀMĪJK	ΩP	722 GTAGA

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YSYEYDADGQLQTVSINDKPLWRYSYDLNGNIHLLSPGNSARLTPLRXDIRDRITRIG
DVQYKMDEDGFLRQRGGDIFEYNSAGLLIKAYNRAGSWSVRYRYDGLGRRVSSKSSHS
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LNHAHYLENLHFTIDGVGALCLAYTKYGFSSEGDLAILGISGGRRTLENGWVYTVSQINTV
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EBGLRAWTBGEKQQVLSTGRVQCSFFVISVEQYPELSDSANNIHFMRQSEMGRR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnSerAlaLeuLysSerValThrThrGlnGlyHisGluLeuAlaMetMetThrTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGln
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 112872)

S Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 112,872 genomic DNA of 11q14

L Published only in DataBase (1999)

2 (bases 1 to 112872)

B Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Submitted (11-NOV-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15; Kitasato, Sagamihara, Kanagawa 228-8555, Japan

(B-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923; Fax:81-42-778-9924)

On Sep 15, 2000 this sequence version replaced gi:8118885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALUUU/16 112872 bp DNA linear HTG 14-SEB-2000
Homo sapiens chromosome 11 clone CMB9-72M1 map 11q14, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                               AsnSerAlaLeuLysSerValThrThrGlnGlyHisGluLeuAlaMetMetThrTyrHis 187
                                                                                                                                                                                                                                                                                                                                                                                              GlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsnGlyTrpThrThrPheTyrGlu 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 CGAAGTGATACAGACAGTTCAGTGCATGTCCAGGTAGAGGACCTCCAGCAAGGATGATGTC 600
                                                                                                                                                                                AspileThrLeuIleThrAspAsnAsnGlyAsnMetValAsnValArgArgAspSerThr
                                                                                                                                                                                                           241 GACAICACACTCATCACAGACAAGAGGCAACATGGTAAATGTCCGCGGGAGACTCTACT
                                                                                                                                                                                                                                                                         148 GlyMetProLeuTrpLeuValValProAspGlyGlnValTyrTrpValThrMetGlyThr
                                                                                                                                                                                                                                                                                                 228 ArgSerAspThrAspSerSerValHisValGlnValGluThrSerSerLysAspAspVal
                                        121 GAGCTGTCTTCACCAATTGACCAGGAGCTCTATCTGTTTGATACCACCGGCAAGCACCTG
                                                                                                                                     181 TACACCCAAAGCCTGCCCACAGGAGACTACCTGTACAACTTCACCTACACTGGGGACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrAspSerPheGlyArgLeuThrAsnValThrPheProThrGlyGlnValSerPhe
                                                                                          108 TyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsnPheThrTyrThrGlyAspGly
GluLeuSerSerProlleAspGlnGluLeuTyrLeuPheAspThrThrGlyLysHisLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 ThrileThribrashLeuSerAlaSerGlyAlaPheTyrThr 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 ACCATAACCACCAACCTGTCTGCCTCAGGTGCCTTCTACACA 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
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Center clone name: CMB9-72M1
------ Summary Statistics
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HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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Egala, T. and Yanamoto, J.

Elsogai, T. and Yanamoto, J.

Direct Submission

Losses (15-7012-2013) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Eubmitted (15-7012-2013) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of appan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- E 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                            Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S.,
Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,
Sugiyana, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Nagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A.,
Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K.
MEDO, human cDNA sequencing project
                                                                                                                                               PRI 09-SEP-2003
highly similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="cloning vector: pME18SFL3~mRNA from NT2 neuronal precursor cells treated 2-weeks mitotic inhibitor after 5-weeks retinoic acid (RA) induction.~majorly NT2 neuron"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                 mRNA linear
clone NT2RI3007095,
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                                                                                                                                                                  Homo sapiens cDNA FLJ45805 fis, clone NT2F to Mus musculus neuregulin 1 (Nrg1).

AK127705
AK127705.1 GI:34534730
Oligo cappien; fis (full insert sequence).
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db xref="reaxon:9606"
/clone="NT2R13007095"
/cell_line="NT2"
/cell_type="teratccarcinoma"
/clone_lib="NT2R13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
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75683. .89456
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89557. .99398
/note="assembly_fragment"
Sequencing vector: PCR products, 100% of reads Chemistry: Dye-terminator ET-amersham, 100% of reads Assembly program: Phrap, version 0.990329 Consensus quality: 111232 bases at least Q40 Consensus quality: 111769 bases at least Q30 Consensus quality: 1120%5 bases at least Q20 Consensus quality: 1120%5 bases at least Q20 Consensus quality: 1120%5 bases at least Q20 Consensus quality: 1120%5 bases at least Q20 Consensus quality: 0.000 pases; sum-of-contigs Quality coverage: 13.62x in Q20 bases; sum-of-contigs
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/note="assembly_fragment"
36955. .60659
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60760. .75582
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/note="assembly_fragment"
105325. .108843
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/note="assembly_fragment"
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/db xref="taxon:9606"
/chromosome="11"
/map="11q14"
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DRAFT SEQUENCE, 23 unordered pieces.
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1 (bases 1 to 165812)
Hattori,M., Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Pupiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Published Only in DataBase (2000)
2 (bases 1 to 165812)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
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                   Matches:
Conservative:
Mismatches:
  Length:
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HTG; HTGS PHASE1; HTGS_DRAFT.
HOmo sapiens (human)
Homo sapiens
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note="assembly_fragment clone_end:SP6 vector_side:right"
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                      Direct Submission
Submitted (08-FEB-2000) Masahira Hattori, The Institute of Physical
Submitted (08-FEB-2000) Masahira Hattori, The Institute of Physical
And Chemical Research (HIKEN), Genomic Sciences Center (GSC);
Attasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-855,
Japan (B-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997819.
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 Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini; Hominidae, Homo.

I (bases I to 170156)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Eujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Homo sapiens 170,156 genomic DNA of 11q

Published Only in Database (2000)

E (bases I to 170156)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

E Hattori,M., Tahii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Submisted (29-MAY-2000) Masamina Hattori, The Institute of Ehysical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Mitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, URL:http://App.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9923,
                                                                                                                                                  Homo sapiens chromosome 11 clone RP11-7H7 map 11q, WORKING DRAFT SEQUENCE, 18 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amerabam; 100% of reads Chemistry: Dye-terminator ET-amerabam; 100% of reads Chemistry: Dye-terminator ET-amerabam; 100% of reads Consensus quality: 159074 bases at least Q40 Consensus quality: 16480 bases at least Q30 Consensus quality: 167092 bases at least Q30 Insert size: 168455; sum-of-contigs Quality coverage: 5.57x in Q20 bases; sum-of-contigs
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Contact: hattori@gsc.riken.go.jp
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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Homo sapiens genomic DNA, chromosome 11q, clone:RP11-673F18,
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consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                            29785: contig of 29785 bp in length 29885: gap of 100 bp 52941: contig of 23056 bp in length 53041: gap of 100 bp 71728: contig of 18687 bp in length 71828: gap of 100 bp 87772: gap of 100 bp 102073: contig of 1844 bp in length 102173: gap of 100 bp 102173: gap of 100 bp 109422: contig of 7249 bp in length 109422: contig of 7249 bp in length 109522: gap of 100 bp 117522: 
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71149 TIGGCCATGATGACATACCATGGCAATTCCGGCCTTCTGGCAACCAAAAGCAATGAAAAC 71090
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SPLTYALDSTDDCPSNCFBADGVGSMOHCFPGFGBPCCSASGCPVLGSGNGQYLKGR
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RGVCVRGECHCFVGWGGPGCESPRASCMBQCSGHGSFLAADTNTCNCDHWWTGHDCSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (06-MAY-1999) Michihiro Mieda, Brain Science Institute,
RIKEN, Lab. for Developmental Gene Regulation; 2-1 Hirosawa,
Wako-Shi, Saitama 351-0198, Japan (E-mail:mieda@brain.riken.go.jp,
Tel:81-48-467-9713, Fax:81-48-467-9714)
Sequence updated (29-Jun-1999).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKVAQLIPPGIFWRSQVFIDHPMYLKFNVSLSKDALVGIYGRRGLPPSHTQFDFVELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mieda,M., Kikuchi,Y., Hirate,Y., Aoki,M. and Okamoto,H. Compartmentalized expression of zebrafish ten-m3 and ten-m4, homologues of the Drosophila ten(m)/odd Oz gene, in the central
                                                                                                                                         181 LeualaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn
                                                        TyrTrpValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGlu
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                                                                                                                                                                                                                                                                                                                                                           9264 bp mRNA Danio rerio mRNA for ten-m4, complete cds. AB026980
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Mech. Dev. 87 (1-2), 223-227 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Danio rerio"
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                                                                                                                                                                                                                             201 GlyTrpThrThrPheTyrGlu 207
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Danio rerio
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The bublished only in Database (2000)

E (bases 1 to 186084)

S Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Submitted (10-701-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-chou,Tsurumi,W., Yokohama, Kanagawa 230-0045, Japan (Email:hattorisquescriken.go.jp, URL:http://hgp.gsc.riken.go.jp/, On Mar 21, 2001 this sequence Version replaced gi:11071944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71689 AAGATCAACCGCATCAGGCAGGTCACCACTAGTGGAGAACTCTCACTGGTTGCTGGGGCC 71630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 ASPThrThrGlyLySHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn 120
                                                                                                                         Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates; Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrAlaLysAspAlaLysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LeuTyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 ProSerClyCysAspCysLysAsnAspAlaAsnCysAspCysPheSerGlyAspAspGly
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Matches:
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ECODILIMERRATATIOCETTASMIGGNEY DEMACRIAL TORNICAL AREDYNYDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEOFGKFGVIYYDINQIIT TAVMTHTKHEDAYGRVKEVQYEIFBSLMYMMAVQPDRMGKVAKELKVGPYANTTRYA PYEDADGQCYQVSINNKEPLMRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDV QYRLDEDGFLRQRGNDFFEYNSGALLVKTYNKONGWTIKYRYDGLGRRVSSRSTOĞHH LQFFYADLSSPTRVTHMYNHSSSEITSLYYDLQGHLFAMELSSGDEFYVACDNIGTPL AVESGAGIMIKQIIHTAFGEVYLDSNPSFQLVIGYQGGIYEPLIKLVHMGRRDYDVLA GRWTTPDHDIRKRLNSDNIVPFNLYMFKNNNPLSNSQETKCYMTDVNSWLVTFGFQLY NVIPGYRKPVTDAMEPSYELVHTQIKTQEWDSTKSVLGVQCEVQRQLKSFVRLERFGQ KASYLQDLHFTIAGLDTHYFVKSGLVEGDLSLLGMTVGQRTLETGVNVTVSQVMMVLG GRSRRITDIQMQYGTLSLNVRYGSSVDEEKVRVLELARQRAVATAMAHERHRLRQGEE IYSASDSGCPPTPLHTLFATGTSLFGKGVKVAIREGRVEADIISLANEDGRRIAAVLD AIGLRFERAPFITQEHĪLMLPWGRFFVMDTIVMRHEVNDIPSCDLŠSFTRPMPIVLPA PLTAPAGTCPERGIVVPEIQTLQEEVRIPGTDMRLGYLSSRTSGYKSLLRITLTHSTI PFSLMKVHLMVAVEGRLFRKWFSAAPNLSYDFVWDKTDVYSQKVYGLSBAFVSVGFBY MDPDCCLQASCHTTSLCVGSPDPLDIIQETQISSSLSTLQSFYQRIHFLVGRDSTHVI PDVNPFDGIHACVIRGQVVTSDGTPLVGVNISFINKPAYGYTITRQDGSFDLVSNGGV GSRAWIDGERQQILSSGRVQGYEGFYIVSVDQFPELIDNINNVHFWRQTEMGRR"

Length:
Matches:
Conservative:
Mismatches:
Indels: 5.15e-100 1103.00 90.04% 74.71% 79.70% Best Local Similarity: Query Match: Percent Similarity: Alignment Scores: Pred. No.: ORIGIN Score:

5254 5014 5074 5134 5194 PheThrTyrThrGlyAspGlyAspIleThrLeuileThrAspAsnAsnGlyAsnMetVal 140 AspThrThrGlyLysHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn 120 100 40 09 80 LyslleAsnArglleArgGlnValThrThrSerGlyGlulleSerLeuValAlaGlyAla ProSerGlyCysAspCysLysAsnAspAlaAsnCysAspCysPheSerGlyAspAspGly TyralalysaspalalysicuasnThrProSerSerLeuAlaValCysAlaAspGlyGlu LeuTyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe CTTTTTATCGCCGATTTAGGAAACATTCGTATTCGATATGTTCGTAGGAACAAAGCGTTC LeuAsnThrGlnAsnMetTyrGluLeuSerSerProlleAspGlnGluLeuTyrLeuPhe US-10-029-020-14\_COPY\_1490\_1750 (1-261) x AB026980 (1-9264) Gaps: 4955 5075 61 5135 5195 101 5255 121 21 41 81 임 Db g à Ωp  $\delta$ g δ ОD  $\delta$  $\delta$ à ŏ

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Eukaryotta, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musmanalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musmanalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musses, L. Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Earlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Cox, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcum Tansey, J., Gill, R., Houx, K., Houx, T., Houz, F., Haller, G., Hernandez, J., Hogues, M., Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R., Ness, E., McLeod, M.D., Marie, G., Morrels, S., Morgan, M., Marish, B., Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Wolley, K. and Gibbs, R., Scherer, S., Sodergren, E., Weinstock, G., Honnission Mus musculus 7 BAC RP23-8M3 (Roswell Park Cancer Institute Mouse BAC Library) complete sequence. Submitted (28-FEB-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA COLLEGE OF E8, 2001 this sequence version replaced gi:12963002. Sequencing is completed to a minimum standard of double strand Submitted (26-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 226256) 5375 AGCATCCGCAGAGACTCCACAGGCCTGCCACTCTGGTTAATGGGGCCCGATGGACAGACC 5434 141 AsnValargargaspserThrGlyMetProLeuTrpLeuValValProAspGlyGlnVal 160 240 TyrTrpValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGlu 181 LeualaMetMetThrTyxHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn :::|||:::|||||||||||||||::: 5495 ATCGCCGTCATGACGTACCATGGCAGCTCGGGCCTGCTGGCCACCAAGAGCAATGAGGAC GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu 241 ThrSerSerLysAspAspValThrIleThrThrAsnLeuSerAlaSerGlyAlaPheTyr Mus musculus (house mouse) Mus musculus AC073599.16 GI:13162472 (bases 1 to 226256) Worley, K.C. Direct Submission Unpublished Worley, K.C. Direct Subm 5735 ACG 5737 161 201 261 221 AC073599/c LOCUS DEFINITION ORGANISM TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS a d  $\overset{>}{\circ}$ g à 엄 ò q 셤 à à à

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                                                                                                                                                                                              .14614
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:756<u>9</u>.
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coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
                                                                                                                                                                  Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.
                                                                                                                    Sequence similarities were identified using Powerblast by Jinghui
                                                                        The repeat regions shown were identified using RepeatMasker by
                                                                                                                                                                                                                                                                                                                          complement(147..670)
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musculus cDNA: BF124644"
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In toases I to 245/21,

In toases I to 245/21,

In toases I to 245/21,

Anylan, H., Alsbrooks, Anin, A., Angulano, D.,

Anyalebechi, Y., Aoyagi, A., Angulan, A., Angulano, D.,

Anyalebechi, Y., Angadi, A., Angulan, B., Baden, H.,

Baldain, D., Bandaranike, D., Barber M., Barastead, H., Benahmed, F.,

Baldain, D., Bandaranike, D., Barber M., Bayah, Brown, M.,

Gardenas, V., Carter, K., Cavazos, I., R., Chen, Y., Chen, Y.,

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Kapath, S., Kelly, S., Kelly, S., Khan, Z., King, L., Li, Li, L.,

Ini, W., Liu, W., Liu, Y., Marrin, R., Marcine, R., Marcine, R.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (05-MR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
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3 (bases 1 to 245722)
Rat Genome Sequencing Consortium.
                      Rattus norvegicus (Norway rat)
Rattus norvegicus
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Worley, K.C.
                                                                                                                                          (bases 1 to 245722)
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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    KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33926 AAGATCAATCGCATCAGCAGGTCACTACAAGTGGTGAGATCTCACTGGTTGCTGGTGCC 33867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33746 CTCTATGTGGCCGACCTGGGAACATCCGAATTCGATTTATCCGGAAGAACAAGCCTTTC 33687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33626 GATACCAGTGGCAAGCATCTGTACACTCAGAGCCTACCCACAGGGGACTACCTGTACAAC 33567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245722 bp DNA linear HTG 15-NOV-2002 Attus norvegicus clone CH230-17M17, WORKING DRAFT SEQUENCE. AC120288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspThrThrGlyLySHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuTyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuAsnThrGlnAsnMetTyrGluLeuSerSerProIleAspGlnGluLeuTyrLeuPhe
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Matches:
Conservative:
Mismatches:
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complement (59294__39403)
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40007__40038
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36263. .36295
/rpt_family="(CCA)n"
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* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Losainon/Qualifiers
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads but he indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap, version 0.990329
Consensus quality: 23443 bases at least Q40
Consensus quality: 234913 bases at least Q20
Consensus quality: 256024 bases at least Q20
Estimated insert size: 256455; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                      Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine
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complement(240061..240644)
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Center clone name: CH230-17M17
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cqn2_1/USB7D0_5900_1/USB020200_runat_06082004_112216_29275/app_query.fasta_1.3519
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                            August 13, 2004, 23:35:57; Search time 1786.37 Seconds (without alignments) 2450.585 Million cell updates/sec
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1 RLFRKWFAAAPDLSYYFIWD.....IQSGILHKGNGENQFVSQQP 101
     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                    using frame_plus_p2n model
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          3470272 seqs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Wang, X.Z., Kuroda, M., Sok, J., Batchvarova, N., Kimmel, R., Chung, P., Zinszner, H. and Ron, D.
Identification of novel stress-induced genes downstream of chop BMBO J. 17 (13), 3619-3630 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrGluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGln 60
Duggan, B.M., Burford, N., Lu, D.A., Richardson, T.W., Tran, U.K., Khare, R. and Walia, N.K.
Proteins associated with cell growth, differentiation, and death Patent: WO 02072830-A 22 19-SEP-2002;
Incyte Genomics, Inc. (US)
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Wang,X.-Z. and Ron,D.
Direct Submission
Submitted (H-APR-1998) Skirball Institute, New York University
Medical Center, 550 First Ave., New York, NY 10016, USA
Location/Qualifiers
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/note="Incyte ID No: 7488573CB1"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                       Gangolli, E. A., Patturajan, M., Vernet, C.A., Malyankar, U.M., Kekuda, R., Stone, D.J., Anderson, D., Shimkets, R.A., Burgess, C.E., Zerhusen, B.D., Liu, X., Spytek, K.A., Casman, S.J., Boldog, F.L., Smithson, G., Lil, and Ji, W. Polypetides and nucleic acids encoding same patent: WO 02057453-A 13 25-JUL-2002; Curagen Corporation (US)
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Yue,H., Yao,M.G., Ison,C.H., Lu,Y., Warren,B.A., Elliott,V.S.,
Baughn,M.R., Ding,L., Xu,Y., Gietzen,K.J., Tang,T.Y., Lal,P.G.,
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Sequence 13 from Patent WO02057453.
AX556500
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Sequence 22 from Patent AX600210
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Conservative: Mismatches: Indels:

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4249 GGCTATGAAATTGATGCCTCCAAGCTGGGGGGTGGAGTCTGGATAAGCACCATGCCCTG 4308

41 TyrGluTyrGluSerCysProAspLeulleLeuTrpGluLysArgThrThrValLeuGln 60

4189 TATGAGTATGAATCCTGCCCAGATCTGATCTGTGGGAGAAAAGGACAGGGGTGCTGCAG 61 GlyTyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu 4309 AACATCCAGAGTGGCATCCTGCACAAAGGGAATGGAGAGAACCAGTTTGTGTCCCAGCAG 4368

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81 AsnileginSerGlyIleLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGln 100

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IPFNLAKVHLMVAVBGRLFRKWFAAADDLSYYFIWDKTDVYNQKVFGLSRAFVGTYF
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PPVIGSIMGNORRRSISCPSCNGLADGNKLLAPVALTGGSDGSLYGGDRYTRSIFOS
GNYTNILEBRHERAHKYTLATDPMGSAPTSLDTNSRRYFKVKSTTVYKDLVKNSEVVA
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PHCGYSMGASSDADLEADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFLVKSGSASLGVAANDHPSSLQNHPRLRTPPPPLPHAHTPNQHHAASINSLNRGNFT
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ETSSKDDVTITTHLSGSGGAFYTLLQDQVRNSYYIGADGSLRLLLLANGWEVALQTEPH
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ELLDGRRLLTQEARSLEGPORQSRGPVPPSSHETGFIQYLDSGIWHLAFYNDGKESEV
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RCLGHSGWKGAECDVPTNQCIDVACSSHGTCIMGTCICNPGYKGBSCEEVDCMDPTGS
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AGRWTSPDHELWKRLSSNSIVPFHLYMFKNNNPISNSQDIKCPMTDVNSWLLFFGFQL
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SGRTRRYTDIQLQYRALCINTRYGTTVDEEKVRVLELARQRAVRQAMAREQQRLREGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to Drosophila melanogaster tenm/odz and
human gamma-heregulin; type II transmembrane protein"
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                                                                                                                                                                                      'note="tunicamycin-treated"
                                                                                                                                                                                                                                                                                                                                            'note="downstream of CHOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAC31807.1"
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/gene="Doc4"
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Oohashi,T., Zhou,X., Feng,K., Richter,B., Moergelin,M., Perez,M.T., Su,W., Chiquet-Ehrismann,R., Rauch,U. and Faessler,R. Mouse Ten-m/Odz is a new family of dimeric type II transmembrane proteins expressed in many tissues
                                                                              ROD 08-MAY-1999
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-MAR-1999) Toshitaka Oohashi, Okayama University Medical School, Dept. Mol. Biol. & Biochem.; 2-5-1 Shikata-cho, Okayama, Okayama, 700-8252, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (E-mail:oohashi@cc.okayama-u.ac.jp, Tel:+81-86-235-7128,
                                                                            linear
                                                                          AB025413 8585 bp mRNA ...
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2 (bases 1 to 8585)
Cohashi m
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Location/Qualifiers
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1. .8585
                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="Ten-m4"
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6.05e-58 544.00

Alignment Scores: Pred. No.:

Score:

ORIGIN

3671 GGCTATGAAATTGATGCCTCCAAGCTGGGGGGTGGAGTCTGGATAAGCACCATGCCTG 3730

3731 AACATCCAGAGTGGCATCCTGCACAAAGGGAATGGAGAGAACCAGTTTGTGTCCCAGCAG 3790

AsnIleGlnSerGlyIleLeuHisLygGlyAsnGlyGluAsnGlnPheValSerGlnGln

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3611 rargagrargaarccrgcccagarcrgarccrgrgggagaaaaggacagcggrgcrg 3670 3550 40 9 61 GlyTyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu 80 LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly TyrGluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGln US-10-029-020-14\_COPY\_1100\_1200 (1-101) x AB025413 (1-8585) 8585 999 0 0 0 Matches: Conservative: Mismatches: Indels: Length: 1.69e-57 540.00 98.02% 98.02% Best Local Similarity: Percent Similarity: Alignment Scores: Pred. No.: 3551 21 41 Query Match: Score: qq g qq  $\delta$ à à

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                            padigaru, M., Li, L., Zerhusen, B.D., Casman, S.J., Shenoy, S., Spytek, K.A., Zhong, M., Gangolli, E.A., Burgess, C.E., Patturajan, M. Vernet, C.A., Taylor, S., Tchernev, V.T., Miller, C.E., Guo, X., Boldog, F.L., Grosse, W.M., Alsobrook, J.P., Gerlach, V., Belingermark, S., Rothenberg, M.E., Ellerman, K., Macdougall, J., Malyankar, U., Millet, I., Peyman, J., Smithson, G., Gunther, E. and
                                                                                                                                                                                                                                                                                                                                         Proteins, polynucleotides encoding them and methods of using the
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MEVKERRPYRSLTSRRDTERRYTSSSADSEDGKINPKSYSSSET
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PHRDYSVSVASDADTETDGIMSPEHAVRLWGRSNTKSGRSSCLFSRANSNIJLTDTEH
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PLTAFAGTCPERGIVVPEIQTLQBEVRIPGTDMRLGYLSSRTSGYKSLLRITLHSTI
PFSLMKVHLMVAVEGRLFRKWFSAAPNLSYDFVWDKTDVYSQKVYGLSBAFVSVGFFY
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NVTSVLELSNSPAHKYYLATSPVSGMLYLSDTSSRRVFKVKKSLYAVKDVAKNLELVAG
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IVAGRPMHCQVPGLDHFLVSKIAIHATLESANALAVSHNGLLYIAESDEKKINRVRQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-MAY-1999) Michihiro Mieda, Brain Science Institute, KIKEN, Lab. for Developmental Gene Regulation; 2-1 Hirosawa, Wako-shi, Saitama 351-0198, Japan (E-mail:mieda@brain.riken.go.jp, Tel:81-48-467-9713, Fax:81-48-467-9714)
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mieda,M., Kikuchi,Y., Hirate,Y., Aoki,M. and Okamoto,H. Compartmentalized expression of zebrafish ten-m3 and ten-m4, homologues of the Drosophila ten(m)/odd Oz gene, in the central
                                                                                             linear
                                                                                         AB026980 9264 bp mRNA Danio rerio mRNA for ten-m4, complete cds.
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99425191
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mol_type="mRNA"

/db xref="taxon:7955"

dev stage="embryo"

1. .9264
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'db_xref="G1:5307785"
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/product="ten-m4"
                                                                                                                                                                                                                                                                                        Danio rerio (zebrafish)
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                                                                                                                                                                                                       AB026980.1 GI:5307784
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                                                                                                                                                                                                                                                                                                                                  Danio rerio
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                                                                                    AB026980
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                                                                                                                                                                                                                                                      ten-m4.
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RESULT
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RMEYDQMGRITEKT FRACKSWRYTYLEKSNWLLLYSQRQYYTE FEDEKUDRLS LKWUREDG
ARQTLETTRS IGYYRNTYR PEDGNATVLLUYSQRQYYTE FEDEKUDRLS SYTHMENV
ARQTLETTRR IGYYRNTYR PEDGNATVLQDYSEDGLLLQT IHQGTGRRUY YKYGKLSR
LLEI LYOTTR ARSYDESAGMKRYUGLSGRGACT RRYGJOFLIDRG I FRESEGRW
NARFDYNYDNS FRYNSGRQA VHET PLEI DLYXYDDYSGKTEQFGKFGVI YYDING I TAVWTHYHFDAYGRVEWGYAFLELKYGPYANTTRYP
TAVWTHYHFDAYGRVEROYFI FRSILMYWMMYQFDNMGRVYAKELKYGPYANTTRYP
YRYDADGCQUYSI NDRYFLWRYSYDLAGNIHLHLSFGNSARLTPLRYD I RDR TTRLGDY
OYRLDEDGFLRQRGNYDRYFYNSAGLLYKTYNKWWGYTI KYRYDGLGHH
LQFFYADLSSFPTRYHNYNGSSETTSLYYDLQGHLFAMELSGSGBFRYACDNI GTPL
ANDROGAGLHRAND REGEVYLDSNPSPGLYJGYGGGLYBPLTKLYHMGRRDYDVILA
                 GNIRIRYVRRNKAFLAPLNMYEISSPIDDELYLFDVAASHVFTQSLTTGDYLYNFTYS
GEGDLSSITDKNKNRVSIRRDSTGLPLMLMGPDGQTFWFTMGTNNALKSVAAQGQEIA
                                                                 VMTYHGSSGLLATKSNEDGWSTFYEYDNYGRLTNVTYPTGRVSSYRTDSDSTVRVQTE
                                                                                            GSNKEDITVTTNLSASGTFYTLMQDQVKNSYYIGLDGSLRLVLANGMEVSLHTEPHLL
                                                                                                              SGTVNPTISKRNVTLPIDNGLNLVEWRQRKEQARGQVTVYGRRIRVHNRNLLSNDFDR
VTRTEKVYDDHRKFTLRIHYDHAGRPTLWAPSSRLNGVNVTYSPGGHIAGIQRGTMSV
                                                                                                                                                                                                                                                                                                                                                                                                     NVI PGYRKPVTDAMEPSYELVHTQIKTQEWDSTKSVLGVQCEVQRQLKSFVRLERFGQ
IYSASDSGCPPTPLHTLFATGTSLFGKGVKVAIREGRVEADIISLANEDGRRIAAVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KASYLQDLHFTIAGLDTHYPVKSGLVEGDLSLLGMTVGQRTLETGVNVTVSQVNMVLG
GRSRRITDIQMQYGTLSLNVRYGSSVDEEKVRVLELARQRAVATAMAHERHRLRQGEE
GSRAWTDGERQQLLSSGRVQGYEGFYIVSVDQFPELTDNINNVHFWRQTEMGRR"
                                                                                                                                                                                                                                                                                                                                                                                 GRWTTPDHDIRKRLNSDNIVPFNLYMFKNNNPLSNSQETKCYMTDVNSWLVTFGFQLY
STNGEISLLAGAPSGCDCKNDANCDCYSGDDGYAKDAKLNAPSSLAVSPDGELFIADI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3926 TTTGAGTATGAATCCTGTCCAGATCTTAATCCTCTGGGAGAAGCGGACGACGGCTGTTCTGCAG 3985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3986 GGATACGAGACCACTGCGTCAAATCTTGGTGGCTGGAGTGTGGACAAACACCATGCGCTG 4045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GlyTyrGlulleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu 80
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S.,
Nakajima,D., Nagase,T., Ohara,O. and Koga,H.
Prediction of the coding sequences of mouse homologues of KIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ArgLeuPheArgLysTrpPheAlaAlaAlaProAspLeuSerTyrTyrPheIleTrpAsp
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                        Query Match:
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ORGANISM
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AF195418
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AEQSWLWFATVYKSLLGKGVWLAVSQGRVQTWVLM1ARBDCTKVKAVLMNAFYLENHHF
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MQFGALALHYRYGWTLDEEKKALLEQARQAKALARAWAREQQRVRDGEEGARLWTEGEK
RQLLSAGKVQGYDGYYVLSVEQYPELADSANNIQFLRQSEIGKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \bar{n}\text{octe="CDS} is predicted by in silico analysis. Start codon is not identified."
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gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries DNA Res. 10, 35-48 (2003)
                                                                                                                                                                                                                                                                             Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
The CREATE program supported by Japan science and technology
corporation; cDNA full insert sequencing: Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
3'-end one pass sequencing.
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ltoyhtvwipmnvfyvmdtlvmkkeendipscdlsgfvrpspiivssplstffrsspe
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                                                                                                                                          2 (bases 1 to 5804)
Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
Direct Submission
Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="adult"
/note="vector:modified_pBC_SK+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | product = "MKIAA1455 protein" | protein id="BAC65795.1" | db_xref="G1:28972758"
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Organism="Mus musculus"
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/db xref="taxon:10090"
/clone="mbg00055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="brain"
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JOURNAL
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Length: Matches: Conservative:

7.98e-47 454.00 91.09%

Score: Percent Similarity: Alignment Scores: Pred. No.:

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GTECDVPTTQCIDPQCGGRGICIMGSCACNSGYKGENCERADCLDPGCSNHGVCHGE
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Ben-Zur,T., Feige,B., Motro,B. and Wides,R.
The mammalian Odz gene family: Homologs of a Drosophila pair rule gene with expression implying distinct yet overlapping developmental roles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 AsnīlegļņSergļyiļeĻeuHisĻysGļyAsnGļyGļuAsņGļnPheValSerGļņGļņ 100
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                                                                                                                                                                                                                                                                                                         TyrgluTyrgluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGln
                                                                                                                                                                                                                                                                                                                                                                                               61 GlyTyrGlulleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu
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                                                                                                                                                       LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-007-1999) Faculty of Life Sciences, Bar-Ilan University, Ramat-Gan, Israel Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                   US-10-029-020-14_COPY_1100_1200 (1-101) x AK122513 (1-5804)
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Mus musculus ODZ3 (Odz3) mRNA, partial cds.
AF195418
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                    Indels:
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/organism="Mus musculus"
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2 (bases 1 to 7816)
Ben-Zur,T., Motro,B. and Wides,R.
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Mus musculus
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78.22%
82.70%
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AB025412

JAPANGELIPOCKWEPASCHILATEINIKUDANUGKYGISEAVUSUULUINIQAVIPEIMMUU
LMYAVUGRIEGOKWEPASCHILATEINIKUUDUNGUILYKGNGENQEISEAVUSUGYEEDELILI
WEKRTAVLQGYELDASNWGGWTLDKHHVLDVQNGILYKGNGENQEISEQDPOVUSSING
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NGRRESI SCPSCHOGADACOKALLAPVALACGIDSELYKGNGENQEISEQDPOVUSSING
SSUPAHRYTAATDPVTGOLLYSDTYRERIYERISTGARDLTKNAEVVAGTGEQCLPF
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HFDAHGRI KEILQYRTINNYTHINDENTILDIXQESSRESILYDS
TAVESTYDENGAVNARFDYST SPFLTQYHTVWIPWNVFYVMDTLVMKKEENDIPSCOLĞGFVRPSPIIVSSPLSTFFRS SPEDSPIIPFTQVLHEETTIFGTDLKLSYLSSRAAGYKSVLKIIMTQAVIPFNLMKVH LQTVYLNEKIMMRYNYDLNGNLHLLNPSSSARIJPLRYDLRDRITRLGDVQYRLDEDG FLRQRGTEIFEYSSKGLLTRVYSKGSGWTVIYRYDGLGRRVSSKTSLGQHLQFFYADL TYPTRITHVYNHSSSEITSLYYDLQGHLFAMEISSGDEFYIASDNTGTPLAVFSSNGL KFDLTEPSYELVKSQQWEDVPP1FGVQQQVARQARAFLSLGKVAAEVQVSRRKAGAEQS WLWFATVKSLIGKGVMLAVSQGRVQTNVLNIANEDCIKVAAVLNNAFYLENLHFT1BG KDTHVFIKTTTPESDLGTLRITSGRKALENGINVTVSGSTTVVNGRTRRFADVEMQFG ALALHVRYGMTLDEEKARILEQARQRALARAWAREQQRVRDGEEGARLWTEGEKRQLL SAGKVQGYDGYYULSVEQYPELADSANNIQFLRQSEIGKR" MLKQIQYTAYGEIYFDSNVDFQLVİGFHGGLYDPLTKLIHFGERDYDILAGRWTTPDI EIWKRIGKDPAPFNLYMFRNNNPASKIHDVKDYITDVNSWLVTFGFHLHNAIPGFPVP

7816 79 13 9 0 Conservative: Mismatches: Indels: Matches: Length: 1.1e-46 454.00 91.09% 78.22% 82.70% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: .. 0 N

1 ArgieuPheArgiysTrpPheAlaAlaAlaProAspieuSerTyrTyrPheIleTrpAsp US-10-029-020-14\_COPY\_1100\_1200 (1-101) x AF195418 (1-7816)

8

2188 40 9 2129 AAGACGGACGCATATAATCAGAAAGTCTACGGCTTGTCAGAGGCAGTTGTCCTCGCGGA 41 TyrdluTyrGluSerCysProAspLeulleLeuTrpGluLysArgThrThrValLeuGln LysThrAspValTyrAsnGlnLysValPheGlyLeuSerCluAlaPheValSerValGly 21 ð 셤 ð g

> à qq 8 g

2369 ĊĊŤ 2371 Pro 101 101 ð 임

RESULT

SATISTE TRELEGIAL LIGAGARIA KAUSARI LAGUAN GAUSA ULLILLISE EL LAMHLE
GLIWHLQOTERDITERIGINANDITYPPINTASIAL CANGAR LAGUAL LILLISE EL LAMHLE
GLIWHLQOTERDITERIGINANDITYPPINTASIAL CAGETHENNITISGELDI GR
RALQEVPEGI FWRSQLFIDOPQFLKFNI SLOKDALIGYGRKGLPPSHITOYDEVBLLD
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FISQQPPVSSI RIMGNRRRAISCSCECCCCCONTONING ROD 08-MAY-1999 Ochashi,T., Zhou,X., Feng,K., Richter,B., Moergelin,M., Perez,M.T., Su,W., Chiquet-Ehrismann,R., Rauch,U. and Faessler,R.
Mouse Ten-m/Odz is a new family of dimeric type II transmembrane proteins expressed in many tissues
J. Cell Biol. (1999) In press
J. (bases I to 8964) /translation="MDVKERRPYCSITKSRREKERRYTNSSADNBECRVPTQKSYSSS ETLKAFDHDYSRLLYGNRVKDLVHREADBYTRQGQNFTLRQLGVCESATRRGTAFCAB MGLPHRGYSISAGSDADTENBAVMSPBHAMRLWGRGVKSGRSSCLSSRSNSALTLTDT EHBNREDSESEGPSNNPGQPTLQPLPPSHKQHPAQHHPSITSLNRNSLTNRRNQSPAP Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. PAALPAELQTTPESVQLODSWVLGSSNVPLESRHFLFKTGTGTTPLFSTATPGYTMASG SVYSPPTRPLPRNTLSRSAFKFKKSSKYCSWRCTALCAVGVSVLLAILLSYFIAMHLF GDMDKALTYOIESSGREEDVSITSNLSSIDSFYTMVQDQLRNSYQIGYDGSLRIFYAS GLDSHYQTEPHVLAGTANPTVAKRNMTLPGENGQNLVEMRFRKEGAQCKVNVPFGRKLR VNGRNLLSVDFDRTTKTEKIYDDHRKFLLRIAYDTSGHPTLMLPSSKLMAVNVTYSST GQIASIQRGTTSEKVDYDSQGRIVSRVFADGKTWSYTYLEKSMVLLLHSQRQYIFEYD AKDLTKNAEVVAGTGEQCLPPDEARCGDGGKAVEATLMSPKGNAIDKNGLIYFVDGTM IRKVDQNGIISTLLGSNDLTSARPLTCDTSMHISQVRLEWPTDLAINPMDNSIYVLDN NVVLQITENRQVRIAAGRPMHCQVPGVEYPVGKHAVQTTLESATAIAVSYSGVLYITE TDEKKINRIRQVTTDGEISLVAGIPSECDCKNDANCDCYQSGDGYAKDAKLNAPSSLA ASPDGTLY1ADLGNIRIRAVSKNKPLLNSMNFYEVASPTDQELY1FDINGTHQYTVSL RIFPSGNVTSVLELRNKDFRHSSNPAHRYYLATDPVTGDLYVSDTNTRRIYRPKSLTG VTGDYLYNFSYSNDNDVTAVTDSNGNTLRIRRDPNRMPVRVVSPDNQVIWLTIGTNGC LKSMTAQGLELVLFTYHGNSGLLATKSDETGWTTFFDYDSEGRLTNVTFPTGVVTNLH Submitted (29-WAR-1999) Toshitaka Ochashi, Okayama University Medical School, Dept. Mol. Biol. & Biochem.; 2-5-1 Shikata-cho, Okayama, Okayama 700-8252, Japan (E-mail:oohashi@cc.okayama-u.ac.jp, Tel:+81-86-235-7128, linear musculus mRNA for Ten-m3, complete cds. organism="Mus musculus" /protein\_id="BAA77398.1" /db\_xref="GI:4760780" 8964 bp /db\_xref="taxon:10090" /tissue\_type="brain" Fax:+81-86-222-7768) Location/Qualifiers /dev\_stage="adult" 1. .8964 Mus musculus (house mouse) /product="Ten-m3" /mol\_type="mRNA" /strain="Balb/c" gene="ten-m3" /gene="ten-m3" /codon start=1 GI:4760779 2 (bases 1 to 8964) Ochashi, T. Direct Submission .8197 . .8964 AB025412.1 (sites) Ten-m3. LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM Source REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS JOURNAL gene CDS FEATURES TITLE

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DRQIFRFSEDGWINAREPDSYDDS PRVTSMQGVINETPLFLDLYQFDDISGKVBQFGK
FGVIYYDINQIISTRAWTYTRHFDBAIGRIKEIQYEIFERSLWWWITOVDDMGRATTREE
IKIGPRANTTKRYATEVDVGQLQTVINERKIMMRIVYDLNGNLHLLINPSSSARLTPLR
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RVRODEEGGARLWTEGEKRQLLSAGKVQQYDGTYVLSVEQYPELADSANNIQFLRQSEI
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highly similar
(Odz3).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
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Matches:
Conservative:
Mismatches:
Indels:
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Isogai, T. and Yanamoto, J.

Isogai, T. and Yanamoto, J.

Isogai, T. and Yanamoto, J.

In Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Submitted (15-JUL-2003) Takao 1892-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kendo human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA ilbrary construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Byaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB; annotation: HRI and ABB.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens mRNA for KIAA1455 protein, partial cds.
AB040888
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Mismatches:
Indels:
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Homo sapiens
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VSSPLEAGYTGEAGYKERPENSPMLAYTTIPETDLALSVISSRAGYKSVIRITWO
SIIPFNLMYWHLMVAAVORLEGWEPASPMLAYTFIWDTTDAYNOKYGLESPAVSVG
CYEYESCLDLTLWERRTAILGGYELDASNWGGWTLDRHYDANDWONGILYTRANG
GOPPWYSSINGMGRRBSISCPEGNGGADGWARCLLAPVALGCIDGSLIYGEDRYVRRIF
PGGNVTSVLELRNKDFRHRSNPAHRYLATDPVTGDLYVSDTNTRIYRPRSTITAM
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UGITBRRQVR.AAGRENGTGGGGAAVEATLASSRGMANOKNGILYTRTDE
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KTINRIRQVRTDGEISLVAGIPSCONDANCDCYGGGGGTYRDHYNGY
DGTTTANGTHOYTTGEISLVAGIPSCONDANCDCYGGGGGAKADALSAFBSSLAASP
DGTLYTRTDLGGRIFRRAVSRRNTLASINGSPRYANGYOLDENYVSPRGYTVSLUG
NYANESYSRONDITAAYTDSRGNTLASINGSPRYANDOLGHYNYGTGGCLED
SHYQTEBHULAGTAARTYARRANTLAGGENGONLVBRRFKERGORGKAVNTTGSRGN
MTAQCLELVLFTYHGNSGLLATKSDETGWTTFPDYDSGRLYINVTFPTGTGGLED
SHYQTEBHULAGTAARTYARRANTLAGGENGONLVBRRFKERGORGKAVNTTSSTQOL
ASIQRCTTSERVONDOGGRIVSRYDHTRYNYTSSTQOL
ASIQRCTTSERVONDOGGRIVSRYDHTRYNYTSSTQOL
ASIQRCTTSERVONDOGGRIVSRYDHYNYTYSSTQOL
ASIQRCTTSERVONDOGGRIVSRYDHYNYDYSSTQOL
ASIQRCTTSERVONDOGGRIVSRYDHYNDYTSSTQOL
ASIQRCTTSERVONDOGGRIVSRYDHYNDEGLILLGTRARQORYTERDWG
VLFKXRRQFRRYNDDOGGRIVSRYDHYNDRYDGGRIVGTTORYNMTONTYSSTQOL
TRYDINGSTRUNDITAATTANGTHYNDPERGNASITTONTNATGTORYNTTONTNATGTORYTTONTNATGTORYNTTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNATGTONTNA
                                                                                                                                                                                                                          Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
Submitted (04-APR-2000) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research, 1532-3, Yana, Kisarazu, Chiba
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
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GPFANTTKYAYEYDVDGQLQTVYLNEKIMWRYNYDLNGNLHLINPSNGARLPFRYDL
RDRITRLGDVQYRLDEDGFLRQRGTEIFEYSSKGLLTRVYSKGSGWTVIYRYDGGRR
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GRWAEVQVSRRAGGAQSWLWFATVKSLIGKGVMLAVSQGRVQTNVLNIANEDCIKVA
AVLNNAFYLENLHFTIEGKDTHYFIKTTTPESDLGTLRLTSGR"
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Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro DNA Res. 7 (2), 143-150 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="Start codon is not identified."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="KIAA1455 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_"fh16070"
/clone_lib="pBluescriptII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
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/gene="KIAA1455"
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             Length:
Matches:
Conservative:
Mismatches:
                                               Indels:
                                                       Gaps:
           9.71e-47
453.00
91.09%
77.23%
82.51%
                                                                     US-10-029-020-14_COPY_1100_1200
                                   Best Local Similarity:
Query Match:
DB:
                          Percent Similarity:
  Alignment Scores:
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Score:

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1 ArgieuPheArgiysTrpPheAlaAlaAlaProAspLeuSerTyrTyrPheIleTrpAsp
                                                                                                                      TyrGluTyrGluSerCysProAspLeulleLeuTrpGluLysArgThrThrValLeuGln
                                                                              Spytek, K.A., Li. L., Wolenc, A.R., Vernet, C.A., Eisen, A., Liu, X., Malyankar, U., Shimkets, R.A., Tchernev, V.T., Spaderna, S.K., Gorman, L., Kekuda, R., Patturajan, M., Gusev, V., Gangolli, E.A., Guo, X., Shenoy, S., Rastelli, L., Casman, S.J., Boldog, F., Burgess, C.B., Edinger, S., Ellerman, K., Gunther, E., Smithson, G., Millet, I. and Macdougall, J.R.
Proteins and nucleic acids encoding same
Pattert. WO 20262999-A 39 15-AUG-2002;
                                                            LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly
                                                                                                                                                                                 61 GlyTyrGlulleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu
                                                                                                                                                                                                      AsnIleGlnSerGlyIleLeuHisLysGlyAsnClyGluAsnGlnPheValSerGlnGln
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Mismatches:
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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sapiens
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                                                       PAT 22-MAR-2003
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Curagen Corporation (US)
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Sequence 35 from Patent WO02062999.
AX662353
AX662353.1 GI:29163216
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                            8645 bp | 1
Sequence 37 from Patent WO02062999.
                                                                                                           AX662355.1 GI:29163217
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Homo sapiens
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Best Local Similarity:
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3446 CCT 3448
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ACCESSION
VERSION
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SOURCE
ORGANISM
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DEFINITION
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VERSION
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JOURNAL
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LOCUS
                               RESULT 14
AX662355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 AsnileGlnSerGlyIleLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGln 100
                                     3390 GATGTACAGAACGGTATACTGTACAAGGGAAACGGGGAAAACCAGTTCATCTCCCAGCAG 3449
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Malyankar,U., Shimkets,R.A., Tchernev,V.T., Spaderna,S.K.,
Gorman,L., Kekuda,R., Patturajan,M., Gusev,V., Gangolli,E.A.,
Guo,X., Shenoy,S., Eastelli,L., Casman,S.J., Boldog,F.,
Burgess,C.E., Edinger,S., Ellerman,K., Gunther,B., Smithson,G.,
Miller,I. and Macdougall,J.R.
Proteins and nucleic acids encoding same
Patent: WO 02062999-A 41 15-AUG-2002;
Curagen Corporation (US)
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                  linear
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Conservative:
Mismatches:
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JOURNAL
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VERSION
KEYWORDS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Spytek, K. A., Li, L., Wolenc, A. R., Vernet, C. A., Eisen, A., Liu, X., Malyankar, U., Shimkets, R.A., Tchernev, V. T., Spaderna, S. K., Gorman, L., Kekuda, R., Patturajan, M., Gusev, V., Gangolli, E. A., Guo, X., Shenoy, S., Rastelli, L., Casman, S. J., Boldog, F., Millet, I. and Macdougall, J. R., Gunther, E., Smithson, G., Proteins and mucleic acids encoding same
Patent: WO 02062999-A 35 15-AUG-2002;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
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Search completed: August 14, 2004, 11:52:10 Job time : 1809.37 secs

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AK556500 Sequence
AK600210 Sequence
BK460712 Homo sapi
AK127101 Homo sapi
AK177101 Homo sapi
AK17551 Sequence
AK122490 Mus muscu
AK075413 Mus muscu
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=(Cqn2_1/USPTPO_spool/US10029020/runat_06082004_112216_29275/app_query.fasta_1.3519
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-DB=CenEmbl -QFMT=fastap -SUFFIX=p2n.reg -MINMATGH=0.1 -LOXOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPRT=ptc -NONN=ext -HEAPSIZE=550 -MINLEN=0 -MAXLEN=200000000
-USRS=US10029020 @CGN 1 119065_@runat_06082004_11221E_29275 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPBLÖCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1 YYIGADGSLRLLLANGMEVA.....YNRAGSWSVRYRYDGLGRRV
                 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                     - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3470272 seqs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                                                                                                                  970 ACCCTTCGGATTCTGTACGACCAGGCGGGCCGCCCAGCCTCTGGTCACCCAGCAGG 1029
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                                                                                                                                                                                                                    Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S.,
Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,
Sugiyama, T., Irie, R., Ocsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Sato, K., Nishikawa, T.,
Ximura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A.,
Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K.
NEDO, human cDNA sequencing project
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                         mRNA linear PRI 09-SEP-2003 clone NT2RI3007095, highly similar
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
Indels:
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Oligo capping; fis (full insert sequence)
Memo sapiens (human)
Homo sapiens
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Homo sapiens cDNA FLJ45805 fis, clo
to Mus musculus neuregulin 1 (Nrg1)
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Location/Qualifiers
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Isogai, T. and Yamamoto, J.
Direct Submission
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Best Local Similarity:
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Pred. No.:
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61 AlaargGlyGlnValThrVal 92 GCTCGGGGCCAGGTCACTGTC 81 SerLeuAspPheAspArgVal 	101 ThrLeuArgileLeuTyrAspGlnAlaGlyArgProSerLeuTrpSerProSerSerArg 120		9 2 2 2 2 9	241 HisThrPheTyrLeuGlyThrGlyArgArgVallleTyrLysTyrGlyDysLeuSerLys 260 [	12 ATTGGGCCCCTGATTGACCGACAGATCTTCCGCTTCACTGAGGAAGGCATGGTCAACGCC 62  21 ArgPheAspTyrAsnTyrAspAsnSerPheArgValThrSerMetGlnalaValileAsn 34  22 ArgPheAspTyrAsnTyrAspAsnSerPheArgValThrSerMetGlnalaValileAsn 34  23 CGTTTTGACTACAACTATGACACTCCGGTGACCAGCTGCAGGCTGTGATCAAC 633  41 GluThrColeudProlleAspLeuTyrArspAspAspValSerGlyLysThrGluGln 36  42 GluThrColeudProlleAspLeuTyrAraspTyrAspAspValSerGlyLysThrGluGln 36  43 GAGACCCCACTGCCATTGATCTCTATCGTATGATGATGATCAGGCAAGACAGAGAGAG
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Db   1930   GAGCTGAAGGTAGGACCCTACGCCAATACCACTACTACTACATGATATGATGATGATCAC   1989     Qy		521 AlaTyrAsnArgadeGeresteAnitiTiGAGIACAATICAGETGGCCTGCTAATICAGETGGCCTGCTGCTCATICAGETGGCCTGCTGCTCATICAGETGGCCTGCTGCTCATICAGETGAATGTyrAsgTyrAsgCTGCTGCTGGCTGGCTGGCTGGCTGGCTGGGGCTGGCTG	7 -	AUTHORS (angolli, E. A., Patturajan, M., Vernet, C.A., Malyankar, U.M., Kekuda, R., Stone, D.J., Anderson, D., Shinkets, R.A., Burgess, C.E., Zerhusen, B.D., Liu, X., Spytek, K.A., Casman, S.J., Boldog, F.L., TITLE Polypetides and uncleic acids encoding same JOURNAL Patent: WO 02057453.A 13 25-JUL-2002; FEATURES Location/Qualifiers Source /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Alignment Scores: Pred. No.: 2845.00 Aatches: Score. Bercent Similarity: 100.00\$ Marches: Percent Similarity: 100.00\$ Mismatches: 0 Conservative: 0 Conservati

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IleMetSerGluArgMetGluTyrAspGlnAlaGlyArgIleThrSerArgIlePheAla 160
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XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 7 (1), 65-73 (2000)
20181126
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Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
Pax:+81-438-52-3914)
On May 9, 2002 this sequence version replaced gi:7242958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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/clone="bf00104"
/clone lib="pBCSRPGW"
/note="This sequence was replaced that of fg06864 cDNA as a representative cDNA sequence for KIAA1302."
                               6631
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                   PheLeuArgGlnArgGlyGlyAspIlePheGluTyrAsnSerAlaGlyLeuLeuIleLys
                                                                                                                                                                                                                                                                        AspileArgAspArgileThrArgLeuGlyAspValGlnTyrLysMetAspGluAspGly
GluLeuLysValGlyProTyrAlaAsnThrThrArgTyrSerTyrGluTyrAspAlaAsp
                   GAGCTGAAGGTAGGACCCTACGCCAATACCACTCGCTACTCCTATGAGTATGTTGTTGA
                                                               GlyGlnLeuGlnThrValSerIleAsnAspLysProLeuTrpArgTyrSerTyrAspLeu
                                                                                                                            AsnGlyAsnLeuHisLeuLeuSerProGlyAsnSerAlaArgLeuThrProLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002 this sequence version replaced gi:7242958 Location/Qualifiers
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Homo sapiens mRNA for KIAA1302 protein, partial cds.
AB037723
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'codon_start=1
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/organism="Homo sapiens"
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Ohara, O., Nagase, T. and Kikuno, R.
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Homo sapiens
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JOURNAL
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(1-8624)

8624 541 0 0 0

Matches: Conservative: Mismatches: Indels:

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D à Length:

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NVAROTLETTR SUGYYRNIYOPPEGARSVIODFTEDGHLLHTFYLGTGRRVIYKYGKL
SKLAETLYDTTKVSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTEBG
WNARREDYNYDNSFRYTSMQAYINETPLDIDYRYDDVSGKTREGFGKFGKTYDYDINQI
ITTAVWTHTKJEDAYGRNKEVQYEIFRSLMYWMTUQYDNMGRVVKKELKVGFYANTTR
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LHNVIFGYPREDMDAMERSYELIHTQWKTGRWNNSKILGGCEVQRCKFYTTERF
                                                                                                  LLAGTVNPTVGKRNYTLPIDNGLNIVEWRORKEQARGOVTVFGRRLRVHNRNLLSLDF
DRVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTYSFGGYIAGIORGIM
SERMEYDQAGRITSRIFADGKTWSYTYLEKSMVLLLHSQRQYIFEFDKNDRLSSVTMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOLYGSTITSCOQAPKTKKFASSGSVFGKGVKPALKDGRVTTDIISVANEDGRRVAAI
ILMHAYLENIHFTIDGVDTHYEVKPGSBGDLALIGLSGGRRTLENGWVTVSCINTV
LNGRTRXTDIOLQYGALCINTRYGTTLDEEKARVLELARORAVRGAMAREQORINEG
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vetsskddvtittnlsasgafytllqdqvrnsyyigadgslrlllangmevalqteph
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PAT 14-FEB-2003
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                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                             Yue, H., Yao, M.G., Ison, C.H., Lu, Y., Warren, B.A., Elliott, V.S., Baughn, M.R., Ding, L., Xu, Y., Gietzen, K.J., Tang, T.Y., Lal, P.G., Duggan, B.M., Burford, N., Lu, D.A., Richardson, T.W., Tran, U.K., Khare, R. and Walla, N.K.
Proteins associated with cell growth, differentiation, and death Patent: Wo 02073310-A 22 119-SEP-2002;
Incyte Genomics, Inc. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValThrLeuprolleAspAsnGlyLeuAsnLeuValGluTrpArgGluArgLysGluGln
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db xref="taxon:9606"

/note="Incyte ID No: 7488573CB1"
                  AX600210
Seguence 22 from Patent WO02072830.
AX600210
                                                    AX600210.1 GI:28400252
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                                                                     Homo sapiens (human)
                                                                                        sapiens
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Best Local Similarity:
Query Match:
DB:
                                                                                    Homo
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                                                                                   ORGANISM
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                                                                                                                    REFERENCE
AUTHORS
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AsnValAlaArgGlnThrLeuGluThrIleArgSerValGlyTyrTyrArgAsnIleTyr
           GlnProProGluGlyAsnAlaSerValIleGlnAspPheThrGluAspGlyHisLeuLeu
                                                        1478 CAGCCCCCTGAGGGCAATGCCTCAGTCATACAGGACTTCACTGAGGATGGGCACCTCCTT
                                                                                     HisThrPheTyrLeuGlyThrGlyArgArgVallleTyrLysTyrGlyLysLeuSerLys
                                                                                                                                  LeuAlaGluThrLeuTyrAspThrThrLysValSerPheThrTyrAspGluThrAlaGly
                                                                                                                                                                             MetLeuLysThrIleAsnLeuGlnAsnGluGlyPheThrCysThrIleArgTyrArgGln
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/map="11q14.1"

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/tissue tVpe="human fetal kidney"

/clone lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host

DH10B; sites SfilA + SfilB"

/dev stage="fetal"
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GQVYWVTMGTNSALKSVTTQGHELAMMTYHGNSGLLATKSNENGWTTFYEYDSFGRLT
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RGQVTVFGRRLRVHNRNLLSLDPDRVTRTRKIYDDHRKFTLRILYDQAGRPSTWSPSS
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LHSQRQYIFBEDKNDRLSSVTMPNVARQTLETIRSVGYYRNIYQPFGGNASVIQDFTE
DGHLLHTFYLGTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGMLKTINLQREGFT
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DDVSGKTEOFGKFGYLYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIFRSLMYWMTV
QYDNMGRVVKKELKVGPYANTTRYSYEYDADGQLQTVSINDKPLWRYSYDLNGNLHLL
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GSWSNRYRYDGLGRRYSSKSSHSHHLQFFYADLTNPTKVTHLYNHSSSEITSLYYDLQ
GHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTDPNFQIII
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SNSQDIKCFWTDVNSMLLTFGFQLHNVIPGYPKPDMDAMEPSYELIHTQMKTQBWDNS
KSILGVQCEVQKQLKAFVTLERFDQLYGSTITSCQQAPKTKKFASSGSVFGKGYKFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone (DKFZp68KX1107) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottemburg, GERMANY; Email: clone@rzpd.de Purther information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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npmdnslyvldnnvvlgisenhqvrivagrpmhcqvpgidhfellskvalhatlesala
lavshngvlyiaetdekkinrirqvtysgeislvagapsgcdockndancdcfsgddgy
akdaklnntpsslavcadgelyvadlgnirirkrkrkpplntqnmyelsspidqelyl
                                                  HSM806812 8993 bp mRNA linear PRI 28-AUG-2003
Homo sapiens mRNA; cDNA DKFZp686K11107 (from clone DKFZp686K11107).
BX640737
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 8993). Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Well, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                       Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                            German Human cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="DKFZp686K11107"
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SVANEDGRRVAAILNHAHYLENI GVANTVSQINTVLNGRTRRYII AMAREQGRLREGEEGLRAWTEG FMRQSEMGRR" FPRGSEMGRR" FPRGSEMGRR" FPRGSEMGRR" FPRGSEMGRR" FPRGSEMGRR" FPRGSEMGRR" FPRGSEMGRR" FPRGSEMGRR" FPRGSEMGRR"	Descent Similarity: 2845.00 Matches: 541  Best Local Similarity: 100.00\$ Conservative: 0 Query Match: 100.00\$ Mismatches: 0 DB: 9 Gaps: 0  US-10-029-020-14_COPY_1760_2300 (1-541) x HSM806812 (1-8993)	LeualaasnGlyMetGluValala 20 	41 41 1288	80	Oy         81 SerLeuAspPheAspArgValThrArgThrGluLysIleTyrAspAspHisArgLysPhe 100           Db         1408 TCTCTGGACTTTGATGGCGTAACACGCACAGAGAACATCTATGATGATCACCACCGCAAGTTC 1467	Oy 101 ThrLeuArgileLeuTyrAspGlnAlaGlyArgProSerLeuTrpSerProSerSerArg 120	Oy 121 LeuAsnGlyValAsnValThrTyrSerFroGlyGlyTyrIleAlaGly1leGlnArgGly 140	Qy       141       IlemetSerGluArgMetGluTyrAspGlnAlaGlyArgIleThrSerArgIlePheAla       160         Db       1588       ATCATGTCTGAAAGAATGGAAIACGACCAGGCGGGCCGCATCACATCCAGGATCTTCGCT       1647	Oy 161 ASPGIYLYSTDRTRDSerTyrThrTyrLeuGluLysSerMetValLeuLeuLeuHisSer 180	Oy 181 GlnargGlnTyrIlePheGluPheAspLysAsnAspArgLeuSerSerValThrMetPro 200	Oy 201 AsnValAlaArgGlnThrLeuGluThrIleArgSerValGlyTyrTyrArgAsnIleTyr 220	Qy 221 GlnProProGluGlyAsnAlaSerVallleGlnAspPheThrGluAspGlyHisLeuLeu 240	Oy 241 HisThrPheTyrLeuGlyThrGlyArgArgVall1eTyrLysTyrGlyLysLeuSerLys 260	

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GluThrProLeuProlleAspLeuTyrArgTyrAspAspValSerGlyLysThrGluGln 360
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Direct Submission

Birect Submission

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

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MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA full insert sequencing: Rey Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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/clone lib="BRAWH3"
/note="cloning vector: pME185FL3"
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Matches:
Conservative:
Mismatches:
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99.82%
99.82%
                                                                                                                                                                                            (bases 1 to 3320)
                                                                                                                                                                   Unpublished
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GALCLNTRYGTTLDEEKARVLELARORAVROMAREGORLREGEEGLRAWTEGEKQOV
LSTGRVQGXDGFFVISVEQYPELSDSANNIHFNRQSEMGRR"
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Mismatches:
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Matches:
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/product="hypothetical_protein"
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FTLRILYDQAGRPSIMSPSSRLNGVNYTYSPGGYTAGIQRGTMSERMEYDQAGRTTSR
FFALGYMSYYYLEKSMVLLLHSQRQYIFEEDKNDRLSSYTMPNVARQTLETIRSVGY
YRNIYQPPGRARSYVLODFTEDGHLHTFYFTGTGRRVTYKYGKLSKATAETFYDTTKVGF
TYDETAGMLKTINLQPREGFTCTIRYRQGIGPLIDRQIFFTEEGMVNARPDNYPNSFR
                         HAMBU6114 3486 bp mRNA linear PRI 17-JUN-2003
Homo sapiens mRNA; cDNA DKFZp686D0412 (from clone DKFZp686D0412).
BX537983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone (DKFZPD866D0412) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="human cervix"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
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GRMKEVQYEIFRSLMYMMTVQYDNMGRVVKKELKVGPYANTTRYSYEYDADGQLQTVS
INDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDEDGFLRQR
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MEPSYELIHTQMKTQEWDNSKSILGVQCEVQKQLKAFVTLERFDQLYGSTITSCOQAP
KTKKFASSGSVFGKGVKFALKDGRVJTDIISVANEDGRRVAAILNHAHYLENLHFTID
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LYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKH
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3486)
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Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
   AlaTyrAsnArgAlaGlySerTrpSerValArgTyrArgTyrAspGlyLeuGlyArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Gunther, E.
                       and methods of
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Malyankar, U., Millet, I., Peyman, J., Smithson, G.,
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Matches:
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                                           Patent: WO 02055704-A 1 18-JUL-2002;
Curagen Corporation (US)
Location/Qualifiers
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/db_xref="taxon:9606"
                        Proteins, polynucleotides
                                                                                                                                                               4.2e-234
2821.50
98.72%
98.72%
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Best Local Similarity:
Query Match:
               Stone, D.J.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                 1265 TITGGGAAGTITGGTGTCATTTACTATGACATTAACCAGATCATCACCACACCAGTGTGTG
      MetLeuLysThrileAsnLeuGlnAsnGluGlyPheThrCysThrileArgTyrArgGln
                                                                                                                                                                                           PheGlyLysPheGlyVallleTyrTyrAsplleAsnGlnllelleThrThrAlaValMet
                                                                                                                                                                                                                                        ThrHisThrLysHisPheAspAlaTyrGlyArgMetLysGluValGlnTyrGluIlePhe
                  IleGlyProLeuIleAspArgGlnIlePheArgPheThrGluGluGlyMetValAsnAla
                                                                ArgPheAspTyrAsnTyrAspAsnSerPheArgValThrSerMetGlnAlaValIleAsn
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Okazaki, N., Kikuno, R., Ohara, R., Inamoto, S., Aizawa, H., Yuasa, S., Nakajima, D., Nagase, T., Ohara, O. and Koga, H.
Prediction of the coding sequences of mouse homologues of KIPA
gene: II. The complete nucleotide sequences of 400 mouse
KIPA-homologues ChNRs identified by screening of terminal sequences of CDNA clones randomly sampled from size-fractionated libraries
LDNA Res. 10, 35-48 (2003)
DNA Res. 10, 35-48 (2003)
SS (Azaki, N., Kikuno, R., Nagase, T., Ohara, O. and Koga, H.
Direct Submission
AL Sthered (07-FEB-2003) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
The CREATE program supported by Japan science and technology
corporation; cDNA library construction, clone selection and 5'- &
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GDITHTDNNGMWANVRRDSTGMELMLVPDFGQVSPREDTDSSVHVQVETS
SKDDVTITTNLSASGAFYTLADOVRNSYYTGADGSLALLLANGMFYALCYBFHLIAG
TVNPPVGKRNVLTPFIDNGLALVBWRQRKEARGQVTVFGRRLRVHRNLLSLDFDRVT
RTEXTYDDHRKFTLRILYDQAGRFSLMSFSRLNGVNVTVSPGGHTAGIQGITMSERM
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RTLYDTRKSGYTWBTAGMLKTVNLQNBGFTCTIRKRQTGFILGHTRICREGRWNA
RFDYXYDNSRRVTSWQAYNIGATBELFDLYRYDDVSGKTTGOFGKFGVTYYDINQIITTRA
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VDADGQLQTVVSINDAVINETPLENDMLHTLADSPGNSARTPPLRYDDRDFRTRIGTVQY
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RANDRAFT BODGGLGTVGT BODGGLGTUDV
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REFERREDRYGRUNGSTANDRALTRYCGNYTY
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FFYADLTNPTKVTHLYNHSSSEITSLYYDLQCHLFAMELSSGDEFYTACDNIGGTPLAV
FSGTGLMYRQLLYTAYGEIYMDTNPNFQIIIGYHGGLYDPLTKLYHMGRRDYDVLAGR
WTSPDHELWKRLSSNSIVPHLYMFRANNDFISNSQDIKCFWTDVNSMLLTFGFQLHNV
IPGYPKPDTDAMEPSYELVHTQMKTQEWDNSKSILGVQCEVQKQLKAFVTLERFDQLY
GSTITSCQQAPETKKFASSGSIFGKGVKFALKDGRVTTDIISVANDDGRRIALINNA
HYLENLHFTIDGVDTHYFVKPGPSBGDLAILGLSGGRRTLENGVNVTVSQINTMLSGR
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RAWTDGEKQQVLNTGRVQGYDGFFVTSVEQYPELSDSANNI HFWRQSEMGRR"
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/note="vector:modified_pBC_SK+"
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="mbg04788"
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/gene="mKIAA1302"
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Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                      6098 AAGTAIGGGAAACTGTCAAAGCTGGCAGAGACGCTCTAIGACACCACCAAGGTCAGTTTC
                                                                                                                                                                                                                            274 ThrTyrAspGluThrAlaGlyMetLeuLysThrIleAsnLeuGlnAsnGluGlyPheThr
                                                                              LysTyrGlyLysLeuSerLysLeuAlaGluThrLeuTyrAspThrThrLysValSerPhe
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PHCGYSMGASSDADLEADTVLSPEHPYRLMGRSTRSGRSSCLSSRANSNLTLTDTEHE
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SLSGEPPAGSAQEPTHAQDNWLLNSNIPLETRNLGKQPFLGTLODNLIEWDILGASRH
DGAYSDGHFLFKPGGTSPLFCTTSPGYPLTSSTVYSPPPRPLPRSTFSRPAFNLKKPS
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GSIMGMGRRRSISCBSCNGLADGNKLLAPVALTGSBGSLYVGDFNYIRRIFPSGNV
INLEMRNKDFHHSHSPARKYYLATDHSGAPTSDTNSRFWFVKFYTVVKDLYNKN
EVVAGTGOGCLFPDDPTRCGGGGKATRATLTNPRGITVDKFGLIYFVDGTMIRRVDQNG
IISTLLGSNDLTSARPLSCDSVMEISQVRLEMPTDLANPMDNSLYVDDNNVYLQISE
NHQVRLVAGRPWHCQVPGIDHFFLSKVAIHATLESATALAVSHNGVLYIAETDEKKIN
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NLMKVHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFGFSEAFVSVGYEYES
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LDFDRVTRTEKIYDDHRKFTLRILYDQAGRPSLWSPSSRLNGVNVTYSPGCHIAGIOR
GIMSERMEYDQAGRITSRIFADGKMWSYTYLEKSMVLHLHSQRQYIFEFDKNDRLSSV
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YVADLGNIRIRFIRKNKPFLNTQNMYELSSPIDQELYLFDTSGKHLYTQSLPTGDYLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEGMVNARFDYNYDNSFRYTSMQAVINETPLFIDLYRYDDVSGKTEGFGKFGVIYYDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVQVETSSKDDVTITTNLSASGAFYTLLQDQVRNSYYIGADGSLRLLLANGMEVALQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQIIÏGYHGGLYDPLTKLVHMGRRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y DVI LAGRWISP DHELWKRISSNSIVP FHLYM FKNNNPISNSQDIK CFMIDVNSWLLTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKL.SKLAĒTLYDTTKVSFTYDETĀGMLKTVNLQNĒGFTCTIRYRQIGPLIDRQIFRFT
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 2.34e-233 2813.00 99.26% 98.52% 98.88% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: Pred. No.:

ORIGIN

US-10-029-020-14\_COPY\_1760\_2300 (1-541) x AB025413 (1-8585)

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1 TyrTyriledlyAlaAspGlySerheuArgheuLeuLeuAlaAsnGlyMetGluValAla 20 d

LeuGlnThrGluProHisLeuLeuAlaGlyThrValAsnProThrValGlyLysArgAsn 40 21

qq	5531 CTGCAGACTGAGCCACCTGCTGGCTGGCACTGTCAACCCCACTGTAGGCAAGAAAI	r.
6	41 ValThrLeuProlleAspAsnGlyLeuAsnLeuValGluTrpArgGlnAr	9
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ζŏ	61 AlaArgGlyGlnValThrValPheGlyArgArgLeuArgValHisAsnAr	80
qq	5651 GCTCGTGGCCAGGTCACCGTCTTTGGACGCCGTCTGCGGGGTTCACAACCGAAACCTCTTG	'n
දු පු	81 SerLeuAspPheAspArgValThrArgThrGluLysIleTyrAspAspHisArgLysPhe	100
٥٧	.E	n ,
qa		5 12
δ,	121 LeuAsnGlyValAsnValThrTyrSerProGlyGlyTyrIleAlaGlyIl	140
Ор	5831 CTGAATGGTGTTAATGTGACCTACTCCCCTGGAGGTCACATTGCTGGAATCCAAAGGGGC	Ŋ
٥٧	141 IleMetSerGluArgMetGluTyrAspGlnAlaGlyArgIleThrSerArg	16
Dp	5891 ATCATGTCTGAGAGAATGGATGATCAGGCGGCGCGCATCACATCCCGGATCTTTGCA	Ŋ
ò	161 AspGlyLysThrTrpSerTyrThrTyrLeuGluLysSerMetValLeuLeuLeuHisSer	euHisser 180
ПÞ	5951 GACGGGAAATGTGGAGCTACTCGTACTTAGAGAAGTCCATGGTGCTTCA	9
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οp	6191 CATACCTICTACTIGGECACCGGCCGCCGGGTGATTTACAAGTATGGCAAGTTGTCAAA	დ. — ლ
à	261 LeuAlaGluThrLeuTyrAspThrThrLysValSerPheThrTyrAspGlu	28
DÞ	6251 CTGGCCGAGACTCTGTATGACACCACTAAGGTAAGCTTCACCTACGACGAGGCGAGGG	63.
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δy	341 GluThrProLeuProlleAspLeuTyrArgTyrAspAspValSerGlyLys	36
qu	6491 GAGACCCCACTGCCCATTGACCTCTACCGCTATGATGATGATGTCAGGGAAGACAGAC	
ζ	361 PheGlyLysPheGlyVallleTyrTyrAspIleAsnGlnIleIleThrThr)	'n
DÞ	6551 TTTGGGAAGTTTGGTGTCATCTACGACATCAACCAGATCATTACCACCGGTCATG	99
λŏ	381 ThrHisThrLysHisPheAspAlaTyrGlyArgMetLysGluValGlnTyrGluIlePhe	ullephe 400
Dp	6611 ACCCACACCAAGCACTTTGATGGCATGAAGGAAGAAGTACAGTATA	9

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LIEMDI FSASRRDGAYSDGHFFFRGGGTSPLFCTTSPGYPLTSSTYVSBPPRPLPRST
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LGNIR IRREITRAVKREPLINTGMYYELSSPIDGENTATTGLESATALAVSHNGYTN
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BTSSKODVTITTHLSGSGAFYTLLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHL
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RVTRTEKIYDDHRKFTLRILYDQAGRPSFWSPSSRLNGVNVTXSPGGHIAGIQRGIMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTAVWTHSKHFDAYGRMKEVQYETTERSLMYMMTVQYDNMGRVVKKELKVGPYANTTRY
SYEYDADGGLGTVSINDKPLMRYSYDLNGNLHLLSPCNSARLTPLRYDLRDRITRLGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGDGDI THI TDNNGNMVNVRRDSTGMPLWLVVPDGQVYWVTMGTNSALRSVTTQGHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERMEYDOAGRITSRIFADGKMWSYTYLEKSMVLHLHSOROYIFEFDKNDRLSSVTMPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAROTLĒTIRSUGYYRNIYOPPEGNASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKLS
KLAETLYDTTKVSFTYDETAGMLKTVNLQNEGFTCTIRYRQIGPLIDRQIFRFTEEGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNARFDYNYDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLOPFYADLTNPTKVTHLYSHSSBITSLYYDLOGHLFAMBLSSGDEFYIACDNIGTP
LAVFSGTGLMIKQILYTAYGBIYMDTNPNFQIIIGYHGGLYDFLTKLVHMGRRDYDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGRWTSPDHELWKRLSSNSIVPFHLYMFKUNNPISNSQDIKCFMTDVNSWLLTFGFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HNVIPGYPKPDTDAMEPSYELVHTQMKTQEWDNSKSILGVQCEVQKQLKAFVTLERFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLYGSTITSCQQAPETKKFASSGSIFGKGVKFALKDGRVTTDIISVANEDGRRIAAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAHYLENLHFTIDGVDTHYFVKFGFSEGDLAILGLSGGRRTLENGVNVTVSQINTML
SGRTRRYTDIQLQYRALCLNTRYGTTVDEEKVRVLELARQRAVRQAMAREQQRLREGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I PGENPEDGGHACVIRGOVMTSDGTELVÖVNÍSFINNÈLFGYTISRODGSFDLVTNGG
ISIILRFERAPFITQEHTLMLPWDRFFVMETIVMRHEENEIPSRDLSNFARPNVVSP
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/ LT anslation = MOVKERKEYRSLTRRRDAERRYTSSSADSEEGKGPOKSYSSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGLRAWIDGEKQOVLNTGRVQGYDGFFVTSVEQYPELSDSANNIHFMRQSEMGRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LeuGlnThrGluProHisLeuLeuAlaGlyThrValAsnProThrValGlyLysArgAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6088 YIGCAGACTGAGCCACACTGCTGGCTGGCACTGTCAACCCCACTGTAGGCAAGAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TyrTyrIleGlyAlaAspGlySerLeuArgLeuLeuAlaAsnGlyMetGluValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6028 TACTACATCGGGGCTGATGGCTCCCTGAGGCTGCTACTAGCCAATGGCATGGAAGGCT
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Conservative:
Mismatches:
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/gene="Doc4"
/note="putative; t
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2785.00
98.52%
97.60%
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Best Local Similarity:
Query Match:
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                                                                   6730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 9722)
Wang, X.Z., Kuroda, M., Sok, J., Batchvarova, N., Kimmel, R., Chung, P., Zinszner, H. and Ron, D.
Edentification of novel stress-induced genes downstream of chop EMBO J. 17 (13), 3619-3630 (1998)
                                                                                                                                                                                                   6790
                                                                                                                                   440
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to Drosophila melanogaster tenm/odz and
human gamma-heregulin; type II transmembrane protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ubases 1 to 9722)
Wang, X.-Z. and Ron, D.
Direct Submission
Submitted (14-APR-1998) Skirball Institute, New York University
Medical Center, 550 First Ave., New York, NY 10016, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheLeuArgGlnArgGlyGlyAspIlePheGluTyrAsnSerAlaGlyLeuLeulleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   521 AlaTyrAsnArgAlaGlySerTrpSerValArgTyrArgTyrAspGlyLeuGlyArgArg
                                                                                                                                                                                                                                                                                                                                                                                             AsnGlyAsnLeuHisLeuLeuSerProGlyAsnSerAlaArgLeuThrProLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASDI16ArgASDArgI1eThrArgLeuGlyASDVAlGInTyrLySMetASpGluASDGlY
                                        6731 GAGCTGAAGGTGGGACCCTATGCCAACACTACCGGCTACTCCTATGAGTATGATGCTGAT
                                                                                                                                                                                                                                                                GlyGlnLeuGlnThrValSerIleAsnAspLysProLeuTrpArgTyrSerTyrAspLeu
                                                                                                                                                                                                                                                                                                                             6791 GGCCAGCTGCAGACAGTCTCCATCAATGACAAGCCACTCTGGCGCTACAGCTATGACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgSerLeuMetTyrTrpMetThrValGlnTyrAspAsnMetGlyArgValValLysLyS
                                                                                                                                      GluLeuLysValGlyProTyrAlaAsnThrThrArgTyrSerTyrGluTyrAspAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus DOC4 (Doc4) mRNA, complete cds. AF059485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="downstream of CHOP 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:10090"
/ceIl_line="NIH-3T3"
/note="tunicamycin-treated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Mus musculus"
'mol_type="mRNA"
'strain="NIH/Swiss"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1/product="DOC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .. .9722
/gene="Doc4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF059485.1 GI:3170614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="Doc4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .9060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ġrk 7093
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JOURNAL
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AF059485
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KEYWORDS
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6147

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GSNKEDI TVTTNLSASGTFYTLMQDOVKNSYY IGLGGSLEUVLANGEVSLEITEPHLL
SGTVNPPI SKRNVTLE IDNGIALLVENRQRKEQARGQVTVYGRRLRVHNRULLSMDFDR
VTRTEKVYDDHRKFTLR IHYDHAGRPTLMAPSSRLNGVNVYSSPGGHTAGIQRGTMSV
RMPYDQMGRITISKI TISKI FADGKSMSYYTLEKSMVLLLYSQRQY I FSFDKNDRLSSVTMPNV
RAQTLETTRSI GYXPMYRPPEGIAATVLQDYSEDGLLLQTIHQGTGRRUY YKYGKLSR
ILLEILLYDTTRI AFSYDESAGMLKTVGLQSEGFACTI RYRQI GPLI DRQI FRESEGWN
NARPDYNYDMSFRVTSMQAVINETPLFI DLYRYDDVSGKTEQFGKFGVI YYDINQI IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYSASDSGCPPTPLHTLFATGTSLFGKGVKVALREGRVEADIISLANEDGRRIAAVLD
KASYLODLHFTIAGLDTHYFVKSGLVEGDLSLLGMTVGQRTLETGVNVTVSQVNMVLG
GRSRRITDIQMQYGTLSLNVRYGSSVDEEKVRVLELARQRAVATAMAHERHRLRQGEE
GSRAWTDGERQQLLSSGRVQGYEGFYIVSVDQFPELTDNINNVHFWRQTEMGRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STNGELSLLAGAPSGCDCKNDANCDCYSGDDGYAKDAKLNAPSSLAVSPDGELFIADL
GNIRLRYVRRNKAFLARLNMYELSSPIDDELYLPDVNASHVFTQSLTTGDYLYNFTYS
GEGDLSSITDKNKNRVSIRRDSTGLPLMLMGPDGQTFWFTMGTNNALKSVAAQGQEIA
VMTYHGSSGLLATKSNEDGWSTFYEYDNYGRLTNVTYPTGRVSSYRTDSDSTYRVQTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAVMTHTKHFDAYGRVKEVQYEIFRSLMYWMMVQFDNMGRVVAKELKVGPYANTTRYA
YEYDADGQLQVVSINDKPLWRYSYDLNGNLHLLSPGNSARLTPLRYDIRDRITRLGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYRLDEDGFLRQRGNDFFEYNSAGLLVKTYNKVNGWTIKYRYDGLGRRVSSRSTQGFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVESGAGLMIKQILHTAFGEVYLDSNPSFQLVĪGYQGGLYEPLTKLVHMGRRDYDVLA
GRWTTPDHDIRKRLNSDNIVPFNLYMFKNNNPLSNSQETKCYMTDVNSKLVTFGFQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGRRILSQGLPGLDGPPPPAQQRSLVPITSHDTGCIQYMDSGIMHLAVYNDGKETEQV
SFLTTAIDSIDDCPSNCFGNGDCVSGNCHCFPGFRGPDCSRASCPVLCSGNGQYLKGR
CMCHSGWKGSECDVPTNQCIDITCSGHGTCIVGTCICNPSYKGENCEBVDCLDPFCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQFFYADLSSPTRVTHMYNHSSSEITSLYYDLQGHLFAMELSSGDEFYVACDNIGTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVI PGYRKPVTDAMEPSYELVHTQIKTQEWDSTKSVLGVQCEVQRQLKSFVRLERFGQ
                                                                                                                                                                                                                                                                            YTORSINESPAPTDSSAFNEGFTSAODSSAODNWILLNSNYPLETRNIAKOTFLETLOD
NFIEMDILATARRDGAYTDGHFLFKFQGTSFLYCTTSPGYPLTSSTVYSPPRFLPRN
                                                                                                                                                                                                                                                                                                                                                                                      YQLTEDNTSGLHLPTDLGLPPLGNTGLEFPDRGSRDDGKLDGFFPEDSF1DMGEIDVG
RKVAQLIPPGIFWRSQVFIDHPMYLKFNVSLSKDALVGIYGRRGLPPSHTQFDFVELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGVCVRGECHCFVGWGGFGCESPRASCMEQCSGHGSFLADTNTCNCDHNWTGHDCSTE
                                                                                                                                    LKAEDQDSRLAYGSRVKDLVHHEADEFSRQGPDFSLRDMAFGDPVPPHMGAYRTEMGL
PHRDYSVSVASDADTETDGIMSPEHAVRLMGRSNTKSGRSSCLFSRANSNLTLTDTEH
                                                                                                                                                                                                                                              SFLVKTGSGNVCTPAAATANEGSFQNHSRLRTPPLPLFHSHSPSQHHTASIGSLSRSN
                                                                                                  translation="MEVKERRPYRSLISRRDIERRYISSSADSEDGKINPKSYSSSET"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCAADCGGHGI CVAGSCRCDEGWMGTGCEQRACHPRCSEHGTCKDGKCECSPGWNGEH
                                                                                                                                                                                                                ENTENGPPLHCSSASSSPVDSPYPPPSHAANQSQGRLLGNSGAQAGRDSESEDEFGPN
                                                                                                                                                                                                                                                                                                                                                    TFSRPAFSLKKPYKHCNWKCAALSAILISVTLVFLLAYFIAMHLFGLNWHLQPVQRQI
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ORIGIN

qq	5885 GTCACGCTGCCCATCGACAATGGACTCAACCTGGTGGAGTGGAGAGAGA	AAAGAGCAG 5944
λά	61 AlaArgGlyGlnValThrValPheGlyArgArgLeuArgValHisAsnAr	Asnleuteu 80
qo	5945 ĠĊĠĊĠĀĠĠĠĊŖĀĠŢĊŔĊĀĠŢĠŢĀĊĠĠĀĊĠĊĸĠĀĊŢĊĊĠĠĠŢŢĊĀŢĀĀŢĀĠ	AATTTGTTA 6004
ò	81 SerLeudspPheAspArgValThrArgThrGluLys1leTyrAspAspHi	Arglysphe 100
q <sub>Q</sub>	6005 TCTATGGATTTCGATCGGGTAACCAGGACTGAGAAAGTGTATGATGACCA	AGGAAGIIC 6064
දු පු	101 ThrLeuArg11eLeuTyrAspGlnAlaG1yArgProSerLeuTrpSerProSerSerArg 120	Serserarg 120            AGTAGCCGG 6124
λ̈́o	121 LeuAsnGlyValAsnValThrTyrSerProGlyGlyTyrIleAlaGlyIl	GlnArgGly 140
Db	6125 CTAAATGGTGTCACCACCTACCAGGTGGCCACATTGCTGGCA	cadadddc 6184
δλ	141 IleMetSerGluArgMetGluTyrAspGlnAlaGlyArgIleThrSerAl	
qq	6185 ACAATGTCAGTCCGAATGGAATATGACCAAAATGGGAGAATCACCTCAAA	ATATTTGCA 6244
δy	161 AspGlyLysThrTpSerTyrThrTyrLeuGluLysSerMetValLeuLe	:::
Ωp	6245 GATGGAAAATCATGGAGCTACATACCTTGAAAAGTCCATGGTGCTGC	CTCTACAGC 6304
λ̈́o	181 GlnArgGlnTyrIlePheGluPheAspLysAsnAspArgLeuSerSerV	ThrMetPro 200
qq	6305 CAGCGACAATCTTCGAGTTTGACAAGAACGACCGCCTTTCTTCAG	ACCATGCCC 6364
δý	201 AsnValAlaArgGlnThrLeuGluThrIleArgSerValGlyTyrTyrA:	AsnileTyr 220
qq	6365 AATGIGGCCAGACAGACCITGGAGACCACCGGTTCCATCGGCTATTACA	AAACACATAC 6424
λ	221 GlnProProGluGlyAsnAlaSerVall1eGlnAspPheThrGluAspG	/HisLeuLeu 240
QQ	6425 CGGCCACCTGAGGCAATGCCACAGTTTGCAAGATTACAGTGAAGATG	ACTGCTTCTG 6484
δλ	241 HisThrPheTyrLeuGlyThrGlyArgArgVallleTyrLySTyrGlyL;	
Db	6485 CAAACCATCCACCAAGGAACAGGACGTAGAGTCATCTATAAGTATGGGA	ACTCTCCCGT 6544
Qy	261 LeuAlaGluThrLeuTyrAspThrThrLysValSerPheThrTyrAspG	uThrAlaGly 280
Db	6545 CIGCTAGAAATCCTTTATGATACGACACGGATTGCCTTTTCTTATGATG	ATCTGCAGGC 6604
δλ	281 MetLeuLysThr11eAsnLeuGlnAsnGluGlyPheThrCysThr11eA	o 1
Dp	6605 AIGCTCAAAACTGTGGGGCTTCAAAGTGAAGGTTTTGCTTGTACCATAC	TTACAGACAG 6664
δλ		EValAsnAla 320
gg	6665 ATCGGACCACTTATCGACAGACAGATCTTTCGTTTTTAGTGAGGGCCA	£2/0 ))51444155
ري اور	321 ArgPheAspTyrAsnTyrAspAsnSerPheArgValThrSerMetGln&laVa 	aVallleAsn 340              AGTGATTAAT 6784
ž č	41 GluThrProLeuProlleAspLeuTyrArgTyrAspAspVal	rGluGln
q	6785 GAAACCCCCTTGCCCATTGACCTCTATGGTGATGACGTCTCAGGGG	GACGGAGCAG 6844
δλ	361 PheGlyLysPheGlyVallleTyrTyrAspIleAsnGln1le1leThrT	leThrThrAlaValMet 380
QQ	secaaatttegaettatatattateatattaaccagat	ATG
ζ	381 ThrHisThrLysHisPheAspAlaTyrClyArgMetLysGluValGlnTyrGlulle	Phe 400
qq	CCACACCAAACACTTTGATGCATACGGAAGAGTTAAAGA	AGATTTTC
Š	401 ArgserLeumetTyrTrpMetThrValGInTyrAspAsnMetGlyArgVal'	vallyslys 

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NGRTRRFADVEMQFGALALHVRYGMTLDEEKARILEQARQ
EGARLWTEGEKRQLLSAGKVQGYDGYYVLSVEQYPELADS
                                                                                                                                                                                   suArgLeuLeuLeuAlaAsnGlyMetGluValAla 20
||||||:::::: |||:::|||
ICAGAATTATCTACGCCAGTGGCCTGGACTCACAC 331
                                                                                                                                                                                                                                   511
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                                                                                                                                                                                                                                                                                    9ThrGlutyslleTyrAspAspHisArgLysPhe 100
                                                                                                                                                                                                                                                                                                                                                                                                             571
                                                                                                                                                                                                                                                                                                                                                                                                                                     aGlyArgProSerLeuTrpSerProSerSerArg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                              631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rProGlyGlyTyrileAlaGlyIleGlnArgGly 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pGlnAlaGlyArgileThrSerArgilePheAla 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rLeuGlulysSerMetValLeuLeuLeuHisSer 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rileargservalgiytyrtyrargasniletyr 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gArgVallleTyrLysTyrGlyLysLeuSerLys 260
|||||||||:::::||||||
3AGGGTCTTATTCAAATACAGAAGGCAGACTAGG 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pLysAsnAspArgLeuSerSerValThrMetPro 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lijeGlnAspPheThrGluAspGlyHisLeuLeu 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                    yArgArgLeuArgValHisAsnArgAsnLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                 :||| ||||||||||:::
                                                                                                                                                                                                                                                                                                                                                   GACAGAAAGATCTATGACGACCACCGTAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCCACAGGTCAAATTGCCAGCATCCAGCGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rLysValSerPheThrTyrAspGluThrAlaGly
                                                                                                                                                             x AX876525 (1-3614)
                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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PQ CJ

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LeuAsnGlyValAsnValThrTyrSerProGlyGlyTyrIleAlaGlyIleGlnArgGly 140
                                                                                                             pc Cl2P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers (149). (3283).
                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGInThrGluProHisLeuLeuAlaGlyThrValAsnProThrValGlyLysArgAsn 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU.
KEIICHI NAGAI, TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                           PD 09-JUL-2002
PP 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI SAITO,
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATI PI KEIICHI NAGAI, TETSUJI OTSUKI
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC 12015/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1 (bases 1 to 3614)

Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Primer for synthesizing full-length cDNA and use thereof Patent; JP 2002191363-A 11018 09-JUL-2002;

HELIX RESEARCH INSTITUTE

S. Homo sapiens (human)

PN JP 2002191363-A/11018
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    GTCCTAAAGACAGTAAACCTCCAGAGTGATGGTTTTATTTGCACCATTAGATACAGGCAA
                                                     ATTGGTCCCCCCGATTGACAGGCAGATTTTCCGCTTTAGTGAAGATGGGATGGTAAATGCA
                                                                                                 IleGlyProLeuIleAspArgGlnIlePheArgPheThrGluGluGlyMetValAsnAla
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Homo sapiens (human)
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PRI 01-AUG-2002

AK001336 3614 bp mRNA linear Homo sapiens cDNA FLJ10474 fis, clone NT2RP2000067.

AK001336

LOCUS

AK001336

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/ translation="WDKAITTYDIESSSREEDVSITSNLSSIDSFYTMVQDQLANSYQI
GYDGSLRIIYASGLDSHYQTEPHVLAGTANFTVAKRNMTLPGENGQNLVEWRFREGQA
GYNVYPGRALRYNGRNLLSVDFDRTTKTRKIYDDRRKFLLRIAYDTSGHPTLMLPSS
KLMAVNVYTSSTGQIASIQRGTTSEKVDYDGQGRIVSRYSPADGCKTWSYTYLEKSMYLL
LHSQRQYIRFYDMNDRLSATTMPSVARHTMQTIRSTGYRNAFTYDETGKMYTLL
LHSQRQYIRFYDMNDRLSATTMPSVARHTMQTIRSTGYRNYPNPESNASIITDSNLE
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NPSNSARLTPLRYDLRDRITRADVGVRLDBGFLRQRGTEIFEYSSRGLTTRYYSKG
SGWTVIRRYGGRRRVSSKTSLGQHLQFYADLITYPTRITHYYNHSSSEITSLYYDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics Laboratory; 1531-37 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomicsehri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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VOQOVARQDRAFLIGIGKMAEVOVSRRAGGAQSWIJMPATVKSLIGKGVMLAVSQGRVO
TNVLNIANEDCIKVAAVLINAFYLENHAFTIERGYDTHYETKTTPREDGIGTHELITSGR
KALENGINVTVSQSTTVONPAFRADVEMDFGALLHVRVGWTLDEEKARILEGARO
RALARGMAREQQRVRDGEEGARLWTEGEKRQLLSAGKVQGYDGYYULSVEQYPELADS
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GFHGGLYDFLTKLIHFGERDYDILAGFWTTPDIEIWKRIGKDPAPFNLYMFRNNNPAS
                                                                                                                                                                                                                                                           Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Naqai,K., Sugano,S., Shiratori,A., Sudo,H.,
Wagatama,M., Hosoiri,T., Raku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
Ishi,S., Takkguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamarsu,A.,
Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/cell_type="NTZ"
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/clone_lib="NTZRP2"
/note="cloning vector: pME18SFL3~mRNA from NT2 neuronal
precursor cells after 2-weeks retinoic acid (RA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 3614)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
oligo capping, fis (full insert sequence). Homo sapiens (human) Ebkarrer
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Mismatches:
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/clone="NT2RP2000067"
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Pred. No.:
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JOURNAL
                                         VERSION
KEYWORDS
SOURCE
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Dβ	1292 GAAA	akceceaciectaticarciciaricagitigaicacatiticigecaaagitigaecae 1351
δ	361 Phe	PheGlyLysPheGlyVallleTyrTyrAspIleAsnGlnIleIleThrThrAlaValMet 380
qq	1352 TT	TITGGAAAGTITGGAGTIATATATATGATATTAACCAGATCATTTCTACAGCTGTAATG 1411
Qy	381 Th	ThrHisThrLysHisPheAspalaTyrGlyArgMetLysGluValGlnTyrGluIlePhe 400
QQ	1412 ACC	
δ	401 Arg	ArgSerLeuMetTyrTrpMetThrValGlnTyrAspAsnMetGlyArgValValLysLys 420
qq	1472 AG	
δy	421 Gl	GluLeuLysValGlyProTyrAlaAsnThrThrArgTyrSerTyrGluTyrAspAlaAsp 440
Dp	1532 GA	
à	441 G1	GlyGlnLeuGlnThrValSerIleAsnAspLysProLeuTrpArgTyrSerTyrAspLeu 460
ΩÞ	1592 GG	GGACAGCTCCAAACAGTTTACCTCAATGAAAGATAATGTGGCGGTACAACTACGATCTG 1651
٥٧	461 As	AsnGlyAsnLeuHisLeuLeuSerProGlyAsnSerAlaArgLeuThrProLeuArgTyr 480
qq	1652 AA	AATGGAAACCTCCATTTACTGAACCCAAGTAACAGTGCGCGTCTGACACCCCTTCGCTAT 1711
Š	481 As	AspileargaspargileThrargLeuGlyAspValGlnTyrLysMetAspGluAspGly 500
qq	1712 GA	::
Qy	501 Ph	PheLeuargGlnArgGlyGlyAspIlePheGluTyrAsnSerAlaGlyLeuLeu1leLys 520
QO	1772 TT	TICCTACGICAAAGGGGGCACGGAAAICTITGAATATAGCTCCCAAGGGGTTCTAACTCGA 1831
δ	521 Al	AlaTyrAsnArgalaGlySerTrpSerValArgTyrArgTyrAspGlyLeuGlyArgArg 540
qq	1832 GT	GTTTACAGTAAAGGCAGTGGCTGGACGAGTGATCTACCGTTATGACGGCCTGGGAAGGCGT 1891
δy	541 Val	1 541
ΩD	1892 GTT	т 1894

Title:

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AB026980 Danio merc
AJ238613 Gallus ga
AB025410 Mus muscu
AF100772 Homo sapi
AJ293019 Gallus ga
AX876360 Sequence
BD16608 Primer fo
AX027473 Homo sapi
AX87749 Sequence
BD156663 Primer fo
AX01749 Homo sapi
AX875525 Sequence
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AB037723 Homo sapi
AX60210 Sequence
BX640737 Homo sapi
AX056511 Homo sapi
AX675551 Sequence
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AX122513 Mus muscu
AF195418 Mus muscu
AB025412 Mus muscu
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AX250065 Sequence
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AX250013 Sequence
AX250008 Sequence
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-Q=Cgn2_1/USPTO_spool/US10029020/runat_06082004_112216_29275/app_query.fasta_1.3519
-Q=Cgn2_1/USPTO_spool/US10029020/runat_06082004_112216_29275/app_query.fasta_1.3519
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-DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIP=0 - ALIGN=15 - MODE=LOCAL
-USFR=TO - NORM==Ext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=2000000000
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-NO_MMAP - LARGEQUERY - NEG SCORES=0 - WAlT - DSPBLOKE=100 - LONGLOG
-DEV_TIMEOUT=120 - WARN_TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FCAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
                                                                                                                                                        August 13, 2004, 23:35:57; Search time 3555.05 Seconds (without alignments) 2450.585 Million cell updates/sec
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                           - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3470272 segs, 21671516995 residues
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Maximum Match 1008
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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140

2435 160

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German Genome Project.
This clone (DKFZp686D0412) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/CDNA/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="human cervix"
/clone_lib==686 (synonym: hloc3). Vector pSportl_Sfi; host
DH10B; sites Sfila + SfilB"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSMB06114 3486 bp mRNA linear PRI 17-JUN-2003
Homo sapiens mRNA; cDNA DKFZp686D0412 (from clone DKFZp686D0412).
BX537983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (17-70N-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
2196 TICCAGCTACACAACGTGATCCCTGGTTATCCCAAACCAGACATGGATGCCATGGAACCC
                                                                  SerTyrGluLeu11eHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerIle
                                                                                                LeuGlyValGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe
                                                                                                                                                                                  2316 CTCGGGGTACAGTGTGAAGTACAGAAGCAGCTCAAGGCCTTTGTCACCTTAGAACGGTTT
                                                                                                                                                                                                                                           141 AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLysPhe
                                                                                                                                                                                                                                                                         161 AlaSerSerGlySerValPheGlyLysGlyValLysPheAlaLeuLysAspGlyArgVal
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/codon_start=2
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/clone="DKFZp686D0412"
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/db_xref="taxon:9606"
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Homo sapiens
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                                    mRNA linear PRI 09-SEP-2003 clone BRAWH3043034, highly similar
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                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="BRAWH3043034"
/tissue type="brain"
/clone="Lib="BRAWH3"
/note="Cloning vector: pMB18SFL3"
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oligo capping; fis (full insert sequence).
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Homo sapiens
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Homo sapiens cDNA FLJ45158 fis, clo
to Mus musculus neuregulin 1 (Nrg1)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Kekuda,R., Stone,D.J., Anderson,D., Shimkets,R.A., Burgess,C.E
Zerhusen,B.D., Liu,X., Spytek,K.A., Casman,S.J., Boldog,F.L.,
Smithson,G., Lii,L. and Ji,W.
Polypetides and mucleic acids encoding same
Patent: WO 20557453-A 13 25-JUL-2002;
Curagen Corporation (US)
Location/Qualifiers
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Sequence 13 from Patent W002057453.
AX556500.1 GI:25899736
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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TLPIDNGLNLVEWRQRKEQARGQVTVFGRRLRVHNRNLLSLGFDRVTRTEKIYDDHRK
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                                                translation="SFGRLTNVTFPTGQVSSFRSDTDSSVHVQVETSSKDDVTITTNI
                                                                                                                            FTLRILYDQAGRPSLWSPSSRLNGVNVTYSPGGYIAGIQRGIMSERMEYDQAGRITSR
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/protein_id="CAD97943...
/db_xref="GI:31874054"
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LAGRWTS PDHELWKHLSSSNVMPFNLYMFKNNNPISNSQDIKCFWTDVNSWLLFFGFO
LHNVI PGYPKPDMDAMEPSYELIHTOMKTOEMDNSKS LIGYQCEVOKQUKAFYTLERF
DQLYGSTITSCQQAPKTKRASASGSYEKRANKFALKGRYATOTI ISVANEDGRRVAAI
INHAHYLENLHFTI DGVDTHY FVKEGPSEGDLA ILGLSGGRRTLENGYNVTVSGINTV
INGRTRRYTD TOLQCYGALCLATRYGTTLDEEKARVLELARQRAVRQAMAREQORLREG
BEGLRAWTEGEKQQVLSTGRVQGYDGFVI SVEQYPELSDSANNIHFMRQSEMGRR"
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                                                                                                                                                                                                                                                                                                                                                                                       ATAGGCTACCATGGTGGCCTCTATGATCCACTCACCAAGCTTGTCCACATGGGCCGGCGA 2797
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheGlnLeuHisAsnValIleProGlyTyrProLysProAspMetAspAlaMetGluPro
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Sequence 22 from Patent WO02072830.
AX600210
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Matches:
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VETSSKDDVTITTNLSASGAFYTLLQDQVRNSYYIGADGSLRLLLANGMEVALQTEH
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DRVTRTERKTYDDHRKFTLLYDQAGRPSLMSPSSRLMGVNVTYSPGGYIAGIORGTH
SERMEYDQAGRITSRTFADGKTWSYYLLEKSWYLLLHSPGRQYIFEPDKNDRLSSVTMF
NVARQTLETIRSVGYYRNIYQPPEGRASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKL
STABTLYDTTKNSFTYDETAGMLKTINLQNEGFTCTIRYRQIGPLIDRQIFFEFEG
MVNARPTRHPDAYGRMKEVQYEIFRSLMYMMTVQYDNMGRVVKKELKVGFYYSYDINQI
ITTAVMTHTKHPDAYGRMKEVQYEIFRSLMYMMTVQYDNMGRVVKKELKVGFYANTTR
SSYEXDADGGQCQTVSTNDKFMRYSYDINGNLALLSFGNSRALFTFLKVTRLG
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HHLQPFRYADLTNPTKVTHLYNHSSSEITSLYYDLQGHLRAMELSSGDEFYIACDNIGT
PLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQIIIGYHGGLXDPLTKLVHMGRRDYDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagase, T., Kikuno, R., Ishikawa, K.I., Hirosawa, M. and Ohara, O. Prediction of the coding sequences of unidentified human genes. XVI. The complete sequences of 150 new cDNA clones from brain which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obara,O., Nagase,T. and Kikuno,R.

Direct Submission

Submitted (1J-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
                                                                                                                                                                                                                                                                                                          PRI 10-MAY-2002
                                                                      7771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .vc=-1111s sequence was replaced that of fg06864 cDNA as representative cDNA sequence for KIAA1302."
                                                                                                                                                    7831
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                                                                                                                                            7772 ACCACAGACATCATCAGGGGCAATGAGGATGGGGGAAGGGTTGCTGCCATCTTGAAC
                                                   ThrThrAspIlelleSerValAlaAsnGluAspGlyArgArgValAlaAlaIleLeuAsn
                              AlaserserglyservalpheglytysglyvaltyspheAlaLeuLysAspGlyArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax:+81-438-52-3914)
On May 9, 2002 this sequence version replaced gi:7242958
Location/Qualifiers
                                                                                                                                                                                                                                                                                                ABU3/723 8624 bp mRNA linear
Homo sapiens mRNA for KIAA1302 protein, partial cds.
AB037723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        code for large proteins in vitro
DAR Res. 7 (1), 65-73 (2000)
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107181198
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/clone_lib="pBCSKPGW"
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/gene="KIAA1302"
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Mammalia; Eutheria;
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Please contact the RZDPI PARTON CONTROL OF THE PLANT IN HELDERWEY 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="human fetal kidney"

/clone lib= 686 (synonym: hlcc3). Vector pSportl_Sfi; host

DH10B; sites SfilA + SfilB"

/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPMDNSLYVLDNNVVLQĪSENHQVRIVAGRPWHCQVPGIDHFLLSKVĀLHATLESAIA
LAVSHNGVLYIAETDEKKINRIRQVTTSGEISLVAGAPSGCDCKNDANCDCFSGDDGY
                 sapiens mRNA; cDNA DKFZp686K11107 (from clone DKFZp686K11107)
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SPGNSARLTPLRYDIRDRITRLGDVQYKMDEDGFLRQRGGDIFEXNSAGLLIKAYNRA
GSWSVRYRYDGLGRRVSSKSSHSHHLQFFYADLTNPTKVTHLYNHSSSEITSLYYDLQ
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                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                            German Genome Project.
This clone (DKFZp686K11107) is available at the RZPD in Berlin.
                                                                                                                                                                                                                                                 Direct Submission
Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                           Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                  Clone from S. Wiemann, Molecular Genome Analysis, German Cance Research Center (DKFZ); Email s wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germanny) within the CDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein, N-terminus elongated, differentially spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
/protein_id="CAB45850.1"
/db_xref="GI:34364829"
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/organism="Homo sapiens"
                                                                                                                                                                                                                                The German Human cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="DKFZp686K11107"
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/db_xref="taxon:9606"
/map="11q14.1"
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                                                   BX640737.1 GI:34364828
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                                                                                     Homo sapiens (human)
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                  Yue, H., Yao, M.G., Ison, C.H., Lu, Y., Warren, B.A., Elliott, V.S., Baughn, M.R., Ding, L., Xu, Y., Gietzen, K.J., Tang, T.Y., Lal, P.G., Duggan, B.M., Burford, N., Lu, D.A., Richardson, T.W., Tran, U.K., Khare, R. and Walia, N.K.
Proteins associated with cell growth, differentiation, and death Patent: WO 02072830-A 22 19-SEP-2002;
Incyte Genomics, Inc. (US)
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/cell Lype="teratocarcinoma"
/clone lib="NTZRP7"
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Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K. Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamanto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagah, K. and Isogai, T., Sugano, S., Manna, CDNA sequencing project
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/note="unnamed protein product"
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Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
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    2685
    organism="Homo sapiens"
    mol_type="mRNA"
    db_xref="taxon:9606"

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
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2685 bp mRNA linear Homo sapiens cDNA FLJ31969 fis, clone NT2RP7008013, to Mus musculus mRNA for Ten-m4.
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Matches:
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                      /gene="DKFZp686K11107"
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DB: 6 Gaps: 1 US-10-029-020-14_COPY_2460_2600 (1-201) x AX675551 (1-8438)	Qy 1 11eGlydyrHisGlyGlyLeuTyrAspProLeuThrLysLeuValHisMetGlyArgArg 20	QY         21 AsplyrAspValLeuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu 40           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 41 SerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer 60	Qy 61 AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly 80	Qy 81 PheGlnLeuHisAsnVallleProGlyTyrProLysProAspMetAspAlaMetGluPro 100	Qy 101 SerTyrGluLeuileHisThrGlmMetLysThrGlnGluTrpAspAsnSerLys 118 	OY 119SerIleLeuGlyValGlnCysGluValGlnLysGlnLeuLys 132	Qy         133 AlaPheValThrLeuGluArgPheAspGlnLeuTyrGlySerThrIleThrSerCysGln 152           Db         7679 GCCTTTGTCACCTTAGAACGGTTTGACCAGCTCTATGGCTCCACAATCACCAGCTGCCAG	172	Qy         173 PheAlaLeuLysAspGlyArgValThrThrAspIleIleSerValAlaAsnGluAspGly 192           Db         7799 TTTGCCTTGAAGGATGGCCGAGTGACCACAGACATCATCAGGCCAATGAGATGG		RESULT 9  AK122490 LOCUS AK122490 LOCUS AK122490 LOCUS AK122490 LOCUS AK122490 AK122490 AK122490 VERSION AK122490 VERSION AK122490 AK122490 AK122490.1 GI:28972711 KEYWORDS FILCONAL. KEYWORDS AK12490.1 GI:28972711 KEYWORDS AK12490.1 GI:28972711 KEYWORDS AK12490.1 GI:28972711	Mus musculus Mus musculus Eukaryota; Me Mammalia; Eut	AUTHORS Okazaki, N., Kikuno, R., Ohara, R., Inamoto, S., Aizawa, H., Yuasa, S., Nakajima, D., Nagase, T., Ohara, O. and Koga, H.  TITLE Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse	KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries DNA Res. 10, 35-48 (2003)  REFERENCE 2 (bases 1 to 5583)  AUTHORS OKAZAKI,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.  TITLE Direct Submission JOURNAL Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics; 2-6-7	Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
Oy 41 SerSerSerAsnValMetDroPheAsnLeuTyrMetPheLysasnAsnAsnAsnLeSer 60	hegly        rrgga			rgPhe       3GTTT		gVal			AX675551	DEFINITION Sequence 1 from Patent W002055704. ACCESSION AX675551 KEYWORDS	SOURCE Homo sapiens (human) ORGANISM Homo sapiens sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Prinates; Catarrhini; Hominidae; Homo.	AUTHORS Dadigaru, M., Li, L., Zerhusen, B.D., Casman, S.J., Shenoy, S., Spytek, K.A., Zhong, M., Gangolli, E.A., Burgess, C.E., Patturajan, M., Vernet, C.A., Taylor, S., Tchernev, V.T., Miller, C.E., Guo, X., Boldog, F.L., Grosse, W. M., Alsobrook, J.P., Gerlach, V., Edingermark, S., Rothenberg, M.E., Bllerman, K., Macdougall, J., Malyankar, U., Millet, I., Peyman, J., Smithson, G., Gunther, E. and Stone, D.J.		ES ource	Alignment Scores:  Alignment Scores:  Pred. No.:  Score:  Score:  Percent Similarity:  96.17*  Mismarches:  Ouery Match:  98.17*  Alignment Scores:  0  Alignment Scores:  0  Alignment Scores:  1.76e-109  Length:  8438  Conservative:  0  Ouery Match:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Length:  1.76e-109  Matches:  1.76e-109  Length:  1.76e-109  Matches:  1.76e-109  Length:  1.76e-109  Le	ייייייייייייייייייייייייייייייייייייייי

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Mouse Ten-m/Odz is a new family of dimeric type II transmembrane proteins expressed in many tissues
J. Cell Biol. (1999) In press
2 (bases 1 to 8885)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                      121 LeuGlyValGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe
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                       PheGlnLeuHisAsnVallleProGlyTyrProLysProAspMetAspAlaMetGluPro
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Mus musculus mRNA for Ten-m4, complete cds.
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Mus musculus
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(codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPGYPKPDTDAMEPSYELVHTQMKTQEWDNSKSIÏGVQCEVQKQLKAFVTLERFDQLY
GSTITSCQQAPETKKFASSGSIFGKGVKFALKDGRVTTDIISVANEDGRRIAAILNNA
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TRRYTDIOLOYRALCINTRYGTTVDEEKVRVLELARQRAVRQAWAREQORLREGEEGL
RAWTDGEKQQVLNTGRVQGYDGFFVTSVEQYPELSDSANNI HFMRQSEMGRR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /t_{\pi\pi\pi} s1ation = "Tonmyelsspidoelyledischutyschutgelptgdylynftytgdgdithitdnngnnvnvrrdstgmplwlvvpdgqvywvtmgtnsalrsyttgghelammgdithitdnngnnvnvrrdstgmplwlvvpdgqvywvtmgtnsalrsyttgghelammgdvymvtmgtnsalrsyttgghelammgdvymvtmgtnsalrsyttgghelammgddithitdnngnnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnngnvrrdstgmplammgddithitdnn
(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918) The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing: Kazusa DNA Research Institute; cDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly 80
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Matches:
Conservative:
Mismatches:
Indels:
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/note="vector:modified_pBC_SK+"
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protein_id="BAC65772.1"
db_xref="GI:28972712"
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                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="mbg04788"
                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="brain"
                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="mKIAA1302"
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7450 7510 7570 7630 1 IleGlyTyzHisGlyGlyLeuTyzAspProLeuThrLysLeuValHisMetGlyArgArg 20 40 9 80 GATTATGATGTGCTGGCTGGACGCTGGACGCCAGACCATGAACTCTGGAAACGCCTG SerSerSerAsnValMetProPheAsnLeuTyrWetPheLysAsnAsnAsnProlleSer AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly 8585 189 10 2 0 US-10-029-020-14\_COPY\_2400\_2600 (1-201) x AB025413 (1-8585) Matches: Conservative: Mismatches: Indels: Length: Gaps: 7.52e-106 1031.00 99.00% 94.03% 95.73% Best Local Similarity: Query Match: DB: Percent Similarity: Alignment Scores: 7391 7451 61 41 Pred. No.: ORIGIN Score: ð 셤 à g  $\delta$ g ò

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/db_xref="G1:3170615"
/translation="WDVKERKPYRSLTRRRDAERRYTSSSADSEEGKGPQKSYSSET
LKAYDQDARLAYGSRVKDMVPQGABEFCRTGTNFTLRELGLGEMTPPHGTLXRTDIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 9722)
Wang,X.Z., Kuroda,M., Sok,J., Batchvarova,N., Kimmel,R., Chung,P., Zinszner,H. and Ron,D.
Zinszner,H. and Ron,D.
Identification of novel stress-induced genes downstream of chop BMBO J. 17 (13), 3619-3630 (1998)
                    LeuGlyValGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe
                                                            SerTyrGluLeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerlle
                                                                                                                                                                                        AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrlysLysPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 9722)
Wang.X.-Z. and Ron,D.
Direct Submission
Submitted (14-APR-1998) Skirball Institute, New York University
Medical Center, 550 First Ave., New York, NY 10016, USA
Location/Qualifiers
                                                                                                                                                                                                                                                       AlaSerSerGlySerValPheGlyLysGlyValLysPheAlaLeuLysAspGlyArgVal
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Mus musculus DOC4 (Doc4) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db xref="taxon:10090"
|cell line="NIH-3T3"
|note="tunicamycin-treated"
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/strain="NIH/Swiss"
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/product="DOC4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="Doc4"
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SOURCE
ORGANISM
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VERSION
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JOURNAL
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AUTHORS
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source AUTHORS TITLE JOURNAL JOURNAL MEDLINE gene PUBMED REFERENCE CDS FEATURES COMMENT 40 9 SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer 1. IleGlyTyrHisGlyGlyLeuTyrAspProLeuThrLysLeuValHisMetGlyArgArg AspTyrAspValLeuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu 1813. .1881 /gene="Doc4" /note="putative; transmembrane-region site" US-10-029-020-14\_COPY\_2400\_2600 (1-201) x AF059485 (1-9722) 9722 189 10 2 0 Length:
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Mismatches:
Indels: Gaps: 8.73e-106 1031.00 99.00% 94.03% Percent Similarity: Best Local Similarity: misc\_feature Alignment Scores: Pred. No.: 21 41 Query Match: ORIGIN Score: 셤 ð q à ð

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//fore="almilar to Drosophila melanogaster tenm/odz and Mus
musculus Doc4"
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Mieda,M.
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Mieda,M.
Subritted (No. Mar. 1999) Michihiro Mieda, Brain Science Institute,
Submitted (No. Mar. 1999) Michihiro Mieda, Brain Science Institute,
RIKEN, Lab. for Developmental Gene Regulation; 2-1 Hirosawa,
RIKEN, Lab. Saitama 351-0198, Japan (E-mail:wieda@brain.riken.go.jp,
Tel:81-84-67-9713, Fax:81-48-467-9714)
Sequence updated (29-0un-1999).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              181 ThrThrAspIleIleSerValAlaAsnGluAspGlyArgArgValAlaAlaIleLeuAsn 200
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mieda, M., Kikuchi, Y., Hirate, Y., Aoki, M. and Okamoto, H.. Compartmentalized expression of zebrafish ten-m3 and ten-m4, homologues of the Drosophila ten(m)/odd Oz gene, in the central
                                                               81 PheGlnLeuHisAsnVallleProGlyTyrProLysProAspMetAspAlaMetGluPro
                                                                                101 SerTyrGluLeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerlle
                                                                                                                                                 8248 TCCTACGAGCTCGTACACACACAGATGAAAACTCAGGAACAACAACAACAACAGCAAC
                                                                                                                                                                                         LeuGlyValGlnCysGluValGlnLysGlnLeuLyshlaPheValThrLeuGluArgPhe
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61 AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly
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Danio rerio mRNA for ten-m4, complete cds.
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1. .9264
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Danio rerio
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NFIEMDILATARRDGAYTDGHPLFKPGGTSPLYCTTSPOYPLTSSTVYSPPPRPLERN
TFSRPAFSLKKPYKHCNWKCAALSAILISVTLVFLLAYFIAMHLFGLNWHLQPVQRQI
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YEYDMYTHTYPDAYGRYKEOYFI IFRSLAYWMYOFDNMGRYVAKELKVGPYANTTRYA
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SFLVKTGSGNVCTPAAATANEGSFQNHSRLRTPPLPLFHSHSPSQHHTASIGSLSRSN
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RMEYDQNGRITSKIFADGKSWSYTYLEKSWVLLLYSQRQYIFEPDKNDRLSSVTMPNV
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LLEILYDTTRIAFSYDESAGMLKTVGLQSEGFACTIRYRQIGPLIDRQIFRFSEEGMV
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GRWTTPDHDIRKRLNSDNIVPFNLYMFKNNNPLSNSQETKCYMTDVNSWLVTFGFQLY
NVIPGYRKFVTDAMEPSYELVHTQIKTQEWDSTKSVLGVQCEVQRQLKSFVRLERFGQ
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KASYLQDLHFTIAGLDTHYFVKSGLVEGDLSLLGMTVGQRTLETGVNVTVSQVAMVLG
GRSRRITDIQMQYGTLSLNVRYGSSVDEEKVRVLELARQRAVATAMAHERHRLRQGEE
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AUTHORS
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Mismatches:
Indels:
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Matches:
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807.00
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71.50%
74.93%
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Submitted (28-APR-1999) Chiquet-Ehrismann R., R-1066.446, Friedrich
Miescher-Institute, Postfach 2543, CH-4002 Basel, SWITZERLAND
Location/Qualifiers
                                                                                                                                                                                                                                                            LeuGlyValGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe 140
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Archosauria, Aves; Neognathae, Galliformes; Phasianidae;
Phasianinae, Gallus.
                 SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer
                                                                                  PheGlnLeuHisAsnValIleProGlyTyrProLysProAspMetAspAlaMetGluPro
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                                                             61 AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly
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/dev stage="Ell, El4, adult"
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AJ238613.
AJ238613. GI:4877312
ten-1 gene; teneurin-1.
Gallus gallus (chicken)
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1, .8118
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Chiquet-Ehrismann, R.
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                                                                                                                                                                                                     YSDGKCYEGVKQPRFAALIEVŶFGKĞIKFAIKDGIVTĀDIIGYANEDSRITAĀILNNAH
YLENLHFTIEGRDTHYFIKLGSLEEDLSLIGNTGGRRILENGYNVTVSÇMISVINGRT
RRFADIQLQHGALCFNVRYGTTVEEEKNHVLEVARQRAVAQAWTKEQRRLQBGEEGIR
AWTDGEKQQLLNTGRVQGYDGYFVLSVEQYLELSDSANNIHFWRQSEIGRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AREDISYNNERVITSMQAMINETPLEIDLYRYUDVSGRTEQFGKFSVINYDLNQVITTT
VMKHTKLI FSANGQVIEVQYELLKSI XYWMT QYDNMGRWYLDLIRVGYDANI TRYFYB
YDDOGQLYTSVNDKTQMRY SYDLIGNINLLEHGNSARLITPLRYDLRDRITRLGEIQY
KMDEDGFLRQRGNET FFYNSWGLLNKAYNKVSGWTVQYCYDGLGRRYABKSSLOGHLQ
FFYADLSNP IRVTHLYNHSSSELTSLYYDLQGHLIAMELSSGEBYYVACDNTGTPLAV
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WTTPNHHIWKHLNAVPQPFNLYSFENNYPVGRIQDVAKYTTDIGSWLELFGFQLHNVL
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                                                                VGSDVDTETEGGASPHALRWWRRGMKSEHSSCLSSRANSALSITDTDHERKSDGEND
MPGSPHNOFTERPLPPPRACTCTRKPPPAADSLQRRSWTTRSQPSPAAPTPPTS
TOSYNLHNSWYLNSWY IBLETHFILFKHGSGSSAIFSAASQNYPLTSNTVYSPPRPT
PRNTFSRPAFTFREYRCCWRKCTALSATAITVTLALLLAYY ANHLFGLTWQLQVPR
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                          /db_xref="SPTREMBL:Q9W6V6"
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GPECDVPEEQC1DPTCFGHGTC1MGVC1CVPGYKGE1CEEEDCLDPMCSGHGVCVQGE
                                                      TLNEYSQELRLNYNSQSRKRKNTDQSTQDMEFCBTPHILCSGYQTDLHGVSBHSYPLE
                                                                                                                                                                KQEPKNSEEPQQAPRNLILTSLQETGFIEYMDQGAWHMAFYNDGKKVEQVFVLTTAIE
                                                                                                                                                I PPGLFWRFQITIHHPVYLKFNISLAKDSLLGIYGRRNI PPTHTQFDFVKLMDGKQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="EGF repeat 1"
1618. :1710
/gene="ten-1"
/note="EGF repeat 2"
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2200. .2304
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gene="ten-1"
note="EGF repeat 5"
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note="EGF repeat 6"
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'gene="ten-1"
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Oohashi,
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7129 AATGCTGTC---CCACAACCATTCAATCTACTCATTTGAAAATAACTACCCAGTTGGC 7185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLysPhe 160
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                                                                                                                                                                                                                                                                                                              21 AsplyrAspValLeuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu
                                                                                                                                                                                                                                                                                                                                                                SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                 81 PheGlnLeuHisAsnVallleProGlyTyrProLysProAspMetAspAlaMetGluPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAATGACCCCCAGGTATAGTGATGCCAAGTGCTATGAGGGAGTGAAGCAACCGAGGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7486 GCAGCTATTCCTTCAGTATTTGGAAAGGCATCAAATTTGCTATCAAGGATGGCATCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrThrAspilelleSerValAlaAsnGluAspGlyArgArgValAlaAlaIleLeuAsn
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118
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Mus musculus mRNA for Ten-m1, complete cds.
AB025410
                                                                                                                                                                Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                       Indels:
                                                                                                                                                     Length:
                       note="YD repeat 24" 730. .6801
                                                            /note="YD repeat 25"
6802. .6867
                                                                                                  /note="YD repeat 26"
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             gene="ten-1"
                                                'gene="ten-1"
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Ten-ml.
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77.61%
58.71%
61.98%
                                  6730.
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Best Local Similarity:
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LOCUS
DEFINITION
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Cohashi,T., Zhou,X., Feng,K., Richter,B., Moergelin,M., Perez,M.T., Su,W., Chiquet-Ehrismann,R., Rauch,U. and Faessler,R. Mouse Ten-m/Odz is a new family of dimeric type II transmembrane proteins expressed in many tissues

Q. Cell Biol. (1999) In press

2. (bases 1 to 8373)
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KWTGSDCSTELCTWEGGSHGYCSRGICOCEGGWGGTCTERSCHSHCAEHGQCKDGKC
BCSFGWEGDHCTIAHYLDAYLDAYDBOTGCLGFGNGRCTLDDNGMHTOYCQVGWGGTGCNIYW
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IFYDELKFLIGWGSTHYVPQDISFDSRRACYITGQVVAVDGTPLVGVNVSFLHHSDYG
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PSCDISNIFSBNPITLLTBSPLTSFGGSCPERGTIYPELQVVQBEIPTPSSFVRLEYLSS
RTPGYKTLLRILTHSTIPYGMIKVHLTVSVEGRLTCKWFPAAINLVYTFAMNKTDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLHEYNQELRRNYNSQSRKRKDVEKSTQE1EFCETPPTLCSGYHTDMHSVSRHGYQLB
MGSDVDTETEGAASPDHALRNWIRGMKSEHSSCLSSRANSALSLTDTDHERKSDGENG
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YNDGKKMEQVFVLTTAIBIMDDCSTNCNGNGECISGHCHCFPGFLGPDCARDSCPVLG
GGNGEYEKGHCVCRNGWKGFBCDVPEBQCIDPTCFGHGTCIMGVCICVPGYKGBICEB
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GOKUWGIJABALVSVOYEYEMCPEFILMEORTVVLOGFEMDASNLGGMSLINKHITENPO
GSUYVGDPRIVVRRI FPEGNENSVELLELENBURTHSTSPARKYTJAMDPROSESIYLSDTN
TRKVYKLKSLVETRODSKNEFWVAGTGOCLFPOGERGOGGKASEASLNSPRGITVD
RHGFIYFVDGTMIRRIDENAVITTVIGSNGLITSTOPLSCOSGMDITQVRLEMPTDLAV
RHGFIYFVDDNIJVLOJESBRRRVRITAGRFHYGOVGGIDHFUJOKVALHSTLESARA
ISVSHGGLLFTARTDERKVNRIQOVTTNGEISIIAGAPTDCDCKIDPNCDCFSGDGGY
AKDAKWAPSSLAVSPDGTLYVADLGAVRITSKROAHLNDNNLYEETASPAJOGELY
FTVNGTHLHYMLITRRYVXNRTYNBEGDLGAITSSNGNSYHIRRDAGGMPILLVVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MEQTDCKPYQPLSKVKHEMDLAYTSSSDESEDGRKPRQSFNSRE
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SQNYPLTSNTVYSPPPRPLFRSTFSRPAFTFNKPYRCCNWKCTALSATALTVTLALLL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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NATFPTGEVSSFHSDLEKLTKVALDTSNRENVLMSTNLTATSTIYILKQENTQSTYRV
SPDGSLRVTFASGMEINLSSEPHILAGAVNPTLGKCNISLPGEHNANLIEWRQRKEQN
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HGNSARLTPLRYDLRDRITRLGEIQYKMDEDGFLRQRGNDIFEYNSNGILGKRYNKYS
GWTVQYYYDGLGRRVASKSSLGQHLQFFYADLANPIRVTHLYNHTSAEITSLYYDLQG
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Submitted (29-MR-1999) Toshitaka Oohashi, Okayama University
Medical School, Dept. Mol. Biol. & Biochem.; 2-5-1 Shikata-cho,
Okayama, Okayama 700-8252, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (E-mail:oohashi@cc.okayama-u.ac.jp, Tel:+81-86-235-7128,
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/db_xref="G1:4760776"
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/dev_stage="adult"
/tissue_lib="brain"
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Location/Qualifiers
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/strain="Balb/c"
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                                                                                                                                                                                                                                                                                                                                                               CDS
                          REFERENCE
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                                                                                TITLE
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GAATTAACTTATGAGCTTCTTCAACTGCAGACAAAACCCCAAGAGTGGGATCCTGGAAAG 7532
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           PHGGIYDFLIKLVHLGQRDYDVVAGRWTTPNIHIWKQLNLLERFFNLYSFENNYPVGK
IQDVAKYTTDIGTWLELFGFQLHNVLPGFPRPELENMELTYELLQLQTKTQEWDPGKM
ILGIQCELQKQLRNFISLDQLPMTPOĞNBGRCLEGKQPRFAVPSFYGFKGIKFAIKE
GLYADLIIGANBEDSRRLAAILNNAHYLENLHFTIGKDTHYFIKLGSLEBDIVLIGN
TGGRRILENGVNYTVSQMISVLNGRIRFRADIQLQLGAGALCFNIRYGTTVEBERGHYLE
NARQRAYAQAWTQEQRELQEGERGTRVWTEGEKQQLLGTGRVQGYDGYFVLSVEGYLE
LSDSANNIHFMRQSEIGRR
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HLIAMELSSGEEYYVACDNMGTPLAVFSSRGQVIKEILYTPYGDIYHDTYPDFEVIIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 ArgPheAspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLys 158
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Conservative:
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KAPSGLAVSPDGTLYVADLGNVRIRTISRNQAHLNDWNIYEIASPADQELYQFTVNGT
HLHTLMLITRDYVNRFTYNSEGDLGAITSSNGNSVHIRRDAGGMPLMLVVPGGQVYWL
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RVTFASGMEIGLSSEPHILAGAVNPTLGKCNISLPGEHNANLEWRQRKEQNKGAVVSA
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YYDGLGRRVASKSSLGQHLQFFVDATANPIRVTHLYNHTSSEITSLYYDLQGHLLAME
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MGSDVDTETEGAASPDHALRMMIRGMKSEHSSCLSSRANSALSLTDTDHERKSDGENG
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AYVIAVHLFGLTWQLQPVEGELYANGVSKGNRGTESMDTTYSFIGGKVSDKSEKKVFQ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                           Strahm, B., Niemeyer, C., Belohradsky, B.H.
                                                                                                                                            Epstein-Barr virus-negative boys with non-Hodgkin lymphoma are mutated in the SH2DIA gene, as are patients with X-linked lymphoproliferative disease (XLP)
                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-OCT-1998) Medizinische Genetik, LMU-Muenchen,
                                                                        Hellebrand, H., Fink, F.M
                                                                                                                                                                                                                                                                                                        2 (bases 1 to 8297)
Brandau,O., Oohashi,T., Faessler,R. and Meindl,A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function="putative receptor molecule"
                                                                                                                                                                                                                               Hum. Mol. Genet. 8 (13), 2407-2413 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                         . 29, Muenchen 80336, Germany
Location/Qualifiers
                                                                              Weiss, M.,
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/db_xref="G1:6165845"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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'product="tenascin-M1"
                               Mammalia, Eutheria, Prima
1 (bases 1 to 8297)
Brandau,O., Schuster,V.,
Kreczy,A., Friedrich,W.,
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/map="Xq24-q25"
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YTTDIRSWLELFGFQLHNVLPGFPKPELENLELTYELLRLQTKTQEWDFGKTIGGDG
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LIGVANEDSRRLAAILNNAHYLBNLHFTIEGRDTHYFTKLGSLEEDLVLIGWTGGRI
LENGVNYTVSQMTSLLNGRTRRFADLDQLQHGALCFNIRYGTVBEEKNHVLEIGRGGRI
LENGVNYTVSQMTSLLNGRTRRFADIQLQHGALCFNIRYGTTVBEEKNHVLEIARQRA
VAQAMTKEQRRLQEGEEGIRAMTEGEKQQLLSTGRVQGYDGYFGLSVEGYLELSDSAN
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LSSGBEYYVACDNTGTPLAVFSSRGQVIKEILYTPYGDIYHDTYPDFQVIIGFHGGLY
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Search completed: August 14, 2004, 12:03:02 Job time : 3600.05 secs

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AC07359 Mus muscu
AK12249 Mus muscu
AB025413 Mus muscu
AF059485 Mus muscu
AC133064 Rattus no
AC133064 Rattus no
AC090378 Homo sapi
AL022718 Human DNA
AF100772 Homo sapi
AB026979 Danio rer
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AP002768 Homo sapi
AK056531 Homo sapi
AJ293019 Gallus ga
AC074048 Mus muscu
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AL163512 Mouse DNA
AL831716 Mouse DNA
BX324192 Mus muscu
AC114058 Rattus no
AX876360 Sequence
BD156088 Primer fo
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AK001748 Homo sapi
AX876525 Sequence
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BX537983 Homo sapi
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AX675551 Sequence
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AX662359 Sequence
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cqm2 1/USTSPTO spool/US10029020/xunat_06082004_112216_29275/app_query.fasta_1.3519
-Q=/Cqm2_1 1/USTSPTO spool/US10029020/xunat_06082004_112216_15/app_query.fasta_1.3519
-DB=GenEmbl -QFWT=fastap -SUPFIX=pbn.rge -MINATGH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-Dits -START=1 -FRVB=-1 --MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=CS10029020 @CGN 1 1 19065 @runat_06082004_112216_29275 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLÖCK=100 -LONGLOG
-DBV_TIMBOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                            ; Search time 1344.2 Seconds (without alignments) 2450.585 Million cell updates/sec
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        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                     nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3470272 seqs, 21671516995 residues
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                                                                                                                                                               August 13, 2004, 23:35:57
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Maximum DB seq length: 200000000
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AK127101

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/codon start="
/prodec="hypothetical protein, N-terminus truncated"
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/prodec="hypothetical protein"
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/clone_lib="686 (synonym: hlcc3). Vector pSportl_Sfi; host
DH10B; sites SfilA + SfilB"
/dev stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   derman Genome Project.

This clone (DKFZp686D0412) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
HSMB06114 3486 bp mRNA linear PRI 17-JUN-2003
Homo sapiens mRNA; cDNA DKFZp686D0412 (from clone DKFZp686D0412).
BX537983
                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                 1 (bases 1 to 3486)
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther.R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2): Email s.wiemann@dkfz.heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
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/gene="DKFZp686D0412"
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/db_xref="taxon:9606"
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S. Chases 1 to 3320)

S. Sagai, T. and Yamamoto, J.

Direct Submission

S. Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Direct Submission

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kean Technology Trade and Industry of Japan; CDNA full insert sequencing: RAB, HRI, and Biotechnology Center etc.); 5-6 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Inceation/Qualifiers

Inceation/Qualifiers
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                                       AK127101
Homo sapiens cDNA FLJ45158 fis, clone BRAWH3043034, highly similar
to Mus musculus neuregulin 1 (Nrg1).
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                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="BRAWH3"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                               oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
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/db_xref="taxon:9606"
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AK127101.1 GI:34533862
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gangolli, E.A., Patturajan, M., Vernet, C.A., Malyankar, U.M., Kekuda, R., Stone, D.J., Anderson, D., Shimkets, R.A., Burgess, C.E., Zerhusen, B.D., Liu, X., Spytek, K.A., Casman, S.J., Boldog, F.L., Smithson, G., Li, L. and Ji, W.
Polypetides and nucleic acids encoding same
Patent: WO 02007453-A 13 25-JUL-2002;
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/db_xref="taxon:9606"
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                                      /gene="DKFZp56400423"
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKPZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp56400423) is available at the RZDD in Berlin.
Please contact the RZDD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens mRNA; cDNA DKFZp56400423 (from clone DKFZp56400423); partial cds.
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/protein id="CAB45719.1"

/db_xxef="61:5262553"

/db_xxef="SPTREMBL: Q9Y452"

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ARVLELARQRAANGAWARECQRLEEEEEGEGLRAWTEGEKQQVLSTGRVQGYDGFFVISV
EQYPELSDSANNIHFMRQSEMGRR"
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1 (bases I to 5269)
Wambutt, R., Heubner, D., Mewes, H.W., Gassenhuber, J. and Wiemann, S. Direct Submission

Direct Submission
Submitted (16-70N-1999) MIPS, Am Klopferspitz 18a, D-82152
                                                                                                                                     SerGln1leAsnThrValLeuAsnGlyArgThrArgArgTyrThrAsp1leGlnLeuGln
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/note="etrong similarity to C-terminus of mouse DOC4"
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X1-2blue; sites NotI + SalI"
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/organism="Homo sapiens"
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/clone="DKFZp56400423"
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LNHAHYLENLHFTIDGYDTHYFYKPGPSEGDLAILGLSGGRRTLENGYNVTVSQINTV
LNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQRAVRQAMAREQQRLREG
BEGLRAWTEGEKQQVLSTGRVQGYDGFFVISVEQYPELSDSANNIHFMRQSEMGRR"
                                                                                                    Nagase,T., Kikuno,R., Ishikawa,K.I., Hirosawa,M. and Ohara,O. Prediction of the coding sequences of unidentified human genes.

XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 7 (1), 65-73 (2000)
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                                                                                                                                                                                                                                                                                                          Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913, Fax:+81-438-52-3913, On May 9, 2002 this sequence version replaced gi:7242958.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="This sequence was replaced that of fg06864 cDNA as representative cDNA sequence for KIAA1302."
                               Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
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                  Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg
                                                                                      LeuargGluGlyGluGlyLeuargalaTrpThrGluGlyGluLys 76
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Homo sapiens mRNA for KIAA1302 protein, partial cds.
AB037723 2 GI:20521827
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
j. .8993
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DH10B; sites Sfilm + Sfilm"
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/protein_id="CAE45850.1"
/db_xref="G1:34364829"
/translation="RIDQNGIISTLLGSNDLTSARPLSCDSVMDISQVHLEWPTDLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPMDNSLYVLDNNVVLQISENHQVRIVAGRPNHCQVPGIDHFLLSKVAIHATLESAIA
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KDGRVTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGDLAIL
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PELSDSANNIHFWRQSEMGRR"
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                               Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Well, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                            Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
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/note="hypothetical protein, N-terminus elongated,
differentially spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        German Genome Project.
This clone (DKFZp686K11107) is available at the RZPD in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="11q14.1"
                                                                                                                                                                                                                                                                                                                                        The German Human cDNA Consortium
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                                                                                            Homo sapiens (human)
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3488 TCCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCAG 3547
                                                                                                                                                            3548 TACGGGGCACTGTGCTTGAACACACTGCGGACAACGTTGCATGAAGAGAAGAAGAGGCACGG 3607
                                                                                                                                                                                                                                                                                  GTCCTGGAGCTGGCCGGAGAGAGCCGTGCGCCAAGCGTGGGCCCGCGAGCAGCAGAGA 3667
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Homo sapiens mRNA; cDNA DKFZp686K11107 (from clone DKFZp686K11107).
BX640737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8031 TCCCAGATCAACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCAG 8090
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Proteins associated with cell growth, differentiation, and death Patent: WO 02072830-A 22 19-SEP-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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                                                                                                   TyrGlyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg
                                                                                                                                                                                                                            41 ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnArg
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                                                                                                                                                                                                                                                                                                                                                  61 LeuArgGluGlYGluGlYLeuArgAlaTrpThrGluGlYGluLys 76
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/db_xref="taxon:9606"
/note="Incyte ID No: 7488573CB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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AX600210

AX600210.1 GI:28400252
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HSM806812
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------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                   * NOTE: This record contains 84 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* Will be sequenced to completion. In the event that

* the record is updated, the accession number will
                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s: gap of 100 bp

r: contig of 704 bp in length

r: gap of 100 bp

: contig of 743 bp in length

: gap of 100 bp
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contig of 722 bp in length
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contig of 693 bp in length
gap of 100 bn
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of 741 bp in
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of 707 bp i
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Center clone name: 886_F_14
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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12: gap of 100 bp

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 170156)

2 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

14 Published Only in DataBase (2000)

22 (bases 1 to 170156)

25 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

2 Diases 1 to 170156)

3 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

2 Diases 1 to 170156)

3 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

3 Direct Submission

3 Lada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

3 Lada,T., Totoki,Y., Genomic Sciences Center (GSC);

3 Lada,T., Lishi,Marsaion

3 Lada,T., Lishi,Marsaion

4 Lada,T., Hattori@ssc.riken.go.jp/, Tel:81-42-778-9923,

4 Pax:81-42-778-9923,
                                                                                                                                                                                                                                                                                                                                                                                                 ARUU2412
Homo sapiens chromosome 11 clone RP11-7H7 map 11q, WORKING DRAFT
SEQUENCE, 18 unordered pieces.
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1168 161267: gap of 100 bp
1268 164102: contig of 2835 bp in length
4103 164202: gap of 100 bp
1203 167603: contig of 3401 bp in length
164 167703: gap of 100 bp
1704 170156: contig of 2453 bp in length.
Location/Qualifiers
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                                        Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 159074 bases at least Q40 Consensus quality: 164580 bases at least Q30 Consensus quality: 167092 bases at least Q20 Inser size: 168456; sum-of-contigs Quality coverage: 5.57x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                          Minomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkwa,B., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Nagahari,K., Masuho,Y., Nawai,B., Suzuki,Y., Sugano,S.,
NBDO human cDNA sequencing project
Unpublished
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NYDNSFRVTSMQAVINETPLPIDLYRYDDVSGKTEQFGKFGTYZDIGGITTANTH
                                                                                                                                                              Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens (human)
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|cell_type="teratocarcinoma"
|clone_lib="NT2RP7"
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Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP7008013"
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
L Published Only in Database (2000)
B C bases 1 to 186084)
B Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Direct Submission
C bubmitted (10-7UL-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEM), Genomic Sciences Center (GSC),
C Suchiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriagsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
On Mar 21, 2001 this sequence version replaced gi:11071944.
                                                                                                                                                                                                  Homo sapiens genomic DNA, chromosome 11q, clone:RP11-673F18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                             115973 CTGCGGGAAGGGGAAGGGCTGCGGGGCTGGACAGAGGGGGAGAAG 115926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27784 CTGCGGGAAGGGGAGGAGGCCTGCGGGCCTGGACAGGGGGAGAAG 27737
   61 LeuArgGluGlyGluGlyJeuArgAlaTrpThrGluGlyGluLys 76
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/mol_type="genomic DNA"
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/clone="RP11-673F18"
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                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens (human)
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AP002768/c
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FEATURES

COMMENT

Pred. No.:

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DRIGIN

LOCUS DEFINITION

RESULT 12

AK056531

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Bukaryoratus Euteleostomi; Bukaryorata; Euteleostomi; Bukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Et Lewis,L.R., Hume,J., Edwards,C., Harris,C., Dadison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J., Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J., Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S., Chen,Z., Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M., Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M., Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,S., Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R., Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R., Neal,D., Nelson,A., Nguyen,M., Oguh,M., Parish,B., Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S., Muzny,D.M., Rives,M., Scherer,S., Sodergren,B., Weinstock,G., Worley,K. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC074048 1.near HTG 16-OCT-2001
Mus musculus chromosome 7 clone RP23-18J2, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                         610 TATGGTGCGCTGTGTCTGAACACTCGCTACGGGACCACTTTGGACGAGGAGGAGGAGGCCCGA 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-JUL-2000) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 25, 2001 Lhis sequence version replaced gi:13162473.

Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                         41 ValleuGluleuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg
                                                     SerGlnIleAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln
                                                                                                                                                                                                                                                                                                                                                                                            61 LeuargGluGlyGluGlyLeuargalaTrpThrGluGlyGluLyS
     US-10-029-020-14_COPY_2650_2725 (1-76) x GGA293019 (1-834)
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HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
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Direct Submission
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AUTHORS
TITLE
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JOURNAL
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AC074048
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/db_xref="GI:9909617"
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                              2132 TACGGGGCACTGTGCTTGAACACACGCTACGGGACAACGTTGGATGAGGAGAAGAACGCGG
                                             SerGlnIleAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln
                                                                             2072 TCCCAGATCAACACAGTACTTAGTGGCAGGACTAGACGCTACACAGACATCCAGCTCCAG
                                                                                                                                                21 TyrdlyalaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg
                                                                                                                                                                                                                                                      41 ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg
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                                                                                                                                                                                                                                                                                                                                                       LeuArgGluGlyGluGlyLeuArgAlaTrpThrGluGlyGluLys 76
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teneurin-4 (TEN4 gene)
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US-10-029-020-14_COPY_2650_2725 (1-76) x AK056531 (1-2685)
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Mismatches:
Indels:
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Matches:
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/evidence=experimental
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Gallus gallus partial mRNA for AJ293019
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TEN4 gene; teneurin-4.
Gallus gallus (chicken)
Gallus gallus
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/gene="TEN4"
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94.88%
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                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).
NOTE: This is a "working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 8.2x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 226256)
Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,
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                                                                                                                                                                                                                                                                103064: contig of 103064 bp in length 103164: gap of unknown length 124754: contig of 21590 bp in length 124864: gap of unknown length 147843: contig of 22989 bp in length 147943: gap of unknown length 168730: contig of 20787 bp in length 192230: contig of 23400 bp in length 192330: contig of 23400 bp in length 192330: gap of unknown length 192330: contig of 16430 bp in length 208760: contig of 16430 bp in length
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/db_xref="taxon:10090"
/chromosome="7"
/clone="RP23-18J2"
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Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Burac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Davis, C., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., Gorrell, J.H., Gunarathe, P., Haller, G., Hernandez, J., Hogues, M., Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, X., Kelly, J., Kelly, S., Kovar, C., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Martin, R., Nassey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S., Neal, D., Nelsen, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B., Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G., Pranch, Lead, C., Liu, S., Sherer, S., Sodergren, E., Weinstock, G., Pranch, Lead, S., Subnission
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Direct Submission
Submitted (28 PFBB-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Feb 28, 2001 this sequence version replaced gi:12963002.
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities or 2 chemistries. If the sequence quality does not meet this standard, it will be indicated in the annotation.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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/organism="Mus musculus"

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/db zref="taxon:10090"

/chromosome="7"
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complement(2209, .2323)
/rpt_family="L2"
2468, .2493
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/rpt_family="B1-F"
3397. .3501
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complement(5737..5848)
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118. .1165
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[family="PB1D10"
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rpt_family="B4A"
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5733. .5800
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Direct Submission
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41 ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg 60
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Matches:
Conservative:
Mismatches:
Indels:
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Job time : 1496.2 secs
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35660. .35869
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36089. .36106
/rpt_family="B4"
36107. .36239
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Best Local Similarity:
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/rpt family="B1-F"
10971 .11355
/rpt family="Lx6"
complement(11571. .13187)
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complement (25094. 25241)
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complement (126937. 27347)
/rpt_family="LIMCc"
27569. 27613
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complement (28594. .28633)
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complement (28841. .28955)
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complement(10121. 10237)
rrpt family="B1-F"
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               rpt_family="(CCTG)n"
0440. .10509
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Mon Aug 16 09:01:03 2004

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Command line parameters:

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-LOOPCLEG -LOÖPEXT=0 -UNITS=bits -START=1 -END=1 - MARTKE-blosming2

-TRANS=human40.cdi -LIST=8.5 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100

-THR MIN=0 -ALIGN=15 -MODE=LOCAL_OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0

-MAXIEN=2000000000 -USRE-MITRA020_0CGN 1 519_@runat_0608204 114103_259

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-LONGLIG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5

-FGAPOP=6 -FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7
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| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 2
4 13 US-10-383-201-43

15 US-10-290-270-13

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1 9 US-09-773-517-12

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Publication No. US20040029226A1
GENERAL INFORMATION:
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1175 GAGATCACGGAGGACACAGCCAGCTTGGCCTGTGCCAACCGACGTCTCCCTATACCCC 1234
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                                                                                                                                                                                                                                                                                       ProGlyTyrProLeuThrSerSerThrValTyrSerProProArgProLeuProArg 320
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               LeuAsnSerAsnIleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThr
                                                                                            LeuGlnAspAsnLeulleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                   341 CysAlaAlaLeuSerAlaIleValIleSerAlaThrLeuValIleLeuLeuAlaTyrPhe
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### TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same CURRENT APPLICATION NUMBER: US/10/029,020

### PRIOR APPLICATION NUMBER: US/10/029,020

### PRIOR FILING DATE: 2000-12-19

### PRIOR PLING DATE: 2000-12-19

### PRIOR PLING DATE: 2000-12-20

### PRIOR PLING DATE: 2001-08-10

### PRIOR FILING DATE: 2001-08-10

### PRIOR FILING DATE: 2001-08-10

### PRIOR PLING DATE: 2001-08-29

### PRIOR PLING DATE: 2001-08-29

### PRIOR PLING DATE: 2001-07-24

### PRIOR PLING DATE: 2001-09-14

### PRIOR PLING DATE: 2001-09-14

### PRIOR PLING DATE: 2001-05-29

### PRIOR PLING DATE: 2001-05-29

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; Publication No. US20040033971A1
; GENERAL INFORMATION:
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LENGTH: 8354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrValleuSerProGluHisProValArgLeuTrpGlyArgSerThrArgSerGlyArg 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 ArgTyrThrSerSerSerAla***SerGluGluGlyLysAlaProGlnLysSerTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 CGCTACACCAGCTCGTCCGCGGACAGCGAGGCAAAGCCCCGCAGAAATCGTACAGC
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
PRIOR FILING DATE: 2002-09-23
PRIOR PEDICATION NUMBER: 10/051,874
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-03-16,928
PRIOR PILING DATE: 2002-03-22
PRIOR PILING DATE: 2002-03-22
PRIOR PILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SOFTWARE: CuraseqList version 0.1
LENGTH: 8354
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2127.00
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ORGANISM: Homo sapiens
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LOCATION: (35)..(8341)
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Best Local Similarity:
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Argiv: 99.25*	215 1155 61 215 81 81 275 275 335		201 ANIMALY 635 AACCGG 221 SerGly 695 TCCGGA 241 LeuAsn 755 CTCAAC 755 LeuGln 815 TTGCAG 281 SerAsp	

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US-09-773-517-12
Sequence 12, Application US/09773517
Sequence 12, Application US/09773517
Sequence 12, Application US/09773517
Sequence 12, Application US/09773517
GENERAL INFORMATION:
APPLICANT: Slivewski, Mark
APPLICANT: Slivewski, Mark
TILE OF INVENTION: USe of Heregulin as a Growth Fact
FILE REFERENCE: P1145R1
CURRENT APPLICATION NUMBER: US/09/773,517
CURRENT FILING DATE: 2001-02-02
PRIOR PILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 14
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Mismatches:
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
   REPRENCE/DOCKET NUMBER: 32171
REPRENCE/DOCKET NUMBER: P1145
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3111 L-1
                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                 NO: 12:
                                                                                                                                                                            TOPOLOGY: Linear MOLECULE TYPE: nucleic acid SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                          LENGTH: 3111 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity:
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994 TCCGGAGAGCCCCTGCCGGCGCGCCCCAGGAGCCTGCCCCACGAGAACTGGCTG
                                                                         LeuAsnSerAsnIleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThr
                                                                                                                                                                                                        1054 CTCAACAGCAACATCCCCCTGGAGACCAGAAACCTAGGCAAGCAGCCATTCCTAGGGACA
                                                    AsnArgGlyAsnPheThrProArgSerAsnProSerProAlaProThrAspHisSerLeu
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APPLICANT: Sliwkowski, Mark
TITLE OF INVENTION: Use of Heregulin as a Growth Factor
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy --
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winterin, (Genentech)
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APPLICATION NUMBER: US/09/792,025
FILING DATE: 23-Feb-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/020,598
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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Patent No. US20020042087A1
GENERAL INFORMATION:
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241 LeuAsnSerAsmilleProLeuGluThrArgAsmiLeuGlyLysGlnProPheteuGlyThr 260  bb 1054 CTCAACAGCAACTCCCCTGGAACCTAGGCAACCTAGGCACTTCTAGGGCACTTCTAGGGCACTTCTAGGCACTTCTAGGCCATTCTAGGCCATTCTAGGCCATTCTAGGCCATTCTAGGCCATTAGTAGGCCATTAGTAGGCCATTAGTAGGCCATTAGTAGGCCATTAGTAGGCCATTAGTAGGCCATTAGTAGGCCATTAGTAGGCCATTAGTAGGCCATTAGTAGGCCATTAGTAGGCCACCTCCCCCCCC	Patent No. USCO200081299A1   APPLICANT: Generatech, Inc.

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1054 CTCAACAGCAACATCCCCCTGGAGACCAGAACCTAGGCAAGCAGCCATTCCTAGGGACA 1113
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                201 AsnArgGlyAsnPheThrProArgSerAsnProSerProAlaProThrAspHisSerLeu 220
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                                                                GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp
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APPLICANT: Sliwkowski, Mark
APPLICANT: Kern, Jeffrey
TITLE OF INVENTION: Use of Heregulin as a Growth Factor
FILE REFERENCE: P1145R1
CURRENT APPLICATION NUMBER: US/10/453,183
CURRENT FILING DATE: 2003-06-03
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                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OOFWARE: Winbatin (Genentech)

CURRENT APPLICATION NOTAE:

APPLICATION NUMBER: US/10/290,578

FILING DATE: 08-No. US20030078389A1-2002

CLASSIFICATION ATAE:

APPLICATION DATA:

APPLICATION AND ADAIS:

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Matches:
Conservative:
Mismatches:
Indels:
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CITY: South San Francisco
STATE: California
                                                                                                     Sliwkowski, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: P1043
TELECOMMUNICATION INFORMATION:
TELEFONS: 415/225-1994
TELEEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: <Unknown>
APPLICATION NUMBER: 60/021640
FILING DATE: 12-Jul-96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
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                                                                              APPLICANT: Schaefer, Gabriele M.
Sequence 1, Application US/10290578
Publication No. US20030078389A1
GENERAL INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity:
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Pred. No.:
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GENERAL INFORMATION:

APPLICANT: Alsobrook II, John et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REPERBENCE: 12402-5698

CURRENT APPLICATION NUMBER: US/10/29020

PRIOR APPLICATION NUMBER: 10/029020

PRIOR APPLICATION NUMBER: 00/372,022

PRIOR APPLICATION NUMBER: 60/372,022

PRIOR APPLICATION NUMBER: 60/372,022

PRIOR PILING DATE: 2002-03-20

PRIOR PILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-13

PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2002-01-16

PRIOR FILING DATE: 2002-01-16

PRIOR FILING DATE: 2002-01-16

PRIOR FILING DATE: 2002-01-16

PRIOR FILING DATE: 2002-01-16

PRIOR FILING DATE: 2002-01-16

PRIOR FILING DATE: 2002-01-16

PRIOR FILING DATE: 2002-01-16

PRIOR FILING DATE: 2002-01-16

PRIOR FILING DATE: 2002-01-16

PRIOR PRIOR PRIOR NUMBER: 10/051,874

PRIOR PRIOR PRIOR DATE: 2002-01-16

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                     340
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261 LeuGlnAspAsnLeuIleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyr
                                                                        SerAspGlyHisPheLeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSer
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 55, Application US/10383201 Publication No. US20040029226A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.24e-204
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ORGANISM: Homo sapiens
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Percent Similarity:
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US-10-383-201-55
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396
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Matches:
Conservative:
Mismatches:
Indels:
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         PRIOR APPLICATION NUMBER: US/09/243,198
PRIOR FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: US 60/073,866
PRIOR FILING DATE: 1998-02-04
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 12
LENGTH: 3111
                                                                                                                                                                                                                                       5.07e-206
2122.00
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                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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US-10-453-183-12
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Best Local Similarity: 98.75*   Mismatches: 5   Query Match: 13   99.16*   Indels: 0   0	4 1 SerSerGlurhitellyaklafyråspollakpalakrjeualafyrölyserkryval 60  21 1 (10)	

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1203
                                                                      1083
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964 AGCACCITCGCCTGGCCGGCCITTAACCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAG
                                                                                                                               1084 GTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGCAGATGACG
                                                                                                                                                                                                        1024 TGCGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCTGCTGGCATACTTT
                                                                                                                                                                                     ----TyrGluIleThrGluAspThrAlaSerSerTrpProValProThrAspValSerLe
                                    341 CyshlaAlaLeuSerAlaIleValIleSerAlaThrLeuValIleLeuLeuAlaTyrPhe
                                                                                                          361 ValAlaMetHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMet-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/290,578
FILING DATE: 08-No. US20030078389A1-2002
CLASSIFICATION: <a href="https://documents.com/">CLASSIFICATION: <a href="https://documents.com/">CLASSIFICATION: <a href="https://documents.com/">CLASSIFICATION: <a href="https://documents.com/">CLASSIFICATION: <a href="https://documents.com/">CURROWN></a>
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Matches:
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APPLICATION NUMBER: US/08/891,845
FILING DATE: «Unknown»
APPLICATION NUMBER: 60/021640
FILING DATE: 12-Jul-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                       US-10-290-578-11; Sequence 11, Application US/10290578; Publication No. US20030078389A1; GENERAL INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2387 base pairs
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STRANDEDNESS: Single
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APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
ITILE OF INVENTION: Proceeins and Nucleic Acids Encoding Same
ITILE OF INVENTION: Proceeins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT PILING DATE: 2003-01-22
PRIOR PELING DATE: 2001-01-22
PRIOR PLILING DATE: 2001-01-22
PRIOR PLILING DATE: 2001-01-04
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                                                                                   1 CATCCGGGCGGCCTGCAGAACCACGCGCGCGCTCCGGACGCCGCCGCCGCCGCTCTCGCAC
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SEQ14-X-AT-28-64-76 (1-400) x US-10-290-578-11 (1-2387)
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Io. US20040022781A1
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Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Wolenc, Adam R
APPLICANT: Wolenc, Adam R
APPLICANT: Wernet, Corine
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Shinkets, Richard A
APPLICANT: Shinkets, Richard A
APPLICANT: Spaderna, Steven K
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Rekuda, Ramesh
APPLICANT: Patturajan, Meera
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Eisen, Andrew J
Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
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Gusev, Vladimir Y
Gangolli, Esha A
Guo, Xiaojia S
Shenoy, Suresh G
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Rastelli, Luca
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Query Match:
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TCAGGCCGCAGCTCCTGCCAGTCGAGTCCAACTCAGCCCTCACCCTGACAGATACG 630
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                                                  GlualaaspThrValLeuSerProGluHisProValArgLeuTrpGlyArgSerThrArg 137
                                                                                                                SerGlyArgSerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThr 157
                                                                                                                                                                                                                                                                                                         195 AlaSerIleAsnSerLeuAsnArgGlyAsnPheThrProArgSerAsnProSerProAla
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US-10-038-854-35
Sequence 35, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spyrek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Vernet, Corine
PUBLICANT: Vernet, Corine
PUBLICANT: Eisen, Andrew J
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APPLICANT: Smithson, Glemda
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT PILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR PILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR PILING DATE: 2010-04-13
PRIOR PILING DATE:
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Matches:
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Mismatches:
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Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
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Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
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Gusev, Vladimir Y
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Gangolli, Esha A
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Shenoy, Suresh G
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Boldog, Ferenc
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Kekuda, Ramesh
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Rastelli, Luca
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Mismatches:
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Matches:
                                                                                                                 APPLICANT: Origene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer
FILE REFERENCE: 3U 103 R1
CURRENT APPLICATION NUMBER: US/10/144,194A
CURRENT FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Version 3.0
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                                                                          ; Sequence 81, Application US/10144194A; Publication No. US20030215809A1; GENERAL INFORMATION:
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43.95%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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; LOCATION: (435)
US-10-144-194A-81
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1219 ACC-
                                                             JS-10-144-194A-81
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                PheThrLeuArgGluLeuGlyLeuGluGluValThrProProHisGlyThrLeuTyrArg
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Mismatches:
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Pred. No.:
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APPLICANT: Vernet, Corine A
APPLICANT: Vernandee, Elma
APPLICANT: Pernandee, Elma
APPLICANT: Pernandee, Elma
APPLICANT: Brimkets, Richard A
APPLICANT: Brimwets, Richard A
APPLICANT: Mishra, John L
APPLICANT: Majurder, Kumud
APPLICANT: Majurder, Kumud
APPLICANT: Majobugall, John
TILLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR PILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 75
LENGTH 2496
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US-09-808-602-75
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880 ACCACĞCCTGAGTCTGTGCAGCTGCAGGACAGCTGGGTGCTC	242 AsnSerAsnIleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThrLeu	922 AACAGCAACGTGCCGCTGGAGACCAGG	262 GlnAspAsnLeulleGluMetAsplleLeuGlyAlaSerArgHisAspGlyAlaTyrSer	948	282 AspGlyHisPheLeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSer		ProGlyTyrProLeuThrSerSerThrValTyr	)3 CCTGGCTACCCACTGACCTCAGGAACAGTTTATACTCCACCTCCCAGGCTGTTACCTAGA	SerThrPhe	:::      :::    3 aatacattttccaggaatgcattcagctgaaaagccctccaagtattgtagctggaaa	11 CysAlaAlaLeuSerAlaileValileSerAlaThrLeuValileLeuLeuAlaTyrPhe	3 TGTGCTGCTTTATCTGCAATTGCTGCTGCAGTCCTGCTTGCCATCCTGCTAGCATATTTC	-	:::	1 Glullerepro 391	3 AGCAACGGGCTGCCGGCCGCGCGCGCGCGCGCACGACGACGGCGCGCGC
88	24	92	26	94	28	949	301	1003	321	1063	341	1123	361	1183	381	1243
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Search completed: August 15, 2004, 00:56:30 Job time : 659 secs

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Sequence Sequence

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Run on:

Sequence:

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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-640-958-11
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08891845;
Patent No. 6096873...
GENERAL INFORMATION:
APPLICANT: Schaefer, Gabriele M.
APPLICANT: S11Wkowski, Mark
ITILE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPENDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REPERENCE/DOCKET NUMBER: P1043
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
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TELEX: 910/371-7168
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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-Q-/cgn2 1/USPTO spool/MITRAQ20/runat 06082004_114102_237/app_query.fasta_1.583
-D8=Issued patents NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0-UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SOORE=pct - THR MAX=100 -THR MIN=0 -ALIGM=15
-WODE=LOCAL -OUTFNT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USFR=MITRAQ20 @CGN 1 1 69 @runat 06082004 114102_237 -NCPU=6 -ICPU=3 -NO_MAPP-LARGEOUSRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -ROAPOP=10 -LONGLOG -FRAPEDST=7
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Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
                                                                    August 14, 2004, 19:26:15; Search time 103 Seconds (without alignments) 2155.149 Million cell updates/sec
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Sequence 2,
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                    nucleic search, using frame_plus_p2n mode]
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US-09-514-573-3
US-08-91-845-1
US-09-514-573-1
US-09-514-573-1
US-09-514-573-11
US-09-231-899-69
US-09-051-899-69
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US-09-095-443-1
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Maximum Match 1008
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Xgapop 10.0 , Ygapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 ValAlaMetHisLeuPheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyr 380
                                                                                                                                                                                                                                                                                                                                                                                                                                      341 CysAlaAlaLeuSerAlaIleValIleSerAlaThrLeuValIleLeuLeuAlaTyrPhe 360
                                     ProGlyTyrProLeuThrSerSerThrValTyrSerProProProArgProLeuProArg
                                                                                                                                                                                                       961 AGCACCTTCGCCCGGCCGGCCGCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAACTGGAAG
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09514573;
Patent No. 6500941
GENERAL INFORMATION:
APPLICANT: Schaefer, Gabriele M. APPLICANT: S14W6wski, Mark
TITLE OF INVENTION: Gamma-Heregulin NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUCHRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/514,573
FILING DATE: 28 FEB 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Genentech, Inc.
STREET: 460 Point San Bruno Bl.
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/891845
FILING DATE: 10 JULY 1997
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415/952-981
TELEX: 910/31-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 160 base pairs
TYPE: Mucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415/225-1994
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TOPOLOGY:
US-09-514-573-3
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CGCTACACCAGCTCGTCGCGGACAGCGAGGGGGAGGCAAAGCCCCGCAGAAATCGTACAGC 120
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Mismatches:
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Matches:
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1680 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity:
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	845 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	COMPUTER READABLE FORM:  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible CORPUTER: WinParin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/891,845 FILING DATE: PLING DATE: PLING APPLICATION DATA: APPLICATION NUMBER: 60/021640 FILING DATE: NAME: Lee, Wendy M. NAME: Lee, Wendy M. REGISTRATION NUMBER: P1043 REFERENCE/DOCKET NUMBER: P1043	TELECOMMUNICATION INFORMATION:   TELERAX: 415/225-1994     TELERAX: 415/225-1994     TELERAX: 415/225-1994     TELERAX: 910/371-7168     INFORMATION FOR SEQ ID NO: 1:   SEQUENCE CHARACTERISTICS:     LENGTH: 3111 Dase pairs     TYPE: Nucleic Acid     STRANDEDNESS: Single     STRANDEDNESS: Single     STRANDEDNESS: Single     STRANDEDNESS: Single     STRANDEDNESS: Single     STRANDEDNESS: Single     SCORE:     SCORE:   STRANDEDNESS: 3396     SCORE:   STRANDEDNESS: 396     Best Local Similarity:   99.00%   Mismatches: 0     DB:   SCORE:   Indels: 0     DB:   SCORE:   OCCUPATION     SEQ14-X-AT-28-64-76 (1-400) x US-08-891-845-1 (1-3111)	1 ACARDY ALLY SALDAT GLAND TATEGORIDE UNITARIGATED AND TATEGORIDE TO THE SALDAT GRAND AND THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIA GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIA GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEGORIDE TO THE SALDAT GRAND AND TATEG
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION DATA:
FILING DATE: 28 FEB 2000
                                                                                      Sequence 1, Application US/09514573
Patent No. 6500941
GENEAL INFORMATION:
APPLICANT: Schaefer, Gabriele M.
APPLICANT: Sliwkowski, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/925-1994
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/891845
FILING DATE: 10 JULY 1997
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno:
CITY: South San Francisco
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
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US-09-514-573-1
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Best Local Similarity:
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                           CGCTACACCAGCTCGTCCGCGGACAGCGAGGGCAAAGCCCCGCAGAAATCGTACAGC
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                       ArgGluLeuGlyLeuGluGluValThrProProHisGlyThrLeuTyrArgThrAspile
                                                CGGGAGCTGGGGCTGGAAGAAGTAACGCCCCCTCACGGGACCCTGTACCGGACACATT
                                                                                           ThrValLeuSerProGluHisProValArgLeuTrpGlyArgSerThrArgSerGlyArg
                                                                                                                                                   ACGGTGCTGTCCCCCTGACACCCCGTGCGTCTGTGGGGCCGGAGCACACGGTCAGGGCGC
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Patent No. 6096873
GENERAL INFORMATION:
APPLICANT: Schaefer, Gabriele M. APPLICANT: Sliwkowski, Mark
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                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches:
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                                                                                                                                                                                                                        SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,845
             AUNKESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Bl
CITY: South San Francisco
STATE: California
ZTATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                      40,378
ER: P1043
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REGISTRATION NUMBER: 40,378
REPERENCE/DOCKET NUMBER: P10.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/925-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2387 base pairs
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100.00%
60.27%
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
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Best Local Similarity:
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OTHER INFORMATION: Description of Artificial Sequence: polynucleotide
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                                                 SEQ14-X-AT-28-64-76 (1-400) x US-09-514-573-11 (1-2387)
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GENERAL INFORMATION:
TITLE OF INVENTION: Polymerase Chimerase
FILE REFERENCE: 4894
CURRENT APPLICATION NUMBER: US/09/623,326
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: DE 198 10 879.6
PRIOR PILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
Indels:
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                                                                                                                                                                                          AlaileValileSerAlaThrLeuValileLeuLeuAlaTyrPheValAlaMetHisLeu 365
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                                         ThrserSerThrValTyrSerProProProArgProLeuProArgSerThrPheAlaArg
                                                                            386 ThralaSerSerTrpProValProThrAspValSerLeuTyrPro 400
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Matches:
Conservative:
Mismatches:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DUTY:
FILLING DATE: 28 FEB 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Schaefer, Gabriele M.
APPLICANT: Sliwkowski, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genettech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STREET: USA
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09514573 Patent No. 6500941
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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100.00%
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EDNESS: Single
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Best Local Similarity:
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US-09-514-573-11
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면 <b>상</b> :	2334	GATCCGGGTCTTCCAGGAGGGGGGGACATCCACACGGAGACCGCCAGCTGGATGTTCGG 239 hrSerProGlyTyrProLeuThrSerSerThrValTyrSerProProArgProLeuP 319
<b>a</b>	2394	CGTCCCCCGGGAGGCCGTGGACCC
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TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
FILE REFERENCE: REG. 31-75-75-75
CURRENT APPLICATION NUMBER: US/09/051,994A
CURRENT FILING DATE: 1998-04-24
EARLIER FILING DATE: 1998-10-25
EARLIER FILING DATE: 1996-10-25
EARLIER APPLICATION NUMBER: 60/007,015
                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SerLeuSerGlyGluPro---ProAlaGlyGlyAla-
                                                               hrLeuThrAspThrGluHisGluAsnThrGluThrAspHisPro-
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Patent No. 6602683
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US-09-051-994-1/C
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CAPLICATION NUMBER: US/07/945,283
FILING DATE: 19920911
1815 No. 5352596th University Street
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Matches:
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NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
TELEFAX: 309-685-4018
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ORIGINAL SOURCE:
ORGANISM: Pseudorabies virus
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Sequence 1. Application US/07945283
Patent No. 535296
GENERAL INFORMATION:
APPLICANT: Cheuny. Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudorabies virus Deletion Mutants
TITLE OF INVENTION: Involving The EPO and LLT Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 CGCCGCCCTGAGCACCCCCTACCAGGTACAGCTT 439
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                                                     Conservative:
Mismatches:
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Matches:
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                                                                                                       ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/04
FILLING DATE: June 12, 195
ATTORNEY/AGENT INFORMATION:
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nucleic acid
NDNESS: single
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Suite 4700
                          Los Angeles
California
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                                                                               Y: U.S.A.
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                          CITY: LOS
STATE: CZ
COUNTRY:
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e***ProGlnGluAlaGluGluPheCysArgThrGly***AsnPheThrLeuArgGluLe 83
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Patent No. 6342593
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Peles, Bior
TITLE OF INVENTION: DIACNOSIS AND TREATMENT
TITLE OF INVENTION: OF ALP RELATED DISORDERS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
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US-09-095-443-1
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Mismatches:
Indels:
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2115 TICACAAGCGT---TIGGGCCTCAGCCCCACAGCAGCCCTTCCACTCCAGA
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APPLICANT: FRASER Claire M.
APPLICANT: PRASER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION UNMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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APPLICANT: FLEESCHMAN, Robert D.
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SEQ ID NO 2
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1333601 GCCGATCGACGCCAATCAGACGAATATTGTGGTGCTCGGCGTAGACCCCGGGCTTCGGTCG 1333542
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    positions throughout the sequence g
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Mismatches:
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Matches:
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Best Local Similarity:
; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-103-840A-2
                                                                                          Alignment Scores:
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1334271 CCAGGGTGTATGGGCCCCGCCCGACAGGCCCACCACCACCATCT---GTGATGCCGA 1334215
                               1334436 AGCTCGCACCAGCCGCAGCGGGGTGCCGCCCACCTGCAGCAGCGGCGCCACCGCCGAAC 1334377
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171 GlnAsnHisAlaArgLeuArgThrProProProProLeuSerHisAlaHisThrProAsn
                                                                         Gln-HisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsnPheThrProArgSerAs
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APPLICANT: Dahlberg, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: 5' Nucleases Derived From Thermostable TITLE OF INVENTION: DNA POlyermase
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
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                                                                                                              1334376 chaggcgchiraaaccgccgcrahrcgcgrccggccgcgcgr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 roArgProLeuProArgSerThrPheAlaArgPro 326
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
PRIOR APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
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APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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     296 -- PheCysThrThrSerProGlyTyrProLeuThrSerSerThrValTyrSerProProP 315
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                                                                                                                      1333494 -- cárcciaragagagagagagaartcagaaagacci 1333462
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Conservative:
Mismatches:
Indels:
                                                                                 roArgProLeuProArgSerThrPheAlaArgPro
                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1
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                                                                                                                                                                                               Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION: APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                      APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
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Best Local Similarity:
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                             Glu---GluGlyLysAlaProGlnLysSerTyrSerSerGluThrLeuLysAlaTyr
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123
92
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Matches:
Conservative:
Mismatches:
Indels:
                                          FORS-01800
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           NAME: Ingolia, Diane E.
REGIETRATION NUMBER: 40,027
REFRENCE/DOCKET NUMBER: FORS.
TELECOMMUNICATION INFORMATION:
TELEPAK: (415) 705-8410
TELEFAK: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ATTORNEY/AGENT INFORMATION:
                                                                                                                       2507 base pairs
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126.00
37.13%
28.65%
5.91%
                                                                                                                    LENGTH: 2507 base pai
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
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Sequence 11748, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
                                                               -CTGGAC 1830
                                                                                                                                                                                                                                        1882 CTGATCCGGGTCTTCCAGGAGGGCGGGGACATCCACACGGAGCCGCCAGCTGGATGTTC 1941
                                                                                                                                                              --CACCTCTCCGGCGACGAGAC 1881
                                                                                                                                                                                                                                                                                                                                                      1942 GGCGTCCCCGGGGGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTC 2001
243 SerAsnlleProLeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThrLeuGln 262
                                                                                                                                                                                                                                                                                                       298 rThrSerProGlyTyrProLeuThrSerSerThrValTyrSerProProArgProLe 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                2002 GGGGTCCTCTACGGCATGTCGGCCCACCCCTCTCCAGGAGCTAGCCATCCCCTTAC 2059
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                                                                                                                                                                                                                                                                                                                                                                                                        318 uProArgSerThrPheAlaArgProAlaPheAsnLeuLysLys---ProSerLysTyr 336
                                                                                              263 AspAsnLeulleGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAsp
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                     283 GlyHisPheLeuPhe-LysProGlyGlyThrSer
                                                                                                                                 1831 TATAGCCAGATAGAGCTCAGGGTGCTGGCC---
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33.42%
22.73%
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Search completed: August 15, 2004, 02:14:11 Job time : 5435 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

(without alignments) 3580.597 Million cell updates/sec 1 MDVKERKPYRSLTRRRDAER......BITEDTASSWPVPTDVSLYP 400 August 14, 2004, 18:05:13 ; Search time 3336 Seconds SEQ14-X-AT-28-64-76 2132 Perfect score: Sequence: :10 Title: Run

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

EST:\* Database :

em\_estba:\*
em\_esthum:\*
em\_estin:\* em\_estmu:\*
em\_estov:\*
em\_estpl:\* em\_estro:\* em\_htc:\* gb\_est1:\*

em\_gss\_rod:\*
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gb\_htc:\*
gb\_est3:\*
gb\_est4:\*
gb\_est5:\*
em\_estfm:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\* em\_gss\_fun:\* em dss hum: \* em\_gss\_mam:\* ₩.: gru em gss mus: em gss pro: 

gb\_gss2:\* 29:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

EST 16-MAY-2003

CB532245 620 bp mRNA linear 756697 MARC 6BOV Bos taurus cDNA 3', mRNA seguence. CB532245.1 GI:29395750 CB532245 EST RESULT 1 CB532245/c LOCUS DEFINITION ACCESSION VERSION ORGANISM KEYWORDS SOURCE

Bos taurus Bos taurus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovinae, Bos.

(bases 1 to 620)

REFERENCE

EST 16-MAY-2003

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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovidae, Bos.

1 (bases I to 620)

Smith, T. P. L., Roberts, A. J., Echternkamp, S. E., Chitko-McKown, C. G., Wray, J. E. and Keele, J. W.
A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified voross_match v0.990329.
Plate: LAM8014 row. K column: 19
Seq primer: GTAATACGACTATAGGG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pooled"
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/clone lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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92 AACACGGAGCCGATCACCCGGGCGGCCTGCAGAACCATTCTCGACTCCCGGACACCGCCG
                                                                                                                                             CB532612 620 bp mRNA linear 757081 MARC 6BOV Bos taurus CDNA 5', mRNA sequence. CB532612
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172
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4399
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                                     /organism="Bos taurus"
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Plate: LAM8014 row: K column: 19
Seq primer: TAGAAGGCAAGTCGAGG.
 Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
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/inclary made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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Mismatches:
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XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Mctabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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Mi.P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
rehensive Collection of Chicken cDNAs
siol. 12 (22), 1965-1969 (2002)
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uuria; Aves; Neognathae; Galliformes; Phasianidae;
ninae; Gallus.
                                                                                                                                                                                                                                                                                                               ATCCGGCCGCCTGCAGAACCACGCGCGCGCTCCGGACGCCGCCGCCGCCGCTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                              LeGluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAspGlyHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       auPhelysProGlyGlyThrSerProLeuPheCysThrThrSerProGlyTyrPro
                                                                                                                                                                                                                                                                                         LsProGlyGlyLeuGlnAsnHisAlaArgLeuArgThrProProProJeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aGlyGlyAlaGlnGluProAlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsn
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gallus cDNA clone
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Matches:
Conservative:
Mismatches:
Indels:
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548F1 CSEQCHN03 Gallus
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2.1 GI:25363728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gallus (chicken)
gallus
                                                                                                                                            8.16e-55
884.00
95.86%
95.86%
41.46%
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ity:
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/done lib="CSEBENR1"
// lone lib="CSEBENR1"
// lone lib="CSEBENR1"
// lone lib="CSEBENR1"
// lone lib="CSEBENR1"
// lone lib="CSEBENR1"
// lone lib="CSEBENR1"
// lone lib="CSEBENR1"
// lone lib sites lone library was constructed from limilion independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction.
// lone library library strand synthesis reaction.
// Rollowing this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with BCORI scompatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., pNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                               BU474934 1inear EST 30-NOV-2002 603364850F1 CSEQRBN21 Gallus gallus clone ChEST262c14 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, Prong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                  gSerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                             160 uAsn-ThrGluThrAspHisProGlyGlyLeuGlnAsnHisAlaArgLeuArg 177
                                                                                                                         878
1139
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100
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ14-X-AT-28-64-76 (1-400) x BU474934 (1-878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PO Box 88, Manchester, M60 1QD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9031"
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1. .878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                            BU474934.1 GI:25968511
                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (chicken)
Gallus gallus
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725.00
90.91%
84.24%
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Best Local Similarity:
Query Match:
DB:
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BU474934
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Pred. No.:
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                           DEFINITION
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JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
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BU474934
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                                                                                                                                                                                                                                                                                                                       /clone="ChEST1010911"
/tissue_type="whole embryo"
/dev_stage="20-21"
/dev_stage="20-21"
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/clone_lib="CSEQCHN03"
/clone_lib="CSEQCHN03"
/clone_lib="CSEQCHN03"
/compatible sites of a custom modified MCS of the pBluescript (K6+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-923 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 CGGGAGCTGGGTCTTGAAGATGTGACTCCCACCCATGGGACTTTGTACCGGACTGATATT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ThrValLeuSerProGluHis-ProValArgLeuTrpGlyArgSerThrArgSerGlyAr 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 ATGGATGTAAAAGAAAGGAAACCGTATCGATCTTCTGACTCGGCGCCGCGACACGGAGCGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetaspValLysGluArgLysProTyrArgSerLeuThrArgArgArgAspAlaGluArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 ArgryrThrSerSerSerAla***SerGluGluGlyLysAlaProGlnLysSerTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerSerGluThrLeuLysAlaTyrAspGlnAspAlaArgLeuAlaTyrGlySerArgVal
                                                            Science and Technology
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1149
112
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="White Leghorn, Hisex"
                                       Department of Biomolecular Sciences
University of Manchester Institute of
                                                                                                      PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ14-X-AT-28-64-76 (1-400) x BU200362 (1-625)
                                                                                                                                                                                                                                             organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                              db xref="taxon:9031"
                    Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.42e-46
769.00
89.94%
83.24%
36.07%
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Best Local Similarity:
                                                                                        (UMIST)
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashud, K., Hayashud, K., Hayashida, K., Hayashud, K., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komo, H., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komo, H., Kawai, M., Misula, M., Komura, M., Miyazaki, A., Mixata, M., Okazaki, X., Saito, R., Saitoh, H., Sakai, K., Shinagawa, A., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Miramatesu, M., and Hayashizaki, Y., Tagamishi, A., Tayahira, S., Miramatesu, M., and Hayashizaki, Y., Toya, T., Tagamishi, A., Toya, T., Tagamishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Pokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLHEYNOELRRNYNSOSRKRKOVEKSTOELBFCETPPTLCSGYHTDMHSVSRHGYQLE
MGSDVDTETBGAASPDHALRRWIRGMKSEHSSCLSSRANSALSLTDTDHERKSDGENG
FKFSPVCCDMEAPADSAQDMQSSPHNOFTFRPLPPPPPPPHACTCARKPPPTVDSLQR
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SQNYPLTSNIVYSPPRPLPRSTFSRPAFTFRKPYRCCNWKCTALSATAITVTLALLL
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RAIDTGEVDIGAQWWQTIPPQLYMRFQITIHPIYLKFRISLAGSLLGIYGRRNIPP
THTQPDFVKLMDGKQUVKQDSKSSDDIQHSPRNLILITSLQETGFIEYNQQGPWYLAFY
                                                                                                                                                                                                                                                                                        The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 3447)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                               The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product; odd Oz/ten-m homolog 1 (Drosophila) (MGD|MGI:1345185, GB|NM_011855, evidence: BLASTN, 99%, match=3037)
                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site for further details. URL.http://genome.gsc.riken.go.jp/
URL.http://fantom.gsc.riken.go.jp/.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues.
                                                                                                                                                                          FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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AUTHORS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            MetAspValLysGluArgLysProTyrArgSerLeuThrArgArgArgAspAlaGluArg 20
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Qy 267 GluMetAspileLeuGlyAlaSerArgHisAspGlyAlaTyrSerAspGlyHisPheLeu 286	287 PheLysProGlyGlyThrSerProLeuPheCysThrThrSerProGlyTyrProLeu 287 Th[	Qy 326 ProAlaPheAsnLeuLysLysEroSerIlysTyrCySAsnTrDLysSySAlaAlaLeulser 345	Oy 366 PheGlyLeuAsnTrpHisLeuGlnProMetGluGlyGlnMetTyr 380	DEFINITION AGENCOURT 8097117 NICHD_XGC_Emb4 Xenopus laevis cDNA clone IMAGE:5542635 5', mRNA sequence.	ACCESSION BQ735622 VERSION BQ735622.1 GI:21874519 KEYWORDS EST. SCHOOLS Amount larvis (African clawed froq)	NISM	REFERENCE 1 (bases 1 to 884) AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	JOURNAL Unpublished (1997) COMMENT Contact: Robert Strausberg, Ph.D. Bmall: Ggapbs-remail.nih.gov	CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: NCI-CGAP clone distribution information can be	found through the I.M.A.G.E. Consortium/LINL at: www.bio.llnl.gov/bbrp/image.html plate: LLAM1242 row: e column: 04 High gnality sequence stop: 373.	FEATURES Location/Qualifiers  Source /organism="Xenopus laevis" //mol + mol +	/db xref="taxon:8355" /clone="IMAGE:5542635" /dev stage="embryo, stage 31-32" /lab host="embryo, stage 31-32" /lab host="PH10R" (bhade-resistant)"	/clone lib="NICHD_XGC Emb4" /note="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1: Not1: Site 2: Sal1; Cloned unidirectionally. Primer: Oligo	Technologies. Note: This is a Xenopus Gene Collection (XGC) library."	Alignment Scores: 5.24e-41 Length: 884 Pred. No.: 5.24e-41 Matches: 160
NDGKKMEQVFVLTTAIGKLPCLLFEFTV" ORIGIN	Alignment Scores: 9.89e-42 Length: 3447  Pred. No.: 720.50 Matches: 169  Score: 720.50 Matches: 169  Percent Similarity: 52.77% Conservative: 50  Best Local Similarity: 40.72% Mismatches: 101  Query Match: 13.73% Indels: 95  DB: 11 Gaps: 15	1 MetaspVallysGluArgLysProfyrArgSerLeuThrArgArgArgAspAlaGlu 1	Db 922 CTAGCTTATACCAGTTCTTCTGATGAGAGAGAGAGAAACCAAGACAGTCATTC 981  Oy 40 SerSerSerGluThrLeuLysAlaTyraspGlnAspAlaArgLeuAlaTyrGlySer 58  Db 982 AACTCCAGGGAAACTCTGCATGAGTATAACCAAGAGCTGAGGAGAATTACAATAGCCAG 1041	rGly 7	Cy 76 ***AsnPheThrLeuArgGluLeuGlyLeuGluGluValThrProProHisGlyThrLeu 95  Db 1096ACACCTCCTACTTTG 1110	Qy 96TyrargThraspIleGlyLeuProGlnCysGlyTyrSerWetGlyAla 111 Db 1111 TGCTCCGGCTACCACACAGACATGCACAGGTTTCTCGACAGACA	Qy 112 GlySerAspalaAspMetGlualaAspThrValLeuSerProGluHisProValArgLeu 131	Oy 132 TrpGlyArgSerThrArgSerGlyArgSerSerCysLeuSerSerArgAlaAsnSerAsn 151	Qy         152 LeuThrLeuThrAspThrGluHisGluAsnThrGluThrAspHisProGlyGlyLeuGln         171           Db         1291 CTGTCCTTGACCGACACTGATGACGGAAGTCTGATGGGGAAAATGGTTTAAA         1347	Qy 171 171 Db 1348 TTCTCTCTGTTTGTTGACATGGAGCTCCAGCTGATTCGGCTCAAGACATGCAAAGC 1407	Oy 172AsnHisAlaArgLeuArgThrProProProLeuSerHisAla 186	Qy 187 HisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsnPheThr 206	Qy 207 ProArgSerAsnProSerProAlaProThrAspHisSerLeuSerGlyGluProProAla 226	Qy 227 GlyGlyAlaGlnGluProAlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsnIleBro 246	Cy 247 LeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThrLeuGlnAspAsnLeuIle 266

KEYWORDS EST. SOURCE Rattus norvegicus (Norway rat.) ORGANISM Rattus norvegicus EUkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Rodentia: Schirocorathi, Mariano, M		AL Unpublished (2003) Contact: Dan Fitzpatrick Amgen, Inc	One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881 Plate: 00003 row: a column: 5. FEATURES Location/Qualifiers	source 1. 402 //organism="Rattus norvegicus" //organism="Rattus norvegicus" //organism="mension" //organism="mensi	//u.z.type="litaxp: /db_xref="taxon:1016" /clone="tryp1-0009-a5"	/tissue_type="prostate" /clone_lib="tryp1 (10582)" /pote="Vector: pYYA-41L; Site_1: HindIII; Site_2: Not1;	ı	: 1.79e-40 Length: 685.00 Matches:	<pre>it Similarity: 99.22% ocal Similarity: 97.67% Match: 32.13%</pre>	14 Gaps:	SBQ14-X-AT-28-64-76 (1-400) x CB544750 (1-402)	QY 250 ArgAsnLeuGlyLysGlnProPheLeuGlyThrLeuGlnAspAsnLeulleGluMetAsp 269		290	Qy 310 ValTyrSerProProArgFroLeuProArgSerThrPheAlaArgFroAlaPheAsn 329	QY 330 LeuLysLysProSerLysTyrCysAsnTrpLysCysAlaAlaLeuSerAlaIleValIle 349	Oy 350 SerAlaThrLeuValIleLeuLeuAlaTyrPheValAlaMetHisLeuPheGlyLeuAsn 369	370		RESULT 9 BU474512 LOCUS BU474512 LOC	BU474512.1 GI:2596808	EST.
Best Local Similarity:       55.56 * Mismatches:       44         Query Match:       32.79 * Indels:       69         DB:       13       Gaps:       8         SEQ14-X-AT-28-64-76 (1-400) x BQ735622 (1-884)	QY     113 SerAspAlaAspMetGluAlaAspThrValLeuSerProGluHisProValArgLeuTrp 132       :::   :::	Qy 133 GlyArgSerThrArgSerGlyArgSerSerCysLeuSerSerArgAlaAsnSerAsnLeu 152	GlnAsn 17	173	Db 134 CATTGAGACTACGAACGCCCCCATAAGCCACCGCAAAACCCCCAC 187	Qy 193 HisAlaSerIleAsnSerLeuAsnArgGlyAsnPheThrProArgSerAsnProSer 212		CCGGCCCCACGACGACCACCACGACCCCCGGGCGGTGGCCCAGGAGTCC	V 23.9 ALAHISALINGHINGHINGHINGSEYSANILEPIOLEGGUTHIARGASHLEU 252  Db 305 GTCCATGACAATIGGCTGCTGAACAGCAACATTCCCCTGGAGACACAG 352	$253~{ m GlyLysGlnProPheLeuGlyThrLeuGlnAspAsnLeuIleGluMetAspIleLeuGly}$	Db 352 352	Qy 273 AlaSerArgHisAspGlyAlaTyrSerAspGlyHisPheLeuPheLysProGlyGlyThr 292  Db 353	293 SerProLeuPheCysThrThrSerProGlyTyrProLeuThrSerSerThrValTyrSer	ACTCC	Qy 332 sproserlystyrcysAsnTrpLysCysAlaAlaLeuSerAlaIleValIleSerAlaTh 352	Trp	371 -HisLeuGlnProMetGluGlyGlnMetTyrGlu-IleThrGluAspThrAlaSerS 38 :::	620	Qy         389 erTrpbrovalpro 393	CB544750 402 bp mRNA linear EST 01-APR	DEFINITION AMGNNUC:TRYP1-00009-A5-A tryp1 (10582) Rattus norvegicus cDNA clone tryp1-00009-a5 5', mRNA sequence. ACCESSION CB544750 GT:29428647	1:00/24/00

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/clone lib lib rain for commodate cDNA produced with the [Stratagene] vector to accommodate cDNA produced with the [Stratagene] libraries from messenger RNA for improved 3/clone cDNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624) cut pBluescript II KS(+) with NotI and BcoRI. Ligate in double stranded adaptor containing Bsgl and BamHI sites [5/ggccgggcaggccggaaccgaaaaaaaag]
[5/aattcttttttcggatccggaaccgaaaaaaaag]
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603143046F1 CSEQCHL16 Gallus gallus cDNA clone ChEST137111 5', mRNA
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Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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Phasianinae, Gallus.
                                                                      GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp
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                        Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
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/mol type="mRNA"
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/db xref="taxon:9031"
/clone="ChEST137111"
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Fax: 0161236040
Email: Simon. Hubbard@umist.ac.uk.
Location/Qualifiers
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10 (Bases 1 to 78);

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs

Courr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                                                                        Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
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                                                                                                                                                                                                                                                                                                 Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                   Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .789
                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:9031"
/clone="ChEST679g24"
/sex="Female"
              gallus (chicken)
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89.70%
83.03%
31.89%
                                                                                                                                                                                                                                                                                                                   Tel: 01612008930
Fax: 01612360409
              Gallus gallus
Gallus gallus
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              SOURCE
ORGANISM
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AL Nature 420, 563-573 (2002)

S dacch, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanadaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanadaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Kasukawa, T., Kasukawa, T., Kasukawa, T., Kasukawa, T., Kasukawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, A., Murata, M., Nishi, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sahato, R., Shinagawa, A., Shirada, K., Shinagawa, A., Shirada, K., Shinagawa, M., Shiradawi, K., Shinagawa, M., Shirada, S., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y. Takahashi, F., Takaku-Akahira, S., Direct Submission Submittee (16-7UL-201) Yoshihide Hayashizaki, Y. Direct Submission Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Okohama Institute 17-72 Suchiro-cho, Tsurumi, Lu, Yokohama, Kanadawa, 230-0045, Janan (F., Manadawa, 230-0045, Janan, 100-0045, Janan, 100-0045, Janan, 100-0045, Janan, 100-0045, Janan, 100-0045,
                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Skonno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishina, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tamaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev stage="adult"
1. .4556
/note="odd Oz/ten-m homolog 1 (Drosophila)
(MGD|MGI:1345185, GB|NM_01185, evidence: BLASIN, 99%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yo
Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222.
Fax:81-45-503-9216)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/strain="C57BL/6J"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
         Length:
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Db 1764CATTTCCTG 1772		Oy 326 ProAlaPheAsnLeuLySLySProSerLySTyrCySASnTrpLySCysAlaAlaLeuSer 345	1953	2013 ATTCTATGTGTCAGCTTTCTTTTT 370 PHisLeuglnProMetGluGlyGlr	Db 2073 TCACTCTCAATGTTGTGACAAATTTGTAGCATA 2109	AL922332/C AL922332 AL922332 AL922332 AL922332 AL922332 PJR-Z1+Z2 Danio rerio cDNA clone 109-E12-2, mRNA sequence.		UKGANISM Danio Terro Danio Terro Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.	AUTHORS Lo.J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W., Mang,W., Wen,Z. and Peng,J.  TITLE 15000 unique zebrafish EST clusters and their future use in microarray for profiling agene expression patterns during	### ##################################		edu.sg ch.sg ch.a-star.edu.sg.	/organism="Danio rerio" /mol_type="mRNA" /strain="local wildtype" /dh_xref="taxon"/955"	/clone="109-E12-2" /tissue_type="whole embryo or fish" /dev_stage="mixed_stages" /clone_lib="puR-21+22"		е	: 70.37% Mismatches: 27.37% Indels: 9 Gaps:
ORIGIN	Alignment Scores: 6.5e-37 Length: 4556 Pred. No.: 657.00 Matches: 163 Score: 657.00 Matches: 51 Percent Similarity: 49.42 Conservative: 51 Best Local Similarity: 37.64% Mismatches: 109 Query Match: 30.82% Indels: 109 DB: 11 Gaps: 14	SEQ14-X-AT-28-64-76 (1-400) x AXO34286 (1-4556)  QY	Qy 20 ArgArgTyrThrSerSerAla***SerGluGluGluGlyLysalaProGlnLysSerTyr 39		Qy 59ArgValLysAspIle***ProGlnGluAlaGluGluPheCysArgThrGly 75 :::	Qy         76 ***AsnPheThrLeuArgGluLeuGlyLeuGluGluValThrProProProHisGlyThrLeu 95           Db         1221ACTTTG 1235	Qy 96TyrargThraspIleGlyLeuProGlnCysGlyTyrSerMetGlyAla 111	112	Qy 132 TrpGlyArgSerThrArgSerGlyArgSerSerCysLeuSerSerArgAlaAsnSerAsn 151	Oy 152 LeuThrLeuThrAspThrGluHisGluAsnThrGluThrAspHisProGlyGlyLeuGln 171	Qy 171 171  Db 1473 TTCTCTCTGTTTGTTGACATGGAGGCTCCAGCTGATTCGGCTCAAGACATGCAAAGC 1532	Qy 172AsnHisAlaArgLeuArgThrProProProProLeuSerHisAla 186	Qy 187 HisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsnPheThr 206	Qy 207 ProArgSerAsnProSerProAlaProThrAspHisSerLeuSerGlyGluProProAla 226	Oy 227 GlyGlyAlaGlnGluProAlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsnIlePro 246	Db 1692 ACCAGCACACAGGATTCAGTTCATCTGCATAACAGCTGGGTCTTGAACAGTAACATACCA 1751  Qy 247 LeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThrLeuGlnAspAsnLeulle 266	Db 1752 CTGGAGACCAGG 1763 Qy 267 GluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAspGlyHisPheLeu 286

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291 GlyThrSerProLeuPheCysThrThrSerProGlyTyrProLeuThrSerSerThrVal 310
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/clone_lib="NIH_MGC_91"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: Not
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens HCM2175 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
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602326960F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4428351 5',
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                                                                                                                                                                                                                                                                  63 Ile***ProGlnGluAlaGluGluPheCysArgThrGly***AsnPheThrLeuArgGlu 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 870)
NIH-MGC http://mgc.nci.nih.gov/.
                                         VallysGluArgLysProTyrArgSerLeuThrArgArgArgAspAlaGluArgArgTyr
                                                                                                               23 ThrSerSerAla***SerGluGluGlyLysAlaProGlnLysSerTyrSerSer
                                                                                                                                                      429 ACCAGCTCATCTGCCGACAGGATGGCAAGATCAACCTAAATCTTACAGCTCGAGT
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Plate: LLAMI0178 row: h column: 16
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/tissue_type="adenocarcinoma, cell line"
     SEQ14-X-AT-28-64-76 (1-400) x AL922332 (1-490)
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Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
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Location/Qualifiers
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181 AACAGAGTGAAGATTTGGTTCACAGAGAGAGAGAGAGTTCACTAGACAAGGACAGAAT 240
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Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                             Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B., Tonenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M. D. and Cargill, M. Direct Submission Cargill, M. Direct Submission Cargill, M. Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 SerArgValLysAspIle***ProGlnGluAlaGluGluPheCysArgThrGly***Asn
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23
32
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Matches:
Conservative:
Mismatches:
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                Science 302 (5652), 1960-1963 (2003)
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/locus_tag="HCM2175"
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gene, VIRTUAL TRANSCRIPT, partial sequence,
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Pan troglodytes
Pan troglodytes
Pan troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
(bases 1 to 511)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Clark,A.G., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
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Conservative:
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APPLICANT: Alsobrook II, John et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE;
FILLE REPERENCE: 21402-268A
CURRENT APPLICATION NUMBER: US/10/383,201
CURRENT FILING DATE: 2003-03-06
PRIOR PELICATION NUMBER: 10/029020
PRIOR PELICATION NUMBER: 60/365,984
PRIOR FILING DATE: 2002-03-20
PRIOR FILING DATE: 2002-04-12
PRIOR PELICATION NUMBER: 60/372,022
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
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Publication No. US20040029226A1
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              August 14, 2004, 01:33:47; Search time 152.319 Seconds (without alignments) 2448.158 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Score

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SEQ ID NO 13
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ORGANISM: Homo sapiens
                                                               TYPE: DNA ORGANISM: Homo sapiens
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CURRENT APPLICATION UNDER:
CURRENT FILING DATE:
2001-12-19
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2001-08-10
PRIOR PELING DATE:
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PRIOR PILING DATE:
2001-08-29
PRIOR PILING DATE:
2001-09-29
PRIOR APPLICATION NUMBER:
60/315,617
PRIOR PILING DATE:
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Mismatches:
Indels:
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Matches:
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        PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 10/051,874
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 60/366,928
PRIOR PILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 10/055,877
PRIOR FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 13, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
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391.00
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, LOCATION: (35)..(8341)
US-10-383-201-43
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Best Local Similarity:
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US-10-029-020-13
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8033 TCCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCAG 8092
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APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Matson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
ITLE OF INVENTION: Methods of Diagnosis of Cancer,
ITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-12
PRIOR FILING DATE: 2001-11-12
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-12-14
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Matches:
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PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION WUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: Patentin Ver. 2.1
LENGTH: 8438
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Publication No. US20030232350A1
GENERAL INFORMATION:
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APPLICANT: Afalz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
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391.00
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CORGANISM: Homo sapiens
US-10-042-865-1
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Best Local Similarity:
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APPLICANT: Stone, David
TITLE OF INVENTION: Droteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
TITLE OF ILIUGHAPPERSON: 21402-537
CURRENT FILING DATE: 2002-05-17
PRIOR PPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR APPLICATION NUMBER: 60/272,338
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/274,876
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                                Length:
Matches:
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Publication No. US20040029216Al
GENERAL INFORMATION:
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APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
APPLICANT: Seman, Stacie J
APPLICANT: Shenoy, Sureeh G
APPLICANT: Spytek, Kimberly
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MacDougall, John
Malyankar, Uriel M
Millet, Isabelle
Peyman, John
Smithson, Glennda
Gunther, Erik
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Best Local Similarity:
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APPLICANT: Bernards, Rene TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients FILLE OF INVENTION: US/10/342,887

CURRENT FILING DATE: 2003-01-15

PRIOR FILING DATE: 2001-06-18

PRIOR PELICATION NUMBER: 10/102,118

PRIOR PELICATION NUMBER: 10/172,118

PRIOR APPLICATION NUMBER: 10/172,118

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 2699

SEQ ID NO 1743

LENGTH: 3614
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 927
                                                                                                                                                                                                                                                                                                                                                                                US-10-029-020-14_COPY_2650_2725 (1-76) x US-10-295-027-927 (1-12880)
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; Sequence 1743, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
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296.00
86.84%
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-295-027-927
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Pred. No.:
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APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Nao, Mao
APPLICANT: Nao, Yu 't 'Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Jennads, Rene
APPLICANT: Bernards, Rene
TILLE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1743
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DATABASE ACCESSION NUMBER: NM_018104
DATABASE ENTRY DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1743, Application US/10172118 Publication No. US20030224374A1 GENERAL INFORMATION:
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Mismatches:
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CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/259,928
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR PLING DATE: 2000-01-02
PRIOR PLING DATE: 2001-01-02
PRIOR PLING DATE: 2001-01-03
PRIOR PRINCE DATE: 2001-01-04
PRIOR PRINCE DATE: 2001-01-04
PRIOR PRILING DATE: 2001-03-29
PRIOR PRILING DATE: 2001-03-29
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PRIOR PELLING DATE: 2001-03-29
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; Sequence 41, Application US/10038654
; Publication No. US20040022781A1
; APPLICANT: Spytek, Kimberly A
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Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
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Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
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Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
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Gusev, Vladimir Y
Gangolli, Esha A
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Wolenc, Adam R
Vernet, Corine
Eisen, Andrew J
Liu, Xiaohong
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Millet, Isabelle
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Kekuda, Ramesh
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             Best Local Similarity:
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SOFTWARE: Patentin Ver. 2.1
                       3104 GTGCGCGACGGCGAGAGGGCGCGCCTCTGGACGGGCGAGAAG 3151
61 LeuArgGluGlyGluGlyLeuArgAlaTrpThrGluGlyGluLys 76
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PPLICANT: Millet, Isabelle
PPLICANT: MacDougall, John R
ITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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Matches:
Conservative:
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CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
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PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR PLILING DATE: 2001-01-04
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PRIOR APPLICATION NUMBER: 60/279,832
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
                                                                                                          Sequence 39, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
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Eisen, Andrew J
Liu, Xiaohong
Malyankar, Uriel M
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Tchernev, Velizar
Spaderna, Steven K
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APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
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Patturajan, Meera
Gusev, Vladimir Y
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Gunther, Erik
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Rastelli, Luca
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ORGANISM: Homo sapiens
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Gangolli,
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Pred. No.:
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LENGTH: 8473
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1 SerGlnileAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspileGlnLeuGln 20
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
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PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
Remaining Frior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SEQ ID NO 41.
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APPLICANT: Mallet, Isabelle
APPLICANT: MacDougall, John R
APPLICANT: Navengall, John R
APPLICANT: Navengall, John R
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Matches:
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Shenoy, Suresh G
Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
Burgess, Catherine E
Edinger, Shlomit R
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Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
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Gusev, Vladimir Y
Gangolli, Esha A
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Li, Li
Wolenc, Adam R
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Gunther, Erik
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Kekuda, Ramesh
                                                                                                                                            TYPE: DNA; ORGANISM: Homo sapiens
US-10-038-854-41
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-10-038-854-37
                                                                                                                               LENGTH: 8487
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Matches:
FILE KEFERENCE 1190 NUMBER: US/10/038,854
CURRENT PEDLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR PELING DATE: 2000-12-29
PRIOR PILING DATE: 2001-12-29
PRIOR FILING DATE: 2001-02
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
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PRIOR FILING DATE: 2001-03-29
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PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
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Query Match:
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US-10-038-854-35
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APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/99/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver: 2.1
LENGTH: 8409
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APPLICANT: Mishra, Vishna
APPLICANT: Mazes, Peter S
APPLICANT: Razelli, Luca
APPLICANT: Razelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-697
US-10-029-020-14_COPY_2650_2725 (1-76) x US-09-808-602-79 (1-8409)
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Conservative:
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                                                                                                                       Sequence 79, Application US/09808602
Patent No. US20020155115A1
GENERAL INFORMATION:
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Publication No. US20030087816A1
GREEAL INFORMATION:
APPLICANT: Vernet, Cornie AM
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Herrmann, John L
                                                                                                                                                                                         APPLICANT: Vernet, Corine A
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Herrman, John L
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishnu
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249.50
75.95$
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Best Local Similarity:
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                                                                                                US-09-808-602-79
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 8675
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                                                                                                                                                                                                                                                                                  APPLICANT: Ellerman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glemnda
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
APPLICANT: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 2003-01-22
PRIOR FLING DATE: 2003-01-29
PRIOR FLING DATE: 2001-12-29
PRIOR FLING DATE: 2001-01-02
PRIOR PLING DATE: 2001-01-02
PRIOR PLING DATE: 2001-01-02
PRIOR PLING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR PLING DATE: 2001-01-04
PRIOR PRILING DATE: 2001-01-04
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-03-29
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PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
                                                                                                                                                                                                                                       Burgess, Catherine
Edinger, Shlomit R
                                        Patturajan, Meera
Gusev, Vladimir Y
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296.00
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Rastelli, Luca
Casman, Stacie J
                                                                  Gusev, Vladimir Y
Gangolli, Esha A
                                                                                                               Guo, Xiaojia S
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ORGANISM: Homo sapiens
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GENERAL MacDougall, John
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                                                                                                TyrGlyAlaLeuCysLeuAsnThrArgTyrGly------ThrThrLeuAspGluGlu
                                                                                                                                                                                                  38 LysAlaArgValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGlu
1 SerGlnIleAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln
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Mismatches:
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Matches:
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Patent No. US20020155115A1
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Best Local Similarity:
Query Match:
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Sequence 13976, Application No. US200309974A1

Sequence 13976, Application No. US200309974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Wang, Youzhen

APPLICANT: Wang, Youzhen

APPLICANT: Wang, Youzhen

APPLICANT: Wang, Youzhen

APPLICANT: Wang, Youzhen

APPLICANT: Wang, Youzhen

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

FILLE OF INVENTION: PORT OF 1409

CURRENT APPLICATION NUMBER: 6/306,220

FRIOR APPLICATION NUMBER: 6/306,220

FRIOR APPLICATION NUMBER: 6/306,220

FRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13976
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          CURRENT APPLICATION NUMBER: US/09/800,198
                                 CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 67
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COGANISM: Gallus gallus
US-09-800-198-67
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Best Local Similarity:
Query Match:
DB:
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Best Local Similari
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ORGANISM: Homo
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Search completed: August 14, 2004, 19:23:12

Job time : 182.319 secs

Mon Aug 16 09:01:14 2004

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64, Appl 41, Appl

Total number

Searched:

Sequence:

Run on:

Appli Appli Appli Appli Appli Appli

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Sequence 407, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: PULTURES WICHAEL

APPLICANT: PULTURES IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
TITLE OF INVENTION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12
PRIOR PELICATION NUMBER: 66/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SEQ ID NO 407

LENGTHARE: PERL PROGRAM
SEQ ID NO 407

TANDEL PERL PROGRAM
TOWNER OF SEQ ID NOS: 1143
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Sequence 1, Appli
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Sequence 1913, Ap
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Sequence 12395, A
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                                                                 US-08-557-309B-5

US-08-834-306-5

US-08-834-306-5

US-08-93-676-5

US-08-06-676B-2

US-08-22-845-1

US-08-22-845-1

US-08-22-845-1

US-08-22-845-1

US-08-22-8414A-4

PCT-US4-00324-2

US-09-397-787-1

US-09-397-787-1

US-09-225-991A-12122

US-09-255-991A-12196

US-09-255-991A-12196

US-09-255-991A-12196

US-09-255-991A-12196

US-09-255-991A-12196

US-09-540-258-1913

US-09-556-002-41

US-09-556-002-41

US-09-556-002-41

US-09-65-479A-1

US-09-65-479A-1

US-09-65-479A-1

US-09-65-479A-1

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US-09-65-479A-1
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 474200.1
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Matches:
Conservative:
Mismatches:
Indels:
                   US-09-252-991A-2384
US-09-621-976-595
US-09-702-251-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-338-907-1
US-09-218-207-1
US-09-338-907-179
US-09-218-207-179
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83.33%
67.95%
66.75%
 TYPE: DNA
ORGANISM: Homo sapiens
17.4
17.4
16.5
16.5
16.5
16.5
16.5
                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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US-09-976-594-407/c_
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   688
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 Score:
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-QCOR201/USPTO spool/US10029020/runat 06082004_112217_29301/app_query.fasta_1.3519
-DB=ISSUEd_PARENTES NA -QENT=fastap -SUFFIX=p2n.rni -MINTATCH=0.1 -LCOPCL=0
-LOOPEXT=0 -UNITS=Ebits -STRAT=1 -END=-1 -MARRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODEL-COAL -OUTFNT=PCT -NORM=ext -HEAPSIZE=500 -MINLENE=0 -MAXLEN=200000000
-USRE-USL0029020 @CGN 1 1_250 @runat_06082004_112217_29301 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NEW TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 6
Sequence 6
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents NA:*
1: /cgn2_6/ptOdata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptOdata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptOdata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptOdata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptOdata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptOdata/2/ina/PCTUS_COMB.seq:*
          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                          OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-976-594-407
US-08-933-750C-90
US-09-234-613-90
US-09-976-594-667
US-09-223-134-1
US-08-992-801-1
US-09-253-55-91
US-09-252-991A-12184
US-09-252-991A-12249
US-09-252-991A-12249
US-09-252-991A-12249
US-09-252-991A-12249
                                                                                                                                                                                                                                                                                                                                                                                   of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                   682709 seqs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                             August 14, 2004, 01:16:21
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Match Length
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68.5
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Database :

11008764321

Result ÑO. υ

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127 CAGGCTCTTCGGGAAGGGAAGAAGAAGGGCCAACCCCTGAAGAAGCAATACAGAA 186
                                                                                                       23 AlaLeuCysLeuAsnThr-----ArgTyrGlyThrThrLeuAspGluGluLys 38
                                                                                                                                                                                                                            39 AlaArgValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGln 58
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                                            US-10-029-020-14_COPY_2650_2725 (1-76) x US-08-933-750C-90 (1-1078)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lial, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Vue, Henry
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCVFe P.
                                                                                                                                                                                                                                                                                                                                                       59 GlnArgieuArgGluGlyGluGluGlyLeuArgAla---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastERO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 90, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO: 90
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 ThrGluGlyGluLys 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SININOTO1
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US-09-234-613-90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-234-613-90
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                                                                                                                                                                                                                      1966 TCGCAGTCCACCGCTGGTGATCGGCAGGACGCGCAGGTTCGCGGACGTGGAGATGCAG 1907
                                                           21 TyrglyhlaleuCysleu-AsnThrArgTyrGlyThrThrleuAspGlu-GluLysAlaA 40
                                                                                                                                                                                   40 rgValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnA 60
                                                                                                                                                                                                                                                                                                                                                    1786 GCGTGCGCGACGCGAGGAGGCGCCCTCTGGACGGAGGGCGAAG 1737
                                                                                                                                                                                                                                                                                                           60 rgLeuArgGluGlyGluGlyLeuArgAlaTrpThrGluGlyGluLys 76
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTERE (OF Windows Version 2.0
CURRING APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arthung Date:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION WUMBER: 36,749
REFERENCY/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
""TREPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 90, Application US/08933750C Patent No. 5932442 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1078 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.50
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36.92%
19.82%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE: SININOTO1
CLONE: 2184712
US-08-933-750C-90
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Best Local Similarity:
Query Match:
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-933-750C-90
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1064 CAGGCTCTTCGGGAAGGGGAAGAAGGAGAAAGGGCCAAACCCCTGAAGAAGCAATACAGAA 1123
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APPLICANT: Weymann, Kris
APPLICANT: Steiner, Henry-York
APPLICANT: Steiner, Henry-York
APPLICANT: Maleck, Klaus
TITLE OF INVENTION: Method For Breeding Disease Resistance
TITLE OF INVENTION: Into Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-029-020-14_COPY_2650_2725 (1-76) x US-09-223-134-1 (1-14113)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/223,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PR-1/luc construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,248
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/002,285
FILING DATE: 08-DAN-1993
ATTORNEY/AGENT INPORMATION:
NAME: Neigs, J. Timochy
REFERENCE/DOCKET NUMBER: 38,241
REFERENCE/DOCKET NUMBER: GGC1673/CIP9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 199-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: No. 6057490artis Corporation: 3054 Cornwallis Road
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/992,801
                                                                                                                                                                      Sequence 1, Application US/09223134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PATENTIN Release #
                                                                                       1124 ACTGAAGGAGACAGA 1138
                                               72 ThrGluGlyGluLys 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 14113 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                           Delaney, Terry
Lawton, Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.4
73.50
45.10%
35.29%
18.80%
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60574
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                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                         Patent No. 6057490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27709
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Best Local Similari
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STATE: NC
COUNTRY:
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                                                                                                                                               US-09-223-134-1
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Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
APPLICANT: Buchbinder, Jenny
APPLICANT: Buchbinder, Jenny
APPLICANT: Buchbinder, Jenny
FILE REPERBNES: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594

PRIOR RELING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
PRIOR PELING DATE: 2000-10-12
SOFTWARR: PERL PROGram
SEQ ID NOS: 1143
SOFTWARR: PERL PROGram
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962 TCCCTGTGTGAGAGACATCACCCTCCCAGGAGCAAGGCGGAAGTCTGGAGGACGCTGAG 1021
                                                                                                                                                                                                                                                                                                     127 CAGGCTCTTCGGGAAGGGGAAGAAGAAGAAAGGACCCCTGAAGAAGAAGAATACAGAA 186
                                                                                                                                                                                                                                                                            39 AlaArgValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGln 58
                                                                                                                                                                                                       ---ArgTyrGlyThrThrLeuAspGluGluLys 38
                                                                                                                                                                                                                                     25 TCCCTGTGTGAGAGACATCACCCTCCCAGGAGCAAGGGGGAAGTCTGGAGGACGCTGAG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AlaLeuCysLeuAsnThr-----ArgTyrGlyThrThrLeuAspGluGluLys 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71
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                                                                                                                                                              x US-09-234-613-90 (1-1078)
                                                                                                                                                                                                                                                                                                                                                         59 GinArgieuArgGluGlyGluGluGlyLeuArgAla----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 240518.42
NAME/KEY: unsure
LOCATION: 748
                                                            Conservative:
Mismatches:
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Conservative:
Mismatches:
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                      Length:
Matches:
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                                                                                                                        Gaps:
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                                                                                                                                                          US-10-029-020-14_COPY_2650_2725 (1-76)
                                                                                                                                                                                                 23 AlaLeuCysLeuAsnThr--
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50.77%
36.92%
19.82%
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                                                      Percent Similarity:
Best Local Similarity:
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Query Match:
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Alignment Scores:
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                                                                                               Query Match:
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2283 AAGACGGCCCTGGACCTCGCCCGCGAGGCGCAGGCGCAGGCCGCGGGGGCGGGACC 2342
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                                                                                                                                                         38 LysAlaArgValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArg--
                                                                                                                 us-10-029-020-14\_copy\_2650\_2725 (1-76) x us-08-992-801-1 (1-14113)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method For Breeding Disease Resistance
Into Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/223,535
                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                 2403 GAGCGCGGCCGTGAGCTTGGACGCTAGGGCAG 2435
                                                                                                                                                                                                                                                                                                                          65 GluGluGlyLeuArgAlaTrpThrGluGlyGlu 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: No. 6232525artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
    Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGC1673/CIP3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,248
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,285
FILING DATE: 08-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Delaney, Terry
APPLICANT: Lawton, Kay
APPLICANT: Lawton, Kay
APPLICANT: Steiner, Henry-York
APPLICANT: Steiner, Henry-York
APPLICANT: Maleck, Klaus
TITLE OF INVENTION: Into Plants
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/992,801
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/09223535; Patent No. 6232525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy
REJSTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 14113 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ryals, John
Uknes, Scott
Ward, Eric
Delaney, Terry
Lawton, Kay
73.50
45.10%
35.29%
18.80%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Ryals,
                       Percent Similarity:
Best Local Similarity:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: N
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APPLICANT:
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US-09-223-535-1
                                                              Query Match:
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                                                  2343 CGCGCCACGGCCCACGAGCGGACGCCGCAGCAGCGCCCAGAAAGGCCCAAGAGAGCC 2402
                           38 LysAlaArgValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArg---
                                                                                                             --GluGlnGlnArgLeuArgGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Method For Breeding Disease Resistance TITLE OF INVENTION: Into Plants NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESSEE: NO. 6107544artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14113
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APPLICATION NUMBER: US/08/992,801
                                                                                                                                                                                                                 2403 GAGGGGGGGGGGGGGTTGGACGCTAGGGCAG 2435
                                                                                                                                                                                            65 GluGluGlyLeuArgAlaTrpThrGluGlyGlu 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PR-1/luc construct'
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1673/CIP3
TELECOMMULCATION INFORMATION:
TELEPHONE: 919-541-8587
TELEPRAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/648,949
FILING DATE: 16-MAX-1996
PRIOR APPLICATION NUMBER: US 08/165,248
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: US 08/02,285
FILING DATE: 08-JAN-1993
ATTORNEY AGENT INFORMATION:
NUMBER: US 08/02,285
FILING DATE: 08-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weymann, Kris
Steiner, Henry-York
Maleck, Klaus
                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08992801
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Ward, Eric
Delaney, Terry
Lawton, Kay
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
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APPLICANT: Ryals, John
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STRANDEDNESS:
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Pred. No.:
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APPLICANT:
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17.52%
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17.39%
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            91504025
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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US-09-252-991A-2453
                      US-09-023-655-969
                                                      Alignment Scores:
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Pred. No.:
        CLONE:
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Patent No. 6607879
CENERAL INFORMATION:
CENERAL INFORMATION:
CACKS, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           38 LysAlaArgValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArg-
                                                                                                                                                                                                            US-10-029-020-14_COPY_2650_2725 (1-76) x US-09-223-535-1 (1-14113)
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                             65 GluGluGlyLeuArgAlaTrpThrGluGlyGlu 75
            MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PR-1/luc construct"
                                                                                                                                                                 Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-055
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 969:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
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73.50
45.10%
35.29%
18.80%
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STRANDEDNESS: single
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TOPOLOGY: linear
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                                                                                                                           Percent Similarity:
Best Local Similarity:
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CLASSIFICATION:
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                                                                           Alignment Scores:
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US-09-223-535-1
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DB:
                                                                                          Pred. No.:
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
NUMBER OF SEQ ID NOS: 33142
IENGTH: 876
                                                                                                                                                                                                                                                           --- CGCAGGAAGGAGATCAAGGAGGCC 1249
                                                                                                                                                                                                                                                                                                                                 54 TrpAlaArgGluGlnGlnArgLeuArgGluGlyGluGluGlyLeuArgAlaTrpThrGlu 73
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                                                                                                                                                                                                        34 LeuAspGluGluLysAlaArgValLeuGluLeuAlaArgGlnArgAlaValArgGlnAla
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Length:
Matches:
Conservative:
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Conservative:
Mismatches:
Indels:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12184, Application US/09252991A Patent No. 6551795
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NS-09-1252-991A-12361/c

| Sequence 12361, Application US/09252991A
| Sequence 12361, Application US/09252991A
| Patent No. 6551798
| GENERAL INFORMATION:
| APPLICANT: Marc J. Rubenfield et al.
| APPLICANT: Marc J. Rubenfield et al.
| TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REFERENCE: 107196.136
| CURRENT RAPLICATION NUMBER: US 60/074,788
| PRIOR PILING DATE: 1999-02-18
| PRIOR APPLICATION NUMBER: US 60/094,190
| PRIOR APPLICATION NUMBER: US 60/094,190
| PRIOR FILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| LENGTH: 1407
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Fatent No. 6551795

GENERAL INFORMATION:
GENERAL INFORMATION:
1TITLE OF INVENTION:
FILE REFERENCE: 107196.136
CURRENT FILEN NAMES: 1999-02-18
CURRENT FILEN NAMES: 1999-02-18
FILE REPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
FRIOR APPLICATION NUMBER: US/00/74,788
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                                                           7 LeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGlnTyrGlyAlaLeuCysLeu 26
                                                                                                                                                                                   27 AsnihrargTyrGlyThrThrLeuAspGluGluLysAlaArgValLeuGluLeuAlaArg 46
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   US-10-029-020-14_COPY_2650_2725 (1-76) x US-09-252-991A-12249
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Matches:
Conservative:
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Indels:
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34.48%
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Best Local Similarity:
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Sequence 12249, Application US/09252991A
Patent No. 6551795
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABSUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12249
      APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR PILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                              RESULT 15
US-09-621-976-595
i Sequence 595, Application US/09621976
j Patent No. 663963
i GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
i CURRENT FILING DATE: 2000-07-21
i SOFTWARE: Patent.pm
SEQ ID NOS: 19335
i LENGTH: 374
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FEATURE:
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US-09-621-976-595
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Sequence 2384, Application US/09252991A

Sequence 2384, Application US/09252991A

Sequence 2384, Application US/09252991A

Fatent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

FRIOR APPLICATION NUMBER: US 60/074,788

FRIOR APPLICATION NUMBER: US 60/074,190

FRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 2384
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1276 ACCTGCTCAAGCTGCGCTACGGCAGTCCCGAGGCCTGCGTATTCACC----- 1323
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                                                                  TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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     1998-07-27
PRIOR FILING DATE: 1998-07-2
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2535
LENGTH: 2205
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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August 14, 2004, 01:13:26; Search time 891.313 Seconds (without alignments) 2546.273 Million cell updates/sec
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- nucleic search, using frame_plus_p2n model
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Xgapop 10.0 , Xgapext
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Command line parameters:
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-Q=/CGT2 1/USTPTO spool/USI0029020/runat 06082004\_112216\_29287/app\_query.fasta\_1.3519
-DB=EST "QFMT=fastap -SUFFIX=p2n.xet "MINMATCH=6.1 -LOOFUL=0 -LOOFEXT=0
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-UNITS=bits -START=1 -END=-1 -MATRIX=blooma62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=1S -MODE=LOCAL
-UNTM==pct -NORM=ext -HEAPSTZE=560 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -LOSPLOCK=100 -LONGLOG
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-NEW TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

em\_gss\_rod:\*
em\_gss\_rod:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Y413475 Homo	77525 227453	56 UI-	134/6 FAII	499 603	32790 TIT-M-EVO	427 60385786·	10132 UI-R-EPO	L58 EST219	580 AV58958	009 AU169909	AW580Z11 RC4-HT041	63 DAFAD434	3493 Tetraod	7897 Mus	54148 603	50 60385988	4 60312095	4 qd40d07	4 qm30d03	qf94c12	w195d07	drysc official		UI-R-	AW044155 wy70e05.x	wi31c06	qo66h01	0 0	h c	4			. qy94c12	8238 qt41h06	7494	04	964 q181d	78290 q178d0	9965	17896 ou35g0
SUMMARIES	ΩI	9 AY41347	0 BF0775	9 AV41347	3 BU38429	3 BU36549	4 CF18279	3 BU38742	3 BQ21013	AI17615	AV58958	AUIESSO	AT-045769	) BB1615	9 CNSC	L AK03	~	3 BU36	BU13	AI184444	A1222954	A1200670	A168/009	AI274285	2 BM717993	AI144798	AW044155	AI910459	A1310370	AT367099	i	AI911042	AW2070	26231	3917	AI33823	AW1374	740	968	77/87	10799	æ
	Query Match Length DB	0 6246 2	היי	5970	881 1	976	621 1	4 913 1	693 1	514	424	4, T	10	608 1	949 2	3038 1	769 1	863 1	946 1	311	7 600	0 000	200	382	7 382 13	390	390	394	395	401	405	406	413	417	421	9 0 6 4	440	44./	450	4.0	454	458
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RESULT 1 AY413475

ALIGNMENTS

GSS 12-DEC-2003 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 6246) AY413475 Homo sapiens HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. AY413475.1 GI:39769437 Homo sapiens (human) Homo sapiens AY413475 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION REFERENCE

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685 bp mRNA linear EST 10-OCT-2002 UI-E-EXO-aim-m-24-0-UI.81 UI-E-EXO Homo sapiens cDNA clone BUT-E-EXO-aim-m-24-0-UI.3', mRNA sequence.
                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
Single pass sequencing. Bases called and alt trimmed with phred
VV.9809044.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRimers
FORWARD: AGGABACAGCTATGACGAT
BACKWARD: GTTTTCCAGTCAGACG
BACKWARD: GTTTTCCAGTCAGACG
Plate: 88 row: F column: 24
Seq primer: ATTTAGACTGACAGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1. (bases 1 to 685)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrGlyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LeuArgGluGlyGluGlyLeuArgAlaTrpThrGluGlyGluLyB 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-029-020-14_COPY_2650_2725 (1-76) x BF077525 (1-499)
Genome Res. 11 (4), 626-630 (2001)
21180013
1128298
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TH: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
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/organism="Bos taurus"
/organism="Bos taurus"
/nol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Homo sapiens
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100.00%
97.37%
98.47%
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Best Local Similarity:
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10. (bases 1 to 499)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Waray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Chitko-McKown, C.G., Pertea, G., Holt, I., Raramycheva, S., Liang, F., Quackenbush, J. and Keele, J.W., Rohrer, G.A.

Chitko-McKown, G.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
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           Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perritera, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, K. Lu, F. Lu, M. Lu, G. Cargill, M. Lu and Cargill, M. Lu and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and M. A. and M. A. and M. A. and M. A. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M
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Direct Submission

Bubmitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5944 TACGGGGGCACTGTGTGTGTGTGTACACGCTACGGGACAACGTTGGATGAGGAGAAGGCACGG
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <1. . >6246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     them based on alignment.
Location/Qualifiers
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BF077525
                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 5970)
Clark, AG., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Toda,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Suckrille, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan. (bases 1 to 5970)

Clark, M.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                    US-10-029-020-14_COPY_2650_2725 (1-76) x AY413476 (1-5970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
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Indels:
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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Science 302 (5652), 1960-1963 (2003)
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gene,
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Pan troglodytes
                                                                                                                                                                                                                                                                                          genomic survey sequence.
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/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/clone lib="UT-E-ENG"
/clone lib="UT-E-ENG"
/note="Organ: eye; Vector: pT/T3-Pac (Pharmacia) with a
modified polylinker; Site 1: ECOR I; Site 2: Not I;
UT-E-ENG is a subtracted CDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an ECOR I adaptor, digested
with Not I, and cloned directionally into pT/T3-Pac
vector. The oligonacleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGARTCAAGA; lens, CGATTAGCGA; eye anterior segment,
AGARTCAACA; lens, CGATTAGCGA; eye anterior segment,
AGARTCAACA; lens, CATTAGCGA; et ina,
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
TAG_IIS-UT-E-ENG
TAG_IESUE=human fetal eyes
TAG_LIB-UT-E-ENG
TAG_LE-ENG
                                                                                                                                          University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
Tel: 319 335 9256
Fax: 319 335 9565
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:9606"
/clone="UI-E-EJO-ain-m-24-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .685
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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385.00
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98.47%
                                                                                               Contact: Soares, MB
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61 LeuargGluGlyGluGluGlyLeuargAlaTrpThrGluGlyGluLys
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Contact: Simon Hubbard
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Best Local Similarity:
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BU365499.1
                                                                                                                                                                    sequence.
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/db.xref="taxon:9031",
/db.xref="taxon:9031",
/clone="Ch87866518"
/dev stage="36"
/dev stage="36"
/dev stage="36"
/dobet="Dost="H108"
/clone lib="CSEQCHN75"
/clone lib="CSEQCHN75"
/clone lib="CSEQCHN75"
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/clone lib="CSEQCHN75"
/clone lib="CSEQCHN75"
/clone lib="CoR1; Site= 2: Not1; This normalized library was Site= 1: ECOR1; million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated Cron in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with ECOR1; size-selected, and cloned into the NotI and ECOR1 compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                      Gallus gallus gallus gallus gallus gallus gallus gallus gallus gallus gallus gallus gallus gallus gallus gallus gallus gallus.

Phasianinae; Gallus.

I (bases 1 to 881)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken CDNAs

Quar. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 TCCCAGATCAACACAGTGCTGGGTGGAACTAGACGTTACACGGACATCCAGCTGCAG 106
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BUJ84298
603858267F1 CSEQCHN75 Gallus gallus cDNA clone ChEST865£18 5', mRNA
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University of Manchester Institute of Science and Technology
(UNIST)
PO Box 88, Manchester, M60 1QD, UK
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Gallus gallus"
/mol type="mRNA"
/strain="White Leghorn, Hisex"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                               GI:25892299
                                                                                                                   Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                 Contact: Simon Hubbard
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Best Local Similarity:
                                                                                   BU384298.1
                                           sequence.
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//clone lib="CSEQCHN12"
//clone lib="CSEQCHN12"
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synthesis was initiated using an oligo (dT) primer, using
methylated C in the first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NoII and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soarse set al., PNAS
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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Gallus gallus (chicken)
Gallus gallus gallus gallus gallus gallus gallus gallus gallus gallus gallus)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
I (bases to Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                    BU365499 976 bp mRNA linear EST 28-NOV-2002
603788050F1 CSEQCHN72 Gallus gallus cDNA clone ChEST747c13 5', mRNA
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Matches:
Conservative:
Mismatches:
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Tel: 01612008930
Fax: 01612360409
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1. .976
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Site_l: ECORI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to Not1 adapters, digested with ECORI size-selected, and cloned into the Not1 and ECORI comparible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
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1 (Dases 1 to 913)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                              1 SerGinileAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln
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University of Manchester Institute of Science and Technology
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                                     Conservative:
Mismatches:
Indels:
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/strain="White Leghorn, Hisex"
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/organism="Gallus gallus"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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BU387427.1 GI:25895415
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Gallus gallus
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Best Local Similarity:
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173 TCCCAGATCAACACAGTGCTGGGTGGAAGGACTAGACGTTACACGGACATCCAGCTGCAG 232
                                                                                                                                                                                                                                            293 GTCCTGGAGCTGGCCCGGCGCGCGCGCGCCCAAGCTTGGGCCCGGGAACAGCAGAAA 352
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 621)
NIH-MCC http://mcc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                    21 TyrGlyalaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg
                                                                                                                                                                                                   41 ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg
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UI-M-EY0-bwz-p-16-0-UI.rl NIH BMAP_EY0 Mus musculus cDNA clone INAGE: 5705343 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                           61 LeuArgGluGlyGluGlyLeuArgAlaTrpThrGluGlyGluLys 76
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF182790.1 GI:33314674
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368.00
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source

FEATURES

Alignment Scores: Pred. No.: Score:

ORIGIN

Bosch, E.,

556

26

9

DEFINITION

CF182790

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL

COMMENT

AUTHORS

REFERENCE

20

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ORIGIN

Score:

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Rattus.
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KEYWORDS
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AI176158/C
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                                                                                                                                                                                                                                                                                              171 TATGGTGCGCTGTGTCTGAACACTCGCTACGGGACCACTTTGGACGAGGAGGACGACCGA 230
                                                                                                                                                                                                                              21 TyrGlyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomí;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 693)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                            UI-R-EPO-cod-1-03-0-UI.SI UI-R-EPO RACTUS norvegicus CDNA clone
UI-R-EPO-cod-1-03-0-UI 3', mRNA sequence.
                                                                                                                                                                             1 SerGlnIleAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln
                                                                                                                                                                                                                                                                               41 ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
(1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                  LeuargGluGlyGluGluGlyLeuargAlaTrpThrGluGlyGlubys 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                               913
70
3
0
                                                                                                                                                       (1-913)
                                                                 Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                       Mismatches:
                                                                                                                                                      US-10-029-020-14_COPY_2650_2725 (1-76) x BU387427
                                                                                                                     Indels:
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97044477
                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics (www.resgen.com)
Seg primer: M13 Forward
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ210132.1 GI:20426597
EST.
                                                                  5e-31
365.00
96.05%
92.11%
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                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
BQ210132/c
                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE
PUBMED
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No.:
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/dev stage="ADDIC"
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/lab_host="ADDIC"
/lab_host="MDIC"
/lab_host="MDIC"
/lab_host="MOIC"
/lab_host="NDIC"
/lab_host="Wetcor: pr713D-Pac (Pharmacia) with a modified
/note="Vector: pr713D-Pac (Pharmacia) with a modified
/note="Vector: pr713D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; UI-R-EPO is a
subtracted cDNA library constructed according to Bonaldo,
Icanon and Soares, Genome Research, 6:791-806, 1996. First
Icanon and Soares, Genome Research, 6:791-806, 1996. First
strand cDNA synthesis was primed with an oligo-dr primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pr773-Pac vector. The oligonucleotide
directionally into pr773-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tags for this
library are: distal colon, GAAGTCCTCC; osteoblast,
AAGARARCAA, cell line R3327 5A, GGACTAGATC; cell line
R3327 5P, CACGTGAGAT; duodenum, TGTGGTTCAT; prostate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514 bp mRNA linear EST 20-JAN-1999 EST219739 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone ROVELS5 3' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 CTGCTGGAGCTGGCCAGGCAGGGCTGTGTACGCCAGGCCTGGGCCCGAGAGAGCAGCAGAGA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 TyrGlyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 ValleuGluleuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 514)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerGlnIleAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LeuargGluGlyGluGlyLeuArgAlaTrpThrGluGlyGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 CTGCGGGAAGGGGAAGAGGCCTCGGGGCCTCGACAGACGGGGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene Index
Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712. Medical Center Drive, Rockville, MD 20850,
Tel: (301)-838-3529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       693
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Mismatches:
Indels:
clone="UI-R-EP0-cod-1-03-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_LIB=UI-R-EP0
TAG_LIB=UI-R-EP0
TAG_SEQ=AAGATATCAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:3726796
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96.05%
92.11%
93.09%
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AI176158.1
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Best Local Similarity:
Query Match:
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EST 29-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                             302 CTGGAGCTGGCCCGGCAAGAGCCGTGCGCCAGGCCTGGGCCCGTGAGCAGCAGCAGCGACTT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryzias latipes (Japanese medaka)
Oryzias latipes
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                       Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Email: kmita@nias.affrc.go.jp
method:uni-directional sequence direction:sequenced from T3 primer
(5, -> 3.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 GlyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArgVal 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 LeuGluieuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArgLeu 61
                                                                                                                                                                                                                                                                                                                                                                                        2 GinileAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGlnTyr
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748 bp mRNA linear EST 29-JAN.
AU169909 Ol-br-ad cDNA Oryzias latipes cDNA clone br5373, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mita,K., Ishikaya,Y. and Yamauchi,M.
Establishment of cDNA database of medaka, Oryzias latipes
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ArgGluGlyGluGlyLeuArgAlaTrpThrGluGlyGluLys
                                                                                                                                                                                                                                              424
8 8 8 0 0 0
                                                                                                                                                                                                                                                                                                                                                               (1-424)
                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                              Length:
Matches:
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/organism="Oryzias latipes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'sex="female/male mixed"
                            organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:8090"
/clone="br5373"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="HNI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU169909
AU169909.1 GI:12591978
                                                                                                                                                                                                                                       3.78e-30
353.00
94.67%
90.67%
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                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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             source
                                                                                                                                                                                                                                       Pred. No.:
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KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 424)
Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H. and Sugimoto, Y.
Establishment of a high throughput BST sequencing system using poly (A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                                                                                                                                                                                                                                                                                                                               383 TACAGGGCACTGTGCCTGAACACCCGCTATGGGACCAGGGGACGAGGAAAAGGTACGG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                           SerginileAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspileGlnLeuGln
                                                                                                                                                            /clone lib="Normalized rat ovary, Bento Soares"
/note="Organ: ovary; Vector: pT/T3Pac; Site_1: EcoRI;
Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrGlyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5725
Email: kazusugi@cccca.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuArgGluGlyGluGlyLeuArgAlaTrpThrGluGlyGluLys 76
                                                                                                                                                                                                                                                                    514
69
3
0
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                                                                            /organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (inhost):2035740"
/db_xref="taxon:10118"
/clone="ROVBLSS"
                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 29 (22), B108 (2001)
                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                               Location/Qualifiers
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Fax: (301)-838-0208
Email: nhlee@tigr.org
Seg primer: M13-21.
                                                                                                                                                                                                                                                             1.35e-30
358.00
94.74%
90.79%
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AV589580
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research (Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
Bequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                713 bp mRNA linear EST 04-SEP-2003
DKFZp434F206 S1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434F206 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 713) Kochrer;K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S. EST (Kochrer, et al.) Unpublished (1999)
                                                                                                                                                                                                                                     320 TGTACGGGGCACTGTGCTTGAACACGCCTACGGGACCAACGTTGGATGAGGGAAGGCAC 261
                                                                                                                                                                                                                                                                                                                                                                      260 GGGTCCTGGAGCTGGCTCCGGCAGAGAGCGGCGCAAGCGTGGGCCCGCGAGCATCAG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rl sequence also available.
This Clone (DKPzp434F206) is available at the RZPD in Berlin.
This Clone (DKPzp434F206) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   1 SerGlnIleAsnThr-ValLeuAsnGly-ArgThrArgArgTyrThrAspIleGlnLeuG
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Acganism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9666"
/clone="DKFSP434F206"
/tissue type="testis"
/dev_stage="adult"
/dev_stage="adult"
/clone lib="434 (synonym: htes3)"
/clone lib="434 (synonym: site_1: Sall"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
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                                                                                                                                                                                  US-10-029-020-14_COPY_2650_2725 (1-76) x AW580211 (1-507)
                                                                 Length:
Matches:
Conservative:
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low stringency conditions."
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Gaps:
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Homo sapiens
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Best Local Similarity:
Query Match:
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RC4-HT0411-080100-013-a03 HT0411 Homo sapiens cDNA, mRNA sequence.
AW580211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 TCTCAGGTCAACACCGTGTTCAACGGCAGGACGACTAGGCGCATCACAGACATCCAGCTGCAG 171
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 507)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LiCR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                              21 TyrclyalaLeucysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg 40
                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                            SerGlnIleAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln
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Mismatches:
Indels:
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                                                                                             Length:
Matches:
          /dev_stage="adult"
/clone_lib="01-br-ad_cDNA"
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/organism="Homo sapiens"
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                                                                                             8.98e-29
344.00
93.42%
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Homo sapiens
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Fax: +55-11-2707001
                                                                                                                               Percent Similarity:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 608)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Iskeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

Unpublished (2001)

On Jun 29, 2000 this sequence version replaced gi:8817476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB161536 RIKEN full-length enriched, 16 days neonate thymus Musculus cDNA clone Al30060L24 3' similar to AB025410 Mus musculus BB161536
                                                                                                                                                                                                                                                   593 GGGGCCTGTGCTTGAACCCCCGCTACGGGCAACGTTGGATTAGGAGAGCC-CGGGTC 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute Institute of Physical and Chemical Research (RIKEN) 1-7-2 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashiazki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-reseges.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Ltoh,M., Komno,H., Okazhi,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
pepare full-length (100), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuki,A., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
                                                                                                                                                                                                                                                                                                                                        41
                                                                                                                                                                                                                                                                                                                                                                                                                               42 LeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArgLeu 61
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Mismatches:
Indels:
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                Percent Similarity:
Best Local Similarity:
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BB161536
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nonredundant cDNA library. Genome Res. . 11 (2), 281–289 (2001)
Kondo,S., Shinagawa,A., Salto,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                              Computational Analysis of Full-Length Mouse CDNAs Compared with
Luman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                         clone_lib="RIKEN full-length enriched, 16 days neonate
                                                                              Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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Conservative:
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                                                                                                                                                                                                                                                                                               tissue type="thymus"
'dev_stage="16 days neonate"
'lab_host="DH10B"
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                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A130060L24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
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Human

Human

BCU0205A BCU0205B Human FCT Human FCT Human FCT Human CTT

OM protein

Run on:

Seguence:

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Human, NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; Cell signal processing; metabolic pathway modulation; metabolic disorder; Cell signal processing; metabolic pathway modulation; metabolic disorder; Cell signal processing; metabolic pathway modulation; disorder; acne; Malbheimer's disease; Parkinson's disease; immune disorder; acneer; Cell memory defect; infertility; congenital heart defect; hair growth; W pigmentation disorder; endocrine disorder; reproductive; neurological disease; health; Cell metapopathy disease; health; Cell metapopathy disease; metapopathy disease; metapopathy disease; metapopathy disease; metapopathy disease; uninary system disorder; age-related disorder; metapopathy disease; uninary system disorder; age-related disorder; metapopathy disease; metapopathy disease; metapopathy disorder; uninary system disorder; age-related disorder; metapopathy disorder; ceceptor kinase; EdF-related protein; SCUBBL; TEN-M4; Cell membrane sushi-containing domain; butyrophilin; type la membrane-sushi domain containing; SNP; gene; ds;
                                                                                      Aas14089 Human FCT
Adb32028 Human FCT
Adb12029 Human FCT
Adb10637 Human FCT
Adb10637 Human CDN
Ab104849 Drosophil
Ac140709 Human foe
Ab129075 Drosophil
Ac28075 Drosophil
Ab129074 Drosophil
Ab129074 Human sec
Adc10764 Human sec
Adc107764 Human cDN
Abk24678 Human cDN
Abk24678 Human cDN
Abb8692 Gene #339
Ab169281 Prostate
Abc0401 Human cva
Abk25440 Human con
Aba3651 Fusion co
Aaa39651 Fusion co
Aaa39651 Fusion co
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Abg82343 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
ABS52100
 Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/Cgn2_1/USTPTO_spool/US10029020/runat_06082004_112215_29265/app_query.fasta_1.3519
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MARRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MX=100 -THR_MIN=0 -ALIGN=15
-MODE_LCOAL_-OUTFYT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Abn85378 Human NOV
Abs78652 Human cDN
Aak52212 Human pol
Aak51828 Human pol
Abh4096 Human cDN
Aah14096 Human cDN
Aah14096 Human cDN
                                                                        August 13, 2004, 17:03:51; Search time 128.916 Seconds (without alignments) 2504.436 Million cell updates/sec
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                                                                                                                                                SQINTVLNGRTRRYTDIQLQ........EQQRLREGEEGLRAWTEGEK
     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                 nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                3373863 seqs, 2124099041 residues
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Ygapop 10.0 ,
Fgapop 6.0 ,
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Score

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Human gen Human mRN Human gen

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Toxicity-Toxicity

TyrGlyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg

21

"Single nucleotide polymorphism (SNP)"

паще≖

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/standard\_name=
replace(260,A)

"Single nucleotide polymorphism (SNP)"

name=

"Single nucleotide polymorphism (SNP)"

'standard name=

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20010S-0288153P.
2001US-0294075P.
2001US-0311590P.
2001US-0311590P.
2001US-03115613P.
                                          19-DEC-2001; 2001WO-US050331
                                                                               2001US-0322358P
                                                  19-DEC-2000; 2
20-DEC-2000; 2
02-MAY-2001; 2
29-MAY-2001; 2
                                                                        10-AUG-2001;
29-AUG-2001;
                                                                     10-AUG-2001;
                                                                                                      Spytek KA,
                                    25-JUL-2002
                                                                                                  Stone DJ,
   variation
              variation
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The present invention relates to new NOVX polypeptides. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, preferably human. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), immune disorders, haematopoletic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, che invention are also useful for treating or preventing cirrhosis, concentitis, learning and memory defects, infertility, congenital heart pancreatitis, learning and memory defects, infertility, congenital heart ceptratory disease, gastro-intestinal diseases, reproductive, health, respiratory disease, bone marrow transplantation, endocrine diseases, alleray and inflammation, nephrological disorders, urinary system disorders, neuropsychiatric disorders and age-related disorders. The consents inclease is the sequence represents a NOVX gene. This sequence
                                                                                                 Liu X;
                                                                                                                                                                                                                                                                                                                                Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease or
                                                        A, Patturajan M, Vernet CAM, Malyankar UM, Kekuda R;
Anderson D, Shimkets RA, Burgess CE, Zerhusen BD, Li
Casman SJ, Boldog FL, Smithson G, Li L, Ji W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8354 BP; 1968 A; 2437 C; 2271 G; 1678 T; 0 U; 0 Other;
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                                                                         Gangolli EA, Patturajan M, Vernet CAM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 50-52; 318pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.53e-39
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(CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                               P-PSDB; ABG70388
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1 SerGinileAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspileGlnLeuGln 20

x ABS52100 (1-8354)

US-10-029-020-14\_COPY\_2650\_2725 (1-76)

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8101
                                                          or
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                                                                                                                                                                                                                                                                                                      Human, NOV1; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive; Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOVX polypeptides and encoding polymucleotides, useful for preventing treating NOVX-associated disorders e.g. cancer, inflammation, or Alzheimer's disease, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                              Gene Therapy, NOV; cancer, heart disease; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; asthma; IgA nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy; wasting disorder; TEN-M4 like protein; chromosome 11; gene; ds.
                                                                                                                                                                                                                                                                                                                                   Antiasthmatic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic; Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a coding sequence for a NOV protein. The NOV
<u>racegecacierectreaacacectacegacaacetregateaaeaaaaaeecacee</u>
                             ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Padigaru M, Li L, Zerhusen BD, Casman SJ, Shenoy S, Spytek KA, Zhong M, Gangolli EA, Burgess CE, Patturajan M, Vernet CAM; Taylor S, Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse WM; Alsobrook JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman K; Macdougall J, Malyankar U, Millet I, Peyman J, Smithson G;
                                                                                                                      LeuargGluGlyGluGlyLeuargalaTrpThrGluGlyGluLys 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/trans_except= (pos: 1138. .1147,aa:Met)
/product= "NOV1 protein"
                                                                                                                                                                                                                                                                             Human NOV1, TEN-M4 like protein, coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 8-9; 358pp; English.
                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JAN-2001; 2001US-0260417P.
10-JAN-2001; 2001US-0260831F.
28-PEB-2001; 2001US-0272338P.
09-MAR-2001; 2001US-0274876F.
18-APR-2001; 2001US-0284704P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JAN-2002; 2002WO-US000554
                                                                                                                                                                                      ABN85378 standard; DNA; 8438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP.
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                                                                                                                              8162
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proteins and coding sequences are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, ALDS, diabetes, obesity, asthma, 19A nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy and other wasting disorders associated with chronic diseases. NOVI is a TEN-M4 like protein and the NOVI gene is localised to chromosome 11
      8888888888888
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Sequence 8438 BP; 2001 A; 2434 C; 2268 G; 1735 T; 0 U; 0 Other;

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8093 TACGGGGCACTGTGCTTGAACACACGCTACGGGACAACGTTGAATGAGGAGAAAGGCACGG 8152
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                                                                                                                SerGln1leAsnThrValLeuAsnGlyArgThrArgArgTyrThrAsp1leGlnLeuGln
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               8438
76
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Conservative:
                                               Mismatches:
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Human cDNA encoding CGDD10, INCYTE 7488573CB1. BP ABS78652 standard; cDNA; 8645 (first entry) 16-DEC-2002 ABS78652: RESULT 3 ABS78652 

Human; ss; gene; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; cell proliferative disorder; arteriosclerosis; atherosclerosis; polirhodas; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thromobocytopaenia; developmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; ADDS; reproductive disorder; Alzheimer disease; Parkinson's disease; asthma; reproductive disorder; infertility; autoimmune disorder; gout; allergy; autoimmune thyroiditis; acquired immunodeficiency syndrome; uveitis; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; multiple sclerosis; osteoarthritis; irritable bowel syndrome; elementicis; contact dermatitis; pancreatitis; rheumatoid arthritis.

Homo sapiens.

WO200272830-A2

19-SEP-2002

08-FEB-2002; 2002WO-US003715.

2001US-0268111P. 2001US-0271175P. 2001US-0274503P. 2001US-0274552P. 09-FEB-2001; 2 23-FEB-2001; 2 08-MAR-2001; 2 09-MAR-2001; 2

(INCY-) INCYTE GENOMICS INC.

Baughn MR; Burford N; Warren BA, Elliott VS, TY, Lal PG, Duggan BM, Khare R, Walia NK; Yao MG, Ison CH, Lu Y, Warr Xu Y, Gietzen KJ, Tang TY, Tran UK, Xu Y, Gietzen Richardson TW, Ding L, Lu DAM, Yue H,

WPI; 2002-723356/78. P-PSDB; ABG97359.

New human proteins associated with cell growth, differentiation death, useful for diagnosing, treating or preventing autoimmune inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atherosclerosis or hepatitis.

Claim 5; Page 175-178; 181pp; English.

The invention relates to an isolated polypeptide comprising GBDD1-12 (cell growth, differentiation and death), a naturally occurring amino caid sequence at least 90% identical to GCDD, a biologically active fragment or an immunogenic fragment. Also included are the comprising a promoter sequence operably linked to the GGD oplynucleotides encoding GGDD1-12, a recombinant polynucleotide an anticody, soreming for compounds which bind to/modulate or are polynucleotides, a cell transformed with the recombinant polynucleotide, a transgenic organism comprising the recombinant polynucleotide, an anticody, soreming for compounds which bind to/modulate or are at the appropriates of GGDD polynucleotide and a naticody, soreming for compounds which bind to/modulate or are compounds antibody, soreming for compounds which bind to/modulate or are compounds antibody, soreming for compounds which bind to/modulate or are antibodies of GGDD polynucleotides, polynucleotide microarray. The polypeptides, polynucleotides of GGDD polynucleotides of GGDD polynucleotides antagonists are useful for diagnosing, treating or preventing disorders are useful for diagnosing, treating or preventing disorders associated with aberrant expression of GGDD, vera, psoriasis, paroxysmal nocturnal haemoglobinuria, polycythaemia disorders (e.g. renal tubular acidosis, anaemia or mental rectardation) contrological disorders (e.g. Alzheimer disease, Parkinson's disease or the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AlbS, contact dermatitis, Crom's disease, diabetes mallitus, contact dermatitis, Crom's disease, diabetes mallitus, cycleoporosis, pancreatiis, pancreatiis, pancreatiis, pancreatiis, pancreatiis, pancreatiis, pancreatiis, fungal, parasitic, protects of cargines or viral, bacterial, fungal, parasitic, protects of contact dermatitis, fungal, parasitic, protects of cargines or proteins associated with cgdDc. The present sequence on codes 

Sequence 8645 BP; 2060 A; 2494 C; 2319 G; 1771 T; 0 U; 1 Other;

8645 76 0 0 0 Matches: Conservative: Mismatches: Indels: Length: 73e-39 391.00 100.00% 100.00% Similarity: Percent Similarity: Alignment Scores: Query Match: Best Local

US-10-029-020-14\_COPY\_2650\_2725 (1-76) x ABS78652 (1-8645)

à	-	1 SerGlnIleAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln 20	
Db	8031	8031 TCCCAGATCAACACAGTACTTAAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCAG 8090	
٥٧	21	21 TyrglyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg 40	
qq	8091	8091 TACGGGGCACTGTGCTTGAACACACGCTACGGGACAACGTTGGATGAGGAGAAAGGCACGG 8150	
à	41	ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArqGluGlnGlnArq 60	
qq	8151 (	8151 GTCCTGGAGCTCGCCCGGCAGAGGCGGTGCGCCAAGCGTGGGCCCGCGAGAGAGA	
δλ	61 ]	61 LeuArgGluGlyGluGlyLeuArgAlaTrpThrGluGlyGluLys 76	
t			

8211 CTGCGOGAAGGGGAAGGGCTGCGGGCCTGGACAGAGGGGGAGAAG 8258

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Homo sapiens.

09-AUG-2001

06-NOV-2001

AAK52812;

RESULT 4
AAK52812

03-FEB-2000; 27-APR-2000;

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78329-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, itssue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or activit/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                      3077 CATGGAGCCCTGTGCTTCAACATCCGGTATGGGACAACTGTCGAAGAAGAAAAGAATCAC 3136
                                                                                                                                                                                                             3137 Grérigsakarraccakacascassakarisseccakassakaraarsakakakakakakakaka 3196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
1 SerGinileAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln
                                                                                  21 TyrGlyAlaLeuCysLeuAsnThrArgTyrGlYThrThrLeuAspGluGluLysAlaArg
                                                                                                                                                                     ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg
                                                                                                                                                                                                                                                                                   3197 CTGCAAGAGGGGGAAAAAGGGGATTAGGGCATGGACAGAAGAGGGGAAAAG 3244
                                                                                                                                                                                                                                                        LeuargGluGlyGluGlyLeuargalaTrpThrGluGlyGluLys 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asundi V, Zhou P, Xi
J, Zhang J, Ren F,
Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1414-1426; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO 373.
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- n. Wang J,
                                                                                                                                                                                                                                                                                                                                                                                              BP.
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27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620225.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00663561.
20-OCT-2000; 2000US-0069325.
30-NOV-2000; 2000US-0069325.
                                                                                                                                                                                                                                                                                                                                                                                            AAK51828 standard; cDNA; 13202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Ma Y, Zhao QA, 1
Xue AJ, Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, hamunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthitis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52881), 2111 (AAK52882) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
Aang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3312 BP; 928 A; 750 C; 739 G; 895 T; 0 U; 0 Other;
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 2341.
                                                                                       AAK52812 standard; cDNA; 3312 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00650325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00653561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00593252.
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2000US-00560875.
2000US-00598075.
2000US-00620325.
2000US-00654936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Liu C, Drmanac RT,
Zhao QA, Wang D, Wang
Yang Y, Wejhrman T,
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311.00
89.47%
75.00%
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                                                                                                                                                                              (first entry)
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Xue AJ,

ΥŢ

Tang 1

Cao Y; R, Wang ZW;

Xu C, (

US-10-029-020-14\_COPY\_2650\_2725 (1-76) x AAK52812 (1-3312)

Alignment Scores:

Pred. No.:

Score:

Query Match:

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8207 TCCCAGATGACTTCTGTGTTGAATGGGAGGACTAGAGGTTTGCAGATATTCAGCTCCAG 8266
                                                                                                                                                                                                                                                                                                      GTGTTGGAGATTGCCAGACAGCGCGCAGTGGCCCAGGCCTGGACTAAGGAACAAGAAGA 8386
                                                                                                                                                                                                                                               (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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                                                                                                                                                                                                                                                                                      09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                                                                               SerGlnIleAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln
                                                                                                                                                                                                                                TyrGlyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg
                                                                                                                                                                                                                                                                                ValleuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prostate tumour tissue; human; mammal; cytostatic;
                                  Sequence 13202 BP; 3921 A; 2764 C; 2865 G; 3652 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                              LeuArgGluGlyGluGlyLeuArgAlaTrpThrGluGlyGluLys 76
                                                                                                                                                            (1-76) x AAK51828 (1-13202)
                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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2001US-0276791P
2001US-027688P
2001US-0281922P
2001US-0281922P
2001US-0081922P
                                                                                                                                                                                                                                                                                                                                                                                                      ABK92230 standard; DNA; 12879
                                                                      1.26e-28
311.00
89.47%
75.00%
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2000US-00733742.
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P-PSDB; ABG61913.
                                                                                           Percent Similarity:
Best Local Similarity:
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16-MAR-2001;
16-MAR-2001;
                                                          Alignment Scores:
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04-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000;
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                                                                                                                                                                                                                                                                                                                                                       8387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prostate
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The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises contexting a biological sample from the patient with prostate cancerassociated polymucleotides (designated PC genes) that selectively thyridise to a sequence that is at least 80% identical to them. The prostate cancerassociated polymucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer or associated genes are useful for diagnosing or treating prostate cancer or segents that in the prostate cancer or associated genes are useful for diagnosing or treating prostate cancer or associated genes are useful for diagnosing or treating prostate cancer or inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABEN22115-ABEN22263 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8000 GIGITIGGAGAITIGCCAGACAGGCGCAGTGGCCCAGGCCTGGACTAAGGAACAAAGG 8059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerGlnIleAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12879 BP; 3852 A; 2674 C; 2768 G; 3585 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8060 CTGCAAGAGGGGGAAGAGGGATTAGGCATGGACAGAAGGGGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuArgGluGlyGluGluGlyLeuArgAlaTrpThrGluGlyGluLys
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Mismatches:
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Matches:
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                                    Claim 22; Page 394-397; 436pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-00116126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999; 99-JP-00248036.
27-A02-1999; 99-D-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-0018376776.
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89.47%
73.68%
78.77%
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Best Local Similarity:
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26-JUN-2001 (first entry)

99JP-00248036.

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AAH14671 standard; cDNA; 3270 BP.
                  sogai T, Nishikawa
Sugiyama T, Wakama
09-JUN-2000; 2000JP-00241899
                                                                                                                                                                                                           1.06e-27
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86.84%
71.05%
75.70%
         (HELI-) HELIX RES INST
                                  WPI; 2001-318749/34.
                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                    present invention
                    Isogai T,
                                                                                                                                                                                                       Alignment Scores:
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                   Ota T, Is
Ishii S,
                                                                                                                                                                                                                               Query Match
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                 Human cDNA sequence SEQ ID NO:12354.
                                                                                                                                                                                                                                                                              27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                        28-JUL-2000; 2000EP-00116126
                                                                                                                  Homo sapiens.
                                                                                                                                                   EP1074617-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                    Ota T,
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The present invention describes primer sets for synthesising 5602 full-
cc [a, an oligo-dr primer and an oligonucleotide complementary to the
cc (a) an oligo-dr primer and an oligonucleotide complementary to the
cc (a) an oligo-dr primer and an oligonucleotide which comprises one of the 5602
cc omplementary strand of a polynucleotide which comprises one of the 5602
cc onplementary strand of a polynucleotide with complementary to the
cc omplementary strand of a polynucleotide which comprising a sequence complementary to the
cc omplementary strand of a polynucleotide which comprising a sequence complementary to a
complementary strand of a polynucleotide which comprising a sequence complementary to the
cc onigonucleotide comprises a 3' end sequence, where the
coligonucleotide comprises a 1 least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence; selected from those defined in the
specification. The primer sets can be used in antisense therapy and in
cspecification. The primer sets can be used in antisense therapy and in
cpection and/or diagnosis of the shormality of the proteins encoded by
the full-length cDNAs. The primers are also useful for the
connas easily without any specialised methods. AAH13628 and
cc halsons assally without any specialised methods. AAH13628 to AAH13628
coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SerGlnIleAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln 20
                                                                                                                                                                       Primer sets for synthesizing polymucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 TyrglyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 ValLeuGluteuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg
                                                                                Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1730 GTGCGCGACGCGAGGAGGCGCGCGCCTCTGGACGGAGGCGAAGAAG 1777
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                                                                                                                                                                                                                                                                    Claim 8; SEQ ID NO 11265; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2157 BP; 544 A; 560 C; 591 G; 462 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LeuargGluGlyGluGluGlyLeuargAlaTrpThrGluGlyGluLys
                                                                              Saito K, Y,
, Otsuki T;
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54
12
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Matches:
Conservative:
Mismatches:
                                                                              илкаwа T, Hayashi K, Si
Wakamatsu A, Nagai K,
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The present invention describes primer sets for synthesising 5602 full-

CC (a) an oligo-dT primer and an oligonucleotide complementary to the

CC complementary strand of a polymucleotide which comprises one of the 5602

CC (a) an oligo-dT primer and an oligonucleotide which comprises one of the 5602

CC complementary strand of a polymucleotide which comprises one of the 5602

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC opplementary strand of a polymucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC sequence and an oligonucleotide comprising a sequence of plynucleotide which comprises a 3'-end sequence of complementary to a

CC sequence and an oligonucleotide comprising a sequence of plynucleotide which comprises a 1'-end sequence', where the

CC sequence and an oligonucleotide comprising a selected from those defined in the

CC sequence of a polynucleotide of plynucleotides

CC particularly full-length cDNAs. The primers are also useful for the

CC particularly full-length cDNAs. The primers are also useful for the

CC particularly without any specialised methods. AAH13628 and

CDNAs easily without any specialised methods. AAH3362 to AAH13628 and

CC particularly condisoned sequences; and AAH13629 to AAH13628 represent

CC oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                    Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 12354; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        852 G; 730 T; 0 U; 0 Other;
                                                    Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-029-020-14_COPY_2650_2725 (1-76) x AAH14671 (1-3270)
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Indels:
                                                        nikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
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Matches:
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                                                               Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.79e-27
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86.84%
71.05%
75.70%
(HELI-) HELIX RES INST
                                                                                           Sugiyama T,
                                                                                                                                                              WPI; 2001-318749/34.
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                                                            Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention
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                                                                                               Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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Conservative: Mismatches: Length: Matches:

Indels:

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Sequence 3614 BP; 967 A; 898 C; 928 G; 821 T; 0 U; 0 Other;
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296.00
86.84%
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/*tag= a
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                                                                                                                                                                                                                                      Best Local Similarity:
                   present invention
                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                Alignment Scores:
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02-JAN-2001;
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DB:
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No..
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length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dry primer and an oligonuclectide complementary to the
complementary strand of a polynuclectide which comprises one of the 5602

(c) an oligonuclectide comprises at least 15 nuclectides; or (b) a combination

oligonuclectide comprising a sequence complementary to the
complementary strand of a polynuclectide which comprises a 5'-end

polynuclectide which comprises a 3'-end sequence complementary to a

complementary strand of a polynuclectide which comprises a 5'-end

polynuclectide which comprises a 3'-end sequence complementary to a

complementary strand of a polynuclectide since therefore the 5'-end sequence and an oligonuclectide comprises a 3'-end sequence complementary to a

complementary strand of a polynuclectide since therefore the 5'-end sequence is selected from those defined in the

complementary. The primer sets can be used in antisense therapy and in

comparing the 11-length cDNAs. The primers are also useful for the

complementary without any specialised methods. AAH13618 end

complementary without any specialised methods. AAH13618 to AAH13628

complementary and a primers allow obtaining of the full-length

complementary and a primers allow a AAH13629 to AAH13612 represent

complementary and an in of which are used in the exemplification of the
                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
21 TyrGlyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg 40
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                                                                                                      41 ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg
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                                                                                                                                                                                                                                                 2760 GTGCGCGACGGCGACGAGGAGGGCGCCTCTGGACGGAGGGCGAGAAG 2807
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                                                                                                                                                                                                               LeuargGluGlyGluGlyLeuargAlaTrpThrGluGlyGluLys
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Otsuki T;
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, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA sequence SEQ ID NO:11430.
                                                                                                                                                                                                                                                                                                                                                                                 AAH14183 standard; cDNA; 3614 BP
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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Ishii S,
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| 1924 TCGCAGTCCACCACGGTGAACGCACGCGCAGGTTCGCGGACGTGGAGATGCAG 2983
                                                                                                                                     3043
                                                                                                                                                                             SerGinileAsnThrValLeuAsnGlYArgThrArgArgTyrThrAspIleGInLeuGln 20
                                                                                                        40
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                                                                                                                 41 ValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnArg
                                                                                             21 TyrglyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg
                                                                                                                                                                                                                                            3104 GTGCGCAACGACGACGCGCGCCTCTGGACGAGAGGCGAGAAG 3151
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                                                                                                                                                                                                                         61 LeuargGluGlyGluGlyGlyGlyLeuargalaTrpThrGluGlyGlyLys
US-10-029-020-14_COPY_2650_2725 (1-76) x AAH14183 (1-3614)
                                                                                                                                                                                                                                                                                                                                                                                                                    Human NOV15c encoding cDNA SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/product= "NOV15c"
                                                                                                                                                                                                                                                                                                                       ABQ82345 standard; cDNA; 8473 BP
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2001US-0279832P.
2001US-0279833P.
2001US-0283889P.
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2001US-0259785P.
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20-FEB-2001;
09-MAR-2001;
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29-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-2001;
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New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
                                                                                                       Spytek KA, Li L, Wolenc AR, Vernet CAM, Bisen A, Liu X;
Malyankar U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;
Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Bilerman K;
Gunther E, Smithson G, Millet I, Macdougall JR;
                                                                                                                                                                                                                                                                   Claim 8; Page 119-121; 444pp; English
                   29-MAY-2001; 2001US-0294080P.
16-AUG-2001; 2001US-0312915P.
17-AUG-2001; 2001US-0313325P.
17-SEP-2001; 2001US-0333350P.
26-NOV-2001; 2001US-0333350P.
2001US-0284447P.
2001US-0286683P.
                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                             WPI; 2002-732706/79.
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            25-APR-2001;
29-MAY-2001;
   18-APR-2001;
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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, cytostatic, anticonvilsant, cerebroprotective, noticathritic, virucide, immunosuppressive, antiallaergic, antianaemic, antibacterial, fungicide, immunosuppressive, antiallaergic, antianaemic, antibacterial, fungicide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers (e.g. Leukaemia, lymphoma, menanoma or cancer of the liver, lung, muscle, covary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or Pick's diabetes mellitus, Grave's disease, or goitre), gastrointestinal disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. ulcerative colitis, viral, bacterial, fungal, helminthic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be biological samples (tissue typing), and in forensic identification of a biological sample. The present sequence encodes human NOVISC, which is ocated on chromosome 4

Sequence 8473 BP; 2301 A; 2017 C; 2145 G; 2006 T; 0 U; 4 Other;

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7842 TTCGGCGCGCTGGCGCTGCGCTACGCCATGACCCTGGACGAGGAGAGAGGCGCGC 7901
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                                                                                                                                                                                                           41 Valieugluleualaargglnargalavalargglnalarpalaarggluglnglnglnarg
                                                                                                            SerGlnIleAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspIleGlnLeuGln
                                                                                                                                                            TyrglyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg
       8473
54
12
10
                                                                                       US-10-029-020-14_COPY_2650_2725 (1-76) x ABQ82345 (1-8473)
       Length:
Matches:
Conservative:
                                          Mismatches:
Indels:
                                                                  Gaps:
          5.92e-27
                     296.00
86.84%
71.05%
75.70%
                                              Similarity:
                               Percent Similarity:
Best Local Similari
Alignment Scores:
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                                                          Query Match:
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Claim 8; Page 123-125; 444pp; English.

diseases.

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New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;
U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;
Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
Smithson G, Millet I, Macdougall JR;
                                                                                                                                                                                                                Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective, nootropic; antidiabetic; antiinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antialersic; virucide; antianemic; antibacterial; protozoacide; antihelminthic; gene therapy, cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy; pick's disease; vesicular transport disease; cystic fibrosis; allergy; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; vaccine; autoimmuna disease; allergic reaction; autoimmune haemolytic anaemia;
                61 LeuargGluGlyGluGluGlyLeuargAlaTrpThrGluGlyGluLyS
                                                                                                                                                                                                                                                                                                                                                                               rheumatoid arthritis; gene; chromosome 4; ss.
                                                                                                                                                                                         Human NOV15d encoding cDNA SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "NOV15d"
                                                                                                ABQ82346 standard; cDNA; 8487 BP
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09-MAR-2001; 2001US-0279863P.
29-MAR-2001; 2001US-0279832P.
29-MAR-2001; 2001US-0279833P.
13-APR-2001; 2001US-0283889P.
18-APR-2001; 2001US-0284647P.
25-APR-2001; 2001US-0286683P.
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04-JAN-2001; 2001US-0259785P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            299. .8140
                                                                                                                                                             17-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kekuda R, Patturajan M
Rastelli L, Casman SJ,
Gunther E, Smithson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
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P-PSDB; ABP53589
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spytek KA,
                                                                                                                                ABQ82346;
                                                                   RESULT 11
                                                                                       ABQ82346
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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, noticopic, cardiovascular, antidiabetic, anticonvulsant, carebroprotective, noticopic, cardiovascular, immunosuppressive, antiallergic, antianthritic, virucide, protozoacide and antihelminthic activities, and can be used in gene the reapy. The NOVX proteins, nucleotides or antibodises can be used in the manufacture of a medicament for treating a syndrome associated with a concers convert disease selected from NOVX-associated disorder, such as cancers covery, testis and uterus), neurological disorder, such as cancers is schaemic cerebrovascular disease, Alzheimer's disease or Pick's disease, disorders of vesicular transport (e.g. cystic fibrosis, disease), disorders of vesicular transport (e.g. cystic fibrosis, disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. ulcerativis), viral, bacterial, fungal, helminthic conduce antibodies and as veccines. The NOVX proteins can be used as immunogens to produce antibodies and as veccines. The NOVX proteins can be used as immunogens to biological sample. The present sequence encodes human NOVISG, which is
¥88888888888888888888888888888
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Sequence 8487 BP; 2306 A; 2029 C; 2148 G; 2001 T; 0 U; 3 Other;

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8487
54
12
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                               Conservative:
Mismatches:
Indels:
                        Matches:
               Length:
             5.93e-27
                       296.00
86.84%
71.05%
75.70%
                                          Best Local Similarity:
                              Percent Similarity:
Alignment Scores:
                                                  Query Match:
DB:
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||||||| | 1778 | TCGCAGTCCACCAGTGAACGCAGGACGCAGGTTCGCGGACGTGGAGATGCAG 7837 SerGinIleAsnThrValLeuAsnGlYArgThrArgArgTyrThrAspIleGlnLeuGln 20 21 TyrclyAlaLeuCysLeuAsnThrArgTyrGlyThrThrLeuAspGluGluLysAlaArg 40 9 ValleuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGluGlnGlnArg 16 61 LeuargGluGlyGluGlyGluGlyLeuargAlaTrpThrGluGlyGlyLyg 41 셤 à g à à

Human NOV15b encoding cDNA SEQ ID NO:37. ABQ82344 standard; cDNA; 8645 (first entry) 17-DEC-2002 RESULT 12 ABQ82344 

Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidabetic; antiinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide; antianaemic; antibartitic; immunosuppressive; antiallergic; virucide; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy; disease; vesicular transport disease; cystic fibrosis; goitre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia;

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rheumatoid arthritis; gene; chromosome 4; ss.
                      Location/Qualifiers
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                                                                   31-DEC-2001; 2001WO-US049976.
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2001US-0269814P.
                                                                              2000US-0258928P
                                                                                                                            25-APR-2001; 2001US-0286683P. 29-MAY-2001; 2001US-0294080P.
                                                                                                                                       2001US-0312915P.
2001US-0313325P.
                                                                                                   2001US-0279863P
                                                                                                        2001US-0279832P
                                                                                                             2001US-0279833P
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                           151. .8316
                                 /*tag= a
                                               WO200262999-A2
           Homo sapiens.
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                                                                                                   09-MAR-2001;
                                                                                                       29-MAR-2001;
                                                                                                             29-MAR-2001;
                                                                                                                                 29-MAY-2001;
                                                                                                                                      16-AUG-2001;
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                                                                                                                                                      26-NOV-2001;
                                                                              29-DEC-2000;
                                                                                         04-JAN-2001;
                                                         15-AUG-2002
                     Key
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Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;
7, Shinkete RA, Tchernev VT, Spaderna SK, Gorman L;
Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
Smithson G, Millet I, Macdougall JR; Spytek KA, Li L, Wolency Spytek KA, Li L, Wolency Malyankar U, Shimkets RA, Tcheiller Kekuda R, Patturajan M, Gusev V, Gar Kekuda R, Patturajan M, Gusev V, Gar Casman SJ, Boldog F, Br

(CURA-) CURAGEN CORP.

WPI; 2002-732706/79. P-PSDB; ABP53587 New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune diseases.

Claim 8; Page 114-117; 444pp; English.

The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, cyforetatic, anticonvulsant, cerebroprotective, noctropic, cardiovascular, antidiabetic, antidinalmantory, antithematic, antibacterial, fungicide, immunosuppressive, antianlengainthe activities, and can be used in gene comparation and antihemanished activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a conference of a medicamia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus, neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or pick's disease, disorders of vesicular transport (e.g. epilepsy, stroke, disease), disorders of vesicular transport (e.g. cystic fibrosis, disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. ulceratives) viral, bacterial, fungal, helminthic conduce antibodies and as vaccines. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX proteins can be used as immunogens to biological samples (tissue typing), and in forensic identification of a conduct on chromosome mapping, and in forensic identification of a located on chromosome apping, and in forensic identification of a located on chromosome and proteins equence encodes human NOVISD, which is

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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, cartidabetic, anticallergic, anticanamatic, anticarthritic, virucide, immunosuppressive, anticallergic, anticanaemic, anticarthritic, virucide, immunosuppressive, anticallergic, anticanaemic, anticarderial, fungicide, protozoacide and antihelminthic activities, and can be used in gene cerebrows. The NOVX proteins a cancers and can be used in the human disease selected from NOVX-associated disorder; such as cancers cerebrovascular, lymphoma, melanoma or cancer of the liver, lung, muscle, cerebrovascular disease, Alzheimer's disease or Pick's ischaemic cerebrovascular tisease, Alzheimer's disease or Pick's disease, disorders of vesicular transport (e.g. cystic fibrosis, disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX mucleotide sequences may be biological samples (tissue typing), and in forensic identification of a biological sample the present sequence encodes human NOVISa, which is
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Gangolli EA, Guo X, Shenoy S;
Burgess CE, Edinger S, Ellerman K;
Macdougall JR;
                                                                                                                                                                                                                                                                                                                                                                                                 New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
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                                                                                                                                                                                                 Liu X;
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Matches:
Conservative:
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                                                                                                                                                                                                                            Tchernev VT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 110-112; 444pp; English.
                                                                                                                                                                                            Li L, Molena
U, Shimkets RA, Tone...
Patturajan M, Gusev V, G
Casman SJ, Boldog F, F
                ; 2001US-0294080P.; 2001US-0312915P.; 2001US-0313325P.; 2001US-0322699P.
2001US-0286683P
                                                                                                              26-NOV-2001; 2001US-0333350P
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86.84%
71.05%
75.70%
                                                                                                                                                                                                                  located on chromosome 4
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Best Local Similarity:
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                       29-MAY-2001;
16-AUG-2001;
                                                                                          17-SEP-2001;
  25-APR-2001;
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                                                                                                                                                                                                                                                                                                           Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular;
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                                                                                                                                                                                                                                                                                                                                                                             21 TyrglyalaleuCysleuAsnThrargTyrGlyThrThrleuAspGluGluLysAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8134 GTGCGCGACGCGAGGAGGCGCGCGCCTCTGGACGGAGGCGAGAAG 8181
         2343 A; 2060 C; 2200 G; 2038 T; 0 U; 4 Other;
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54
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0
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Mismatches:
                                                                                                         Matches:
                                                                                 Length:
                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NOV15a encoding cDNA SEQ ID NO:35.
                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Socation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ82343 standard; cDNA; 8675 BP
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09-MAR-2001; 2001US-0279863P.
29-MAR-2001; 2001US-0279832P.
29-MAR-2001; 2001US-0279833P.
13-APR-2001; 2001US-0283889P.
18-APR-2001; 2001US-0283889P.
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02-JAN-2001; 2001US-0259415P.
04-JAN-2001; 2001US-0259785P.
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The invention relates to isolated polynucleotides which are differentially-regulated in breast cancer. The methods and compositions of the present invention are useful for detecting, diagnosting, staging, monitoring, prognosticating, preventing and/or treating diseases and conditions relating to breast cancer, and may be used in gene therapy or clinical medicine and forensic medicine. Sequences given in records ACC72012-ACC72074 represent polynucleotides of the invention that are differentially-regulated in breast cancer. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human differentially-regulated breast cancer polynucleotide and polypeptide, useful for diagnosing, staging, prognosticating, preventing and/or treating diseases and conditions relating to breast
                                                                                                                                                                                                                          Breast cancer; cytostatic; gene therapy; antisense therapy; regulated; drug discovery; clinical medicine; forensic medicine; gene; chromosome 5q33.3; ds.
                     8146 GTGCGCGACGGCGAGGAGGCGCGCGCTCTGGACGGAGGCGAGAAG 8193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9058 BP; 2387 A; 2430 C; 2263 G; 1978 T; 0 U; 0 Other;
           96
61 LeuArgGluGlyGluGlyLeuArgAlaTrpThrGluGlyGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; SEQ ID NO 79; 127pp + Sequence Listing; English.
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                                                                                                    9058
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                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-2001; 2001US-0326526P.
                                                                                                                                                              (first entry)
                                                                                                                                                                                           BCU0205A gene #SEQ ID 79.
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                                                                                               ACC72051 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotides which are differentially-regulated in breast cancer. The methods and compositions of the present invention are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and/or treating diseases and conditions relating to breast cancer, and may be used in gene therapy or allineal medicine and forensic medicine. Sequences given in records ACC72012-ACC72074 represent polynucleotides of the invention that are differentially-regulated in breast cancer. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
38 LysAlaArgValLeuGluLeuAlaArgGlnArgAlaValArgGlnAlaTrpAlaArgGlu
                                                                                                                                                                                                                                                     drug discovery; cytostatic; gene therapy; antisense therapy; regulated; drug discovery; clinical medicine; forensic medicine; gene; chromosome 5q33.3; ds.
                                                                 92
                                                        GinglinArgLeuArgGluGlyGluGluGlyLeuArgAlaTrpThrGluGlyGluLys
                                                                         Sequence 9695 BP; 2567 A; 2582 C; 2434 G; 2112 T; 0 U; 0 Other;
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                                                                                                                                           ACC72052 standard; DNA; 9695 BP
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14-MAY-2002; 2002US-00144194.
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Best Local Similarity:
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||||||| | TCCCAGCCCACGCTGTTGACGGCAGGACTCGAAGGTTCACGAACATTGAGTTCCAG 7387

21 TyrGlyAlaLeuCysLeuAsnThrArgTyrGly-----ThrThrLeuAspGluGlu 37

1 SerGinileAsnThrValLeuAsnGlyArgThrArgArgTyrThrAspileGlnLeuGln 20

(1-9058)

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8 8 8

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.31e-20 246.50 75.95% 62.03%

Similarity:

Query Match:

Best Local

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Alignment Scores:

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Search completed: August 14, 2004, 02:35:01 Job time : 153.916 secs

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Sequence 1, Appli
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Sequence 1301, Ap
Sequence 301, App
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Sequence 59, Appl
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           13 US-10-383-201-43
13 US-10-0383-201-43
13 US-10-002-020-13
13 US-10-002-865-1
14 US-10-0383-201-55
13 US-10-038-865-1
15 US-10-342-887-1743
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11 US-09-81-495-75
12 US-10-369-493-41803
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14 US-10-156-761-201
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; Sequence 43, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                  OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

0.5 0.5 7.0

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

Searched:

**BLOSUM62** 

Scoring table: Perfect score: Sequence:

Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Jatabase :

SUMMARIES

Query Score Match Length DB

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 SerTyrGluLeuIleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 AspTyrAspValLeuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu
     US-10-25-020-15, Application US/10029020; Sequence 13, Application US/10029020; Publication No. US20040033971A1
GENERAL INFORMATION:
APPLICANT: Gangolil et al.; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: 00/256,704
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-08-10
PRIOR PRIOR APPLICATION NUMBER: 60/257,314
PRIOR PRILING DATE: 2001-08-10
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PRIOR FILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-08-24
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PRIOR PRILING DATE: 2001-05-24
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PRIOR PRILING DATE: 2001-05-29
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Mismatches:
Indels:
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Matches:
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
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Mismatches:
Indels:
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PRIOR FILING DATE: 2002-01-16
PRIOR PILING DATE: 2002-03-22
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PRIOR PILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-01-22
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US-10-383-201-43
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Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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Gaps:

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APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
                                                                                                                                                                            PheGlnLeuHisAsnValIleProGlyTyrProLysProAspMetAspAlaMetGluPro
                                                                                                                                                                                                                                                  AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly
                                                                                                                                                                                                                                                                                                 101 SerTyrGluLeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLys----
                                                                                                                                                                                                                                                                                                                                                                                119 ------SerIleLeuGlyValGlnCysGluValGlnLysGlnLeuLys
                                                     SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer
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Publication No. US20040029216A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Padigaru, Muralidhara
APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
APPLICANT: Casman, Stacie J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
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Miller, Charles E
Guo, Xiaojia
Boldog, Ference L
Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
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MacDougall, John
Malyankar, Uriel M
Millet, Isabelle
Peyman, John
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Gunther, Erik
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| CURRENT APPLICATION NUMBER: US/10/29020 |
| PRIOR PELICATION NUMBER: US/02020 |
| PRIOR PELICATION NUMBER: US/0365,984 |
| PRIOR PELICATION NUMBER: 2001-012-19 |
| PRIOR PELICATION NUMBER: 60/372,022 |
| PRIOR PELICATION NUMBER: 60/312,022 |
| PRIOR PELICATION NUMBER: 60/312,022 |
| PRIOR PELICATION NUMBER: 60/312,022 |
| PRIOR PELICATION NUMBER: 60/391,739 |
| PRIOR PELICATION NUMBER: 60/391,739 |
| PRIOR PELICATION NUMBER: 60/410,755 |
| PRIOR PELICATION NUMBER: 60/412,957 |
| PRIOR PELICATION NUMBER: 10/051,874 |
| PRIOR PELICATION NUMBER: 10/051,874 |
| PRIOR PELICATION NUMBER: 10/055,877 |
| PRIOR PELICATION NUMBER: 10/055,877 |
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141 AspGlnLeuTyrGlySerThrlleThrSerCysGlnGlnAlaProLysThrLysLysPhe
                           AlaSerSerGlySerValPheGlyLysGlyValLysPheAlaLeuLysAspGlyArgVal
                                                                                                                                                               ThrThrAspilelleSerValAlaAsnGluAspGlyArgArgValAlaAlaIleLeuAsn
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Matches:
Conservative:
Mismatches:
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Publication No. US20040029226A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-383-201-55
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                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Afar, Daniel
APPLICANT: Afar, Natasha
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Peter A.
APPLICANT: Murray, Fichard
APPLICANT: Mack, David H.
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APPLICANT: Mack, David H.
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Matches:
Conservative:
Mismatches:
; Sequence 927, Application US/10295027; Publication No. US20030232350A1; GENERAL INFORMATION:
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Indels:
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Matches:
         TITLE OF INVENTION: Using the Same FILE REFERENCE: 21402-537
CURRENT APPLICATION WUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
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ORGANISM: Homo sapiens
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                                                                   21 AspTyrAspValLeuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu 40
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                                                                                                                                                             41 SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer
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APPLICANT: He, Yudong
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Non't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT APPLICANION NUMBER: COREAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLys--
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Publication No. US20030224374A1
GENERAL INFORMATION:
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DATABASE ACCESSION NUMBER: NM 018104
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1743
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PRIOR FILING DATE: 2002-05-14
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
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Sequence 1743, Application US/10342887

Publication No. US20040058340A1

GENERAL INFORMATION:

APPLICANT: Dai, Hongyue

APPLICANT: He, Yudong

APPLICANT: Mao, Mao

APPLICANT: Wan de Vijver, Laura Johanna

APPLICANT: Van de Vijver, Marc J.

APPLICANT: Van de Vijver, Marc J.

APPLICANT: Van de Vijver, Marc J.

APPLICANT: Bernards, Rene

TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

FILE REPRENCE: 9301-188 999

CURRENT APPLICATION NUMBER: 60/298,918

PRIOR APPLICATION NUMBER: 60/298,918

PRIOR FILING DATE: 2001-66-18

PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-06-14

SRIOR FILING DATE: 2002-06-14

SRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 2699

SEQ ID NO 1743

LENACHU: 26.4
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7604 AGGTTTGCTGCTGTCTGTTTTTGGGAAAGGTATAAAATTTGCCATCAAGGATGGC
                                                                        PheGlyPheGlnLeuHisAsnValIleProGlyTyrProLysProAspMetAspAlaMet
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US-10-342-887-1743
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Best Local Similarity:
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Boldog, Ferenc
Burgess, Catherine E
Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
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   Guo, Xiaojia S
Shenoy, Suresh G
Rastelli, Luca
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LENGTH: 8473
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2645 CTGTGGTTCGCCACGGTCAAGTCGCTAATCGGCAAGGGCGTCATGCTGGCCGTCAGCCAG 2704
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2312 ---GGGAAGGACCCAGCTCCTTTAACTTGTACATGTTTAGGAATAACAACCCTGCAAGC 2368
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           Length:
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Sequence 39, Application US/10038854
Publication No. US20040022781A1
GENERAL INPORMATION:
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Kekuda, Ramesh
Patturajan, Meera
Gusev, Vladimir Y
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APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Stabelle
APPLICANT: Millet, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
FILE APPLICATION NUMBER: 60/259,928
FRIOR PILING DATE: 2000-11-29
FRIOR APPLICATION NUMBER: 60/259,415
FRIOR APPLICATION NUMBER: 60/259,785
FRIOR PILING DATE: 2001-01-04
FRIOR PILING DATE: 2001-01-04
FRIOR FILING DATE: 2001-01-04
FRIOR FILING DATE: 2001-03-29
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FRIOR PEDICATION NUMBER: 60/279,833
FRIOR PILING DATE: 2001-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IleGlyTyrHisGlyGlyLeuTyrAspProLeuThrlysLeuValHisMetGlyArgArg
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Matches:
Conservative:
Mismatches:
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                         PRIOR FILING DATE: 2001-03-29

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PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-04-13

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2001-04-18

PRIOR PILING DATE: 2001-04-25

Remaining Prior Application data removed - 5

NUMBER OF SEC ID NOS: 411

SOFTWARE: PatentIn Ver. 2.1

LENGTH: 8487
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               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-854-41
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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| 7503 CTGTGGTTCGCCACGGTCAAGTCGCTGATCGGCAAGAGGCGTCATGCTGGCCGTCAGCCAG 7562
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                                                                                                                                 121 LeuGlyValGinCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe 140
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APPLICANT: Suithbor, Glemida
APPLICANT: Milter, Isabelle
APPLICANT: Milter, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REPERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
FRIOR APPLICATION NUMBER: 60/259,928
FRIOR APPLICATION NUMBER: 60/259,415
FRIOR APPLICATION NUMBER: 60/259,415
FRIOR APPLICATION NUMBER: 60/259,785
FRIOR FILING DATE: 2001-01-04
FRIOR FILING DATE: 2001-01-04
FRIOR APPLICATION NUMBER: 60/269,814
FRIOR APPLICATION NUMBER: 60/269,814
FRIOR APPLICATION NUMBER: 60/269,814
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FRIOR APPLICATION NUMBER: 60/279,832
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Publication No. US20040022781A1
SPELICANT: SPYCEK, Kimberly A
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Vernet, Corine
APPLICANT: Vernet, Corine
APPLICANT: Vernet, Corine
APPLICANT: Lisen, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Malyankar, Uzitel M
APPLICANT: Toherney, Velizar
APPLICANT: Toherney, Velizar
APPLICANT: Spaderna, Steven K
APPLICANT: Spaderna, Steven K
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
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Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
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Shenoy, Suresh G
Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
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Gusev, Vladimir Y
Gangolli, Esha A
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7623 GTGCTCAACAAC 7634
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178 GlyargvalThrThrAspIlelleServalAlaAsnGluAspGlyArgArgValAlaAla 197
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                                                               141 AspGlnLeuTyrGlySerThrIleThrSerCy8GlnGlnAlaProLysThrLysLys--- 159
                                                                                                                    21 AspIyrAspValLeuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu 40
                                                                                                                                                                                                41 SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProIleSer 60
                                         1 IleGlyTyrHisGlyGlyLeuTyrAspProLeuThrLysLeuValHisMetGlyArgArg 20
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US-10-029-020-14_COPY_2400_2600 (1-201) x US-10-038-854-37 (1-8645)
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RESULT 1.

UG-10-038-854-35

; Sequence 35, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: E.i. Li
; APPLICANT: Li, Li
; APPLICANT: Vernet, Corine
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaobong
; APPLICANT: Liu, Xiaobong
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Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
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Boldog, Ferenc
Burgess, Catherine E
Edinger, Shlomit R
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Gusev, Vladimir Y
Gangolli, Esha A
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Shenoy, Suresh G
Rastelli, Luca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Boldog, Ferenc
APPLICANT: Edinger, Shlomit R
APPLICANT: Guther, Brik
APPLICANT: Guther, Brik
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR PAPLICATION NUMBER: 60/259,928
PRIOR FILING DATE: 2000-12-29
PRIOR PELING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR APPLICATION NUMBER: 60/259,835
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
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PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/289,889
PRIOR APPLICATION NUMBER: 60/289,889
PRIOR APPLICATION NUMBER: 60/289,889
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR APPLICATION NUMBER: 60/286,683
                                                     Sequence 37, Application US/10038854; Publication No. US20040022781A1; GENERAL INFORMATION: APPLICANT: Spytek, Kimberly A
                                                                                                                                     Li, Li,
Wolenc, Adam R
Vernet, Corine
Eisen, Andrew J
Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Rekuda, Ramesh
Patturajan, Meera
Gusev, Vladimir Y
Gangolli, Esha A
Guo, Xiaojia S
Shenoy, Suresh G
Rastelli, Luca
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LENGTH: 8645
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APPLICANT: Pechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Howes, Steven H.
APPLICANT: Graham, James R.
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                                                                                      141 AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLys---
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Matches:
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APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: 566,604,734,779
OTHER INFORMATION: n = a,t,g, or c
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7807 GTGCTCAACAAC 7818
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ORGANISM: Homo sapiens
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Best Local Similarity:
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SOFTWARE: PatentIn Ver. 2.1
                                                                             APPLICANT: MILIEC, ISADELLE
APPLICANT: MACDOUGALI, John R
ITILE OF INVENTION: Proceeding and Nucleic Acids Encoding Same
ITILE OF INVENTION: Proceeding and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR PELICATION NUMBER: 60/259,415
PRIOR PELING DATE: 2001-01-04
PRIOR PELING DATE: 2001-01-04
PRIOR PELING DATE: 2001-01-04
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               Gunther, Erik
Smithson, Glennda
Millet, Isabelle
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ORGANISM: Homo sapiens
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LENGTH: 8675
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APPLICANT: Herrman, John L
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishnu
APPLICANT: Mishra, Vishnu
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. U820020155115Alel Proteins and Nuclec Acids Encoding Same
TITLE OF INVENTION: NO. U820020155115Alel Proteins and Nuclec Acids Encoding Came
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
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                                               81 pheglnieuHisAsnValileProGlyTyrProLysProAspMetAspAlaMetGluPro 100
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                                                                                                                  7427 GGCAAGGAGCCAGCC---CCCTTCAACCTGTACATGTTCAAGAACAACAATGTTCTGTGGG
                                                                                                                                                                                                                                                                                                                        7604 CCCTATGAACTGTCAGAGAGCAAGCAAGC-----GAGAACGGACAGCTCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------GGACAGGTCATCACTAAAAAGCTCCATGCCAGCATCCGAGAGAAAGCA
                              AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly
3307 ATTGGCTTCCACGGAGGCCTCTATGACCCCCTCACCAAGCTCGTCCACTTTACTCAACGT
                                                                                               41 SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer
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PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 77
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Patent No. US20020155115Al
GENERAL INFORMATION:
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APPLICANT: Fernandes, Elma
APPLICANT: Shimkers, Richard A
APPLICANT: Herrman, John L
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishnu
APPLICANT: Mass, Peter S
APPLICANT: Mass, Peter S
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7874 TCCGTGTTGAACAAT 7888
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US-09-808-602-77
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Pred. No.:
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GENERAL INFORMATION:

APPLICANT: Vernades, Elma
APPLICANT: Shimtets, Richard A
APPLICANT: Merem, John I
APPLICANT: Mishra, Vishnu
APPLICANT: Mishra, Vishnu
APPLICANT: Maces, Peter S
APPLICANT: Maces, Peter S
APPLICANT: Macougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                       161 AlaSerSerGlySerValPheGlyLysGlyValLysPheAlaLeuLysAspGlyArgVal 180
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                                                                         PheGlnLeuHisAsnValileProGlyTyrProLysProAspMetAspAlaMetGluPro 100
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Conservative:
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CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
PRIOR PILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.1
SENGTH: 8797
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Patent No. US20020155115A1
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US-09-808-602-74
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                     LENGTH: 8797
TYPE: DNA
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US-09-800-198-62
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         SEQ ID NO 62
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Publication No. US20030087816A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vernet, Cornie AM
APPLICANT: Wajumder, Richard A
APPLICANT: Majumder, Kunud
APPLICANT: Majumder, Kunud
APPLICANT: Majumder, Kunud
APPLICANT: Mastes, Perer S
APPLICANT: Mastes, Perer S
APPLICANT: Mastes, Perer S
APPLICANT: Mastes, 1596-697
CURRENT APPLICANT: Rastelli, Luca
FILE REFERENCE: 1596-697
CURRENT APPLICATION NUMBER: 60/186,596
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR SEQ ID NOS: 98
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
                                                                           US-10-029-020-14_COPY_2400_2600 (1-201) x US-09-808-602-77 (1-8797)
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     Length:
Matches:
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Mismatches:
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Sequence Sequence

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Sequence

136, App 1, Appli

Seguence

Sequence Sequence

Sequence

Sequence:

Run on:

Searched:

Sequence

16, Appl 14, Appl

Sequence

1309, Ap 284, App

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Sequence 134, .... Sequence 1342, A Sequence 5, Appli Sequence 2472, Appli Sequence 170, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli
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Sequence 54, Application US/08961527

Patent No. 6420135

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INFORTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:
US-09-717-926-3

US-09-717-926-1

US-09-817-514A-5

US-09-817-512A-3

US-09-202-832-2

US-09-202-832-3

US-09-202-832-3

US-09-202-832-3

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US-09-202-832-3

US-09-202-832-3

US-09-202-1136

US-09-245-041-18

US-09-245-041-16

US-09-245-041-14

US-09-245-041-14

US-09-252-931A-1332

US-09-252-931A-1332

US-09-252-058-5
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                   4 US-08-916-4218-1

US-09-134-000C-570

US-08-540-804-13

US-08-521-872-13

US-08-59-399-13

US-09-251-645-32

US-09-134-010C-1309

US-09-134-010C-1309

US-08-55-785-2

US-08-55-785-2

US-08-55-785-2

US-08-25-785-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FLING DATE:
FLING DATE:
NAME:
BEOGREY INFORMATION:
NAME:
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8515
INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: HP Vectra 486/
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE:
SEQUENCE CHARACTERISTICS:
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                                   Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cogn21/USPETO spool/US10029020/runat 06082004 112217 29301/app_query.fasta_1.3519
-D=|Cogn21_1/USPETO spool/US10029020/runat_06082004_112217_29301/app_query.fasta_1.3519
-DB=ISBUEG PATENTG NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCH=0
-LOOPEXT=0 -UNITS-Dits -START=1 -END=-1 -HATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-USER=US10029020 @CGN 1 1.258 @runat_06082004_112217_29301 -NGPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGIGG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAFEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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8, Appli
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                                                                                August 14, 2004, 01:16:21; Search time 59.4656 Seconds (without alignments) 1875.793 Million cell updates/sec
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2392, Ap
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/ cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                     - nucleic search, using frame_plus_p2n model
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US-09-245-041-8
US-09-245-041-1
US-09-433-681A-548
US-09-453-702B-116
US-09-453-702B-115
US-08-961-527-12
US-08-961-527-12
US-08-162-809-15
US-08-162-809-115
US-09-252-991A-2392
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Score Match Length DB
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Database :

110 110 110 111

Result

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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
FILE REFERENCE: 7853-136
CURRENT APPLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1999-02-05
EARLIER FILING DATE: 1998-07-21
EARLIER FILING DATE: 1998-10-20
NUMBER: OF SEQ ID NOS: 131
SOFTWARE: FESTERE OF THE WINDOWS: 131
SOFTWARE: FESTERE OF THE WINDOWS: 131
SOFTWARE: FESTERE OF THE WINDOWS VETSION 3.0
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                                                 1824 TACAAGGCTTTCAGCGCCAACAATACCGGCTTGCAGATGACCTCTACAGATÁGÁÁÍGÍG 1883
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                                                                                                   LeuAlaGlyArgTrpThr---SerProAspHisGluLeuTrpLysHisLeuSerSerSer 43
                                                                                                                                                                                                      44 AsnValMetProPheAsnLeuTyrMetPheLysAsnAsn-----AsnProlleSerAsn 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.24
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APPLICANT: Nagle, D.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
FILE REFERENCE: 7853-136
CURRENT APPLICATION WUMBER: US/09/245, 041
CURRENT FILING DATE: 1999-02-05
EARLIER FILING DATE: 1999-02-05
EARLIER FILING DATE: 1998-07-21
EARLIER PILING DATE: 1998-07-21
SARIER PILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Fatesey for Windows Version 3.0
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13267 AAGAATATCTTAAGAAATGACATTTCGAATTCTCTTTCT-----TTTTTAACAGCA 13217
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Matches:
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Matches:
Conservative:
Mismatches:
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'Sequence 8, Application US/09245041

'Patent No. 6274339

'GENERAL INFORMATION:
LENGTH: 20986 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TOPOLOGY:
US-08-961-527-54
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|---AAGGTGACGGCTTCTGACTTTGTATAGTTGGCAAGATA-----GTTGATCCA 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 LeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerIleLeuGlyVal 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 GlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPheAspGlnLeu 143
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                                                                                                                                                                                                                                                                                                    45 ValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSerAsnSerGlnAsp 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 GAAGCCATTGATGAAAAACGTTAAAA-----GTTACCTTAGAACGACCTGTTCCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562 TICCCIAGITIAGCGACCAATITITCACITIAICCIGIACCCIAAACACACAAICGAAAA
                                                                                                                                                                                    US-10-029-020-14_COPY_2400_2600 (1-201) x US-09-543-681A-548 (1-1650)
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WEDDUW TYPE: DISKETLE, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
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679 AAAGAICGCGTIGIGAAIGAGAAAAIIGIGITAACGCCAAAC 720
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                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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:77 GTGGCAATCATGGCGAACAGAAAAACCGGGTTTGG-
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STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 ATTATTGATGGTAAATTAAAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 116, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
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Plunkett, Guy
                                                        0.83
82.50
41.38%
25.29%
7.66%
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                                                                                          Percent Similarity:
Best Local Similarity:
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US-09-453-702B-116
                                     Alignment Scores:
Pred. No.:
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                                                                                                                               Query Match:
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Patent NO. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 548

LENGTH: 1650
                                                                                                                                                                                                                                1824 TACAAGGCTTTCAGGGGCCAACAATACGGGCTTGCAGATGACCTCTACAGATACGATGTG 1883
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                                                                                                                                             1884 GATACTCAGATGTGGACCATTCTTAAGGACAGCCGATTTTTCCGTTACTTGCATACAGCT 1943
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|2004 AGCCACGGIGCCAATGCTICTCCICGGACTICATGGCTIATGACATIGCTIGTGACGA 2063
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2160 TICAACAGCCICCICCICAGIGACGICITIAGICITIACCICGGAGCAGGGGAIGCACAC 2219
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|----CTAAAAGAACCCTTGACCATGACAGATGT 2378
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                                                                                                                 2 GlyTyr---HisGlyGlyLeuTyrAspProLeuThrLys-----LeuValHisMetGly 18
                                                                                                                                                                                                                                                                     25 LeuAlaGlyArgTrpThr---SerProAspHisGluLeuTrpLysHisLeuSerSerSer 43
                                                                                                                                                                                                                                                                                                                                              44 AsnValMetProPheAsnLeuTyrMetPheLysAsnAsn----AsnProlleSerAsn 61
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                                                                                                                                                                                                      --AspTyrAspVal
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1220 CGCAGTGAAGCTGCTTGTGTGGCAGCAGGACCTGGTATCCGGTGTCTGTGGGACACACAG
                                                                                      (1-8827)
                                                                            US-10-029-020-14_COPY_2400_2600 (1-201) x US-09-245-041-1
               86
53
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2064 TGGTCAGTGCTTCCCAGACCTGAGCTCCATCAT----
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                             Indels:
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Best Local Similarity: 24.22%
Ouerv Match: 7.80%
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; ORGANISM: Proteus mirabilis
US-09-543-681A-548
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3137 GAİGİĞGATĞCAĞĞAACATTGACGGTACCATCCATÖĞÜĞĞĞGGACAAATGAGGTTATC 3078
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                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Mismatches:
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REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
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Matches:
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
                                                                                                                                                                                                                                     ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                             APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
            Sequence 60, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                              Burland, Valer.
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 63657
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS:
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JS-09-453-702B-60/c
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12437 GTGGAAGCTGAACCATCTGTAGAGGGGTGAAGGACCATTTTATTTGGTCTTTACCGATAAG 42496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
                                                                                                                                NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DRA (genomic); SEQUENCE DESCRIPTION: SEQ ID NO: 116: US-09-453-702B-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
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                             CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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81.00
39.25%
23.66%
7.52%
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3253 GCCTTGGATGAGGGGCTTTGTGTGAAACTGTAGCACCAGAACTTTATCAAGGTTTCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 AspAlaMetGluProSerTyrGluLeuIleHisThrGlnMetLysThrGlnGluTrpAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3193 GATGAGACCAACCGTATGATGCGCATGGTGACGGATCTCCTCCATCTTTCACGTATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AsnSerLysSerIleLeuGlyValGlnCysGluValGlnLysGlnLeuLysAlaPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3133 AATGCTACCAGTCACCTAGATGTGGAACTG-----ATTAACTTCACTGCTTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 IleSerAsn---SerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeu--
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35
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COMPUTER READABLE FORM:
MEDIUM TYPE: Disketce, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

COMPUTER: HP Vectra 486/33

CORRENTING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII TAXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,527
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Mismatches:
Indels:
                          1804 CAGAAAGCAAATGATGAAGCTACAAAAATT 1833
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                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB340P1
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                          Sequence 12, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
                                                                                                                                                                  APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strepto
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome S:
STREET: 9410 Key West Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
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EDNESS: double
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                        US-08-961-527-12/c
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                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-961-527-12
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DB:
                                                                      RESULT 8
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US-09-328-352-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 2280
                            ---GACCAGAGCTCTACTGATGCTCTCCAGCGTCAGCA 2847
                                                                                                        2846 GCACAAACT---GCTCCAGTGGAGACGGCAGAATCCGATACTCAAAAAAAATGAAATCCTG 2790
                                                                                                                                                                                        2789 GIGGAAGCTGAACCATCTGTAGAGCGTGAAGGACCATTTTATTICGICTTTACCGATAAG 2730
                                                                                                                                                                                                                                                                             ----AGGCCAAACAACTTTCTGGT 2691
                                                                                                                                                                                                                                                                                                                                   83 LeuHisAsnVallleProGlyTyrProLysProAspMetAspAlaMetGluProSerTyr 102
                                                                          103 GluLeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerlleLeuGly 122
                                                                                                                                                    123 ValGlnCysGluValGlnLysGlnLeuLysAla-----PheValThrLeuGluArg 139
                                                                                                                                                                                                                                                                                                           ---ThriysLysPheAlaSerSerGlySerValPheGlyLysGlyValLysPheAlaLeu 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1564 AATAGCAAGCACGCAACAGGTAATGCATTTGACTTCACGCTAGATGATGCGAAAAAGTCT 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .624 GGTGAGGCTGTTACACAACTTGAGCAAATGGCTAAAAGATACGGCTTTGTCATTGGCGTT 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1744 CTTGGCTACAAAGGCACAGCAGATGCATTAAAAGATGCAAATGCAGAGCTTGATATTGTT 1803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 LeulysAlaPheValThrLeuGluArgPheAspGlnLeuTyrGlySerThr1]eThrSer
                                                                                                                                                                                                                               140 PheAspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLys----
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 115, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                         2630 AAAATGGCACATACACG 2613
                                                                                                                                                                                                                                                                     2729 GGCGGGAAAATACGGC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Acinetobacter baumannii FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                       176 LysAspGlyArgValThr 181
                                      2897 GAACATGAAGAAACA-----
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Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-328-352-115
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1542 GAAGTGGACCCCAAGCTCGTGTCTAATCTGATGCCCTTTCAGAGAGCTGGAGTCAATTT 1601
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                                                                                                                                                                                                                                                                                                                                                             :::
------TCACAGGACCTTATTGCGCTTTTTAAACAGATGGATTCCAGAAGATATGAT 1361
                                                                                                                                                                                                                                                                                                                                                                                                                         -----LysLysPheAlaSerSerGlySerValPheGlyLys---GlyValLysPhe 173
                                                                                                                                                                                                                                                                                                                                   89 GlyTyrProLysProAspMetAspAlaMetGluProSerTyrGluLeuIleHisThrGln 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ValThrLeuGluArgPhe 140
                                                                                                                                                                                                                                                                     69 MetThrAspValAsnSerTrpLeuLeuThrPheGlyPheGlnLeuHisAsnValllePro 88
     ProLeuThriysLeuValHisMetGlyArgArgAspTyrAspValLeuAlaGlyArgTrp 29
                                                                    ThrSerProAspHisGluLeuTrpLysHisLeuSerSerAsnValMetProPheAsn 49
                                                                                                                                                                                                                                                                                                                                                                                                    109 MetLysThrGlnGluTrp------AspAsnSerLysSerlleLeuGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThr---
                                     1077 cchgacaccadaaccrogaactrogcargaardachahagrocchgarg---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USE
                                                                                                                                       50 LeuTyrMetPheLysAsnAsnAsnProlleSerAsnSerGlnAsplle----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOVEL EPH-RELATED TYROSINE KINASES, NUCLEOTIDE SEQUENCES, AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IB: CAMPBELL AND FLORES 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 GlnCysGluValGlnLysGlnLeuLysAlaPhe-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1602 GCCATAGCCAAAGGAGGCCGCCTG 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 AlaLeu---LysAspGlyArgVal 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-162-809-15; Sequence 15, Application US/08162809; Sequence 15, Application US/08162809; Patent No. 5457048; GENERAL INFORMATION: APPLICANT: Pasquale, Elena B. APPLICANT: Sajjadi, Fereydoun G. TITLE OF INVENTION: NUCLEOTIDE SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                           1293 GAGGCAGACATCAGTTAT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
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STATE: Californ
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| ATTGGGTACAATGCGGAACTCATTGCAGTGTTTAAGACCCTGCCCAGCAAGAATTATGAT 1076
                                                                                                                        ::::::: |||:::::: CAGGTTGTCGACATATTAAGTATTCGCCACATGGGGGTAAAATC 2903
                                                                                                                                                                                      1022 TIGGIGAGALTATCCCAİCAATİCİATCIGGAIGGAAAITGAIACAGAIAAGAIGACG 2963
                                                                                                162 Ser---SerGlySerValPheGlyLysGlyValLysPheAlaLeuLysAspGlyArgVal 180
                                                                                                                                                                   ThrThrAspilelleSerValAlaAsnGluAspGlyArgArgValAlaAlaileLeuAsn 200
                                -----ThrileThrSerCysGlnGlnAlaProLysThrLysLysPheAla 161
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448
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73
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                   Sequence 86, Application US/09620312D
Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
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John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong
                                                                                                                                                                                                                                                                                                                                                                                   Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
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Wang, Jian-Rui
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US-09-620-312D-86
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Wang, Dunrui
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Best Local Similarity:
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105 CCGGCAACGAAGTTAATCTGCTGGATTCAAAACAATTC-----AAGGGGAGCTGG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 CTCCAATCAGAACTTACCAAGAGGAATGTTATGGATCACAGTCAAAACAATTGGCTGG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335
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| ACCAATTTACGAAGAITGACACCATGGCGGCTGATGAGAGCTTCACCCAGATGGATCTTG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      euTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLysPheAlaSerS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AlaLeuLysAspGlyA 179
                                                                                                                                                                                                                                                                                                                                                                                             29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AspileLysCysPhem 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 ProLeuThriysLeuValHisMetGlyArgArgAspTyrAspValLeuAlaGlyArgTrp
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|276 GAACAAACTGGATTCCACGCAATTCAGGGCAGAAGATATATGTGGAGGTCAAGTTTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 TGAGGGACTGCAATAGTATCCCTCTAGTTCTTGGCACTTTGCAAAGAGACTTTCAATCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       561 GCTTTTACTTGGCTTTCCAAGATGTAGGTCCATGTGTTTGCCTTAGTCTCGGTGCG-AGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               520 TACTICAAGAAGIGCCCITICACIGICAAGAACCICGCCAIGITICCAGAIACAGIICCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            880 ATGGACTCCCAGTCCCTGGTGGAGGTGCGGGGTTCTTGTGTCAATCATTCCAAGGAGGAA
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                                                                                                                                                                                                                                                                                                                                                       US-10-029-020-14_COPY_2400_2600 (1-201) x US-08-162-809-15 (1-3254)
                                                                                                                                                                                                                                                                                                                                                                                                                                             30 Thr --- SerProAspHisGluLeu--TrpLysHisLeuSer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 eulleHisThrGlnMetLysThrGlnGluTrpAspAsnSer-
                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 --LysSerIleLeuGlyValGlnCysGluValGln---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 etThrAspValAsnSerTrpLeuLeuThrPheGly-
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                                                                                                                                                                                                                                                                                                                  [ndels:
             REFERENCE/DOCKET NUMBER: P-L 9503
TELECOMMUNICATION INFORMATION:
TELEFHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3254 base pairs
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REGISTRATION NUMBER: 31,815
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78.00
39.17%
24.17%
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32..2980
                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
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Best Local Similarity:
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Pred. No.:
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US-08-162-809-15
                                                                                                                                                                 FEATURE:
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### PILLE OF INVENTION: BRETHODS OF USE

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Matches:
Conservative:
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Sequence 11, Application US/09738946
Patent No. 6579701
GENERAL INFORMATION:
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LENGTH: 5706
TYPE: ...
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25.64%
7.20%
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Best Local Similarity:
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lry ig	pplication 69657 69657 69657 69657 69657 69767 6977 6977 6977 6977 6977 6977 6977 6977 6977 6977 6977	ORGANISM: Homo sapiens   FEATURE:   NAME/KEY: CDS   LOCATION: (1)(2772)   UCCATION: (1)(2772)   USCATION: (1)(2772)   Alignment Scores: (1)   Length: (2772)   Pred. No.: (76.50   Matches: 31   Score: (28   Mismatches: 48   Mismatches: 48   Best Local Similarity: (24.60%   Indels: 29   Mismatches: 29   Mismatches: (29   Mismatches: 29   Mismatches: (29   Mismatches: (29   Mismatches: (29   Mismatches: (29   Mismatches: (29   Mismatches: (29   Mismatches: (29   Mismatches: (29   Mismatches: (20   Mi	: -10-029-020- 88 631	13 13 79	OY 136 ThrLeuGluArgPheAspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaPro 155  Db 799TATGGCTCGACATTACGACTCGACTCCTCTCTCTCTCTCT
4109 G 134 - 4142 G 148 G 4202 T	G TO E			US-10-029-020-14_COPY_2400_2600 (1-201) x US-09-252-991A-2392 (1-1119)  QY	120 GTCGCCAAGTCGGT   42 SerSerAsnValMe   180 GTCGGCGGC   62 SerGlnAspileLy   1:1:1:   222 GCGACGCGTACG   82 Gln-LeuHisAsnV   82 GGCGCTCATTCAT   101SerTyrG

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963 GGAGAACCACTGGAAATTAAAGGTGCCAAGAAGCCTĠĠTCTCĠTTACCAAAAATĠĠĀĊTT 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 ThrLeuGluArgPheAspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaPro 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 LysPheAlaLeuLysAspGlyArgValThrThrAspIleIleSerValAlaAsnGluAsp 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 ------LysThrLysLysPheAlaSerSerGlySerValPheGlyLysGlyVal 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 759 ccrcgraracccagccagaagaaggggca-----acarargaaggraraccagaaa
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APPLICANT: ffrench-Constant, Richard
APPLICANT: Bowen, David
APPLICANT: Rocheleau, Thomas
APPLICANT: Waterfield, Nicholas
TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-029-020-14_COPY_2400_2600 (1-201) x US-09-717-926-1 (1-7220)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 GlnMetLysThrGln---GluTrpAspAsnSerLysSerIleLeu-----
                                                                                       APPLICANT: Meyers. Rachel
APPLICANT: Meyers. Rachel
APPLICANT: Cook, William J.
TITLE OF INVENTION: 32140, A No. 6569657el Human Aldehyde
TITLE OF INVENTION: Dehydrogenase
FILE REFERENCE: 35800/205243
CURRENT APPLICATION NUMBER: US/09/717,926
CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/214,707
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 4
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Matches:
Conservative:
Mismatches:
                                      Sequence 1, Application US/09717926
Patent No. 6569657
GENERAL INFORMATION:
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7.10%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
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RESULT 14
US-09-717-926-1
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Search completed: August 14, 2004, 21:40:27

Job time : 121.466 secs

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Mismatches:
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CURRENT FILING DATE: 2000-03-26
PRIOR PILING DATE: 2000-03-24
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SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                             TYPE: DNA
ORGANISM: Photorhabdus luminescens
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43.33%
36.67%
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; LOCATION: (1)..(2745)
US-09-817-514A-5
FILE REFERENCE: 61645
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Best Local Similarity:
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BU234988 603408474
AK037897 MLS muscu
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BE819779 MR3-BN036
CE578819 AMGNNUC:N
CA777388 ipp9co6.x
AY405420 Homo sapi
BX506934 DKFZp7791
CB720876 AMGNNUC:N
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AY413476 Pan trog1
BQ553239 g101b09.Y
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CF171639 B0845C10-
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AL046228 DKFZp434E
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BB576857 BB576857
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 6246)
                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Homo sapiens HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                             SUMMARIES
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BX308610
CB519165
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AL045768
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AY413475.1 GI:39769437
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ORGANISM
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AY413475
LOCUS
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KEYWORDS
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                         - nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Xgapop 10.0 , Xgapext
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Pan troglodytes HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence,
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             5674 ACCACAGACATCATCAGTGGGCCAATGAGGATGGGCGAAGGGTTGCTGCCATCTTGAAC 5733
                                                                                                                                                                                                                                                           Pan troglodytes (chimpanzee)
Pan troglodytes
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Pan.
1 (bases 1 to 5970)
1 (bases 1 to 5970)
1 (bases 1 to 5970)
1 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
                                                                                                                                                                                                                                                                                                                                                                                                   Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer
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ThrThrAspIleIleSerValAlaAsnGluAspGlyArgArgValAlaAlaIleLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1-5970)
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/db_xref="taxon:9598"
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Science 302 (5652), 1960-1963 (2003)
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AY413476.1 GI:39769438
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      Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perritara, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                      Taylor, 20 (bases 1 to 6246)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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//dev stage="Post nata" |
//dev stage="Post nata" |
//dow stage="Post nata" |
//dow stage="Post nata" |
//dow lib="Mouse Organ of Corti; CDNA pBluescript" |
//dow="Down" Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-nata" (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
from P6; 60 from P7; 46 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
                                                                                                                                                                                                                                    141. AspGlnLeuTyrGlySerThr11eThrSerCysGlnGlnAlaProLysThrLysLysPhe 160
                                                                                                                                                                                                                                                                                                                   161 AlaserserGlyservalPhedlyLysglyvalLysPheAlaLeuLysAspGlyArgVal 180
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1765
Fax: 301-402-1765
PheGlnLeudisAsnVallleProGlyTyrProLysProAspMetAspAlaMetGluPro
                                   5098 TTCCAGCTACACAACGTGATCCCTGGTTATCCCAAACCAGACATGGATGCCATGGAACCC
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Plate: 01 row: b column: 09
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/mol_type="mRNA"
/strain="BALB/c"
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and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fastrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 15 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
primed with the linker- primer and transcribed using
Woloney murine laukemia virus reverse transcribed using
Woloney murine laukemia virus reverse transcribed using
Woloney murine laukemia virus reverse transcribed using
Woloney with the linker- primer and transcribed using
Woloney with DNA polymerase and RMSas H. Complementary
DNA was blunt ended with Ptb DNA polymerase, ligated with
ECOR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Chontech, Palo Alto, CA)
columns to enrich for cDNAs greater than 400bp and 1000
bp, respectively. The cDNA was then directionally ligated
to the Uni-ZAP KR vector, which had been predigested with
ECOR I and Xho I. The phagemid was packaged with Gigapak
III Gold and, upon tiration on XLI Blue MRF, cells, the
recombinants. Stratagene's Exhsaist Interference
resistance helber phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the ConcertS6 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTS from the 5' end of the CDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATCACC) and 25% strength Bigbye terminator sequencing chemistry (Applied Blosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Blosystems, Foster City, CA). The frequency distribution of the library is a follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function, 33% have hits in GenBank, but do not have assigned function; 12% are uncharacterized BSTS and 20% are unidentified."

Conservative: Mismatches: Length: Indels:

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61 AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly 80

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CF171639 MRNA linear EST 25-JUL-2003 B0845C10-5 NIA Mouse Newborn Kidney cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0845C10 IMAGE:30471777 5', mRNA sequence.
methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to Not1 adapters, digested with BCORI, size-selected, and cloned into the Not1 and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1994) 191, except that a significantly longer reannealing hybridization was used."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
/note="Organ: heads; Noti: This normalized library was
EccR; Site_2: Not!; This normalized library was
constructed_from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU233488 11near EST 26-NOV-2002 603408464F1 CSEQCHN24 Gallus gallus cDNA clone ChEST321p15 5', mRNA
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                  Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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/strain="White Leghorn, Hisex"
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PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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clone="chEST321p15"
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/lab_host="DH10B"
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Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
        Mus.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 637)
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                                                                                                                    National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U
                                                                                                                                                                                                                               /mol_type="mRNA"
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Matches:
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Plate: B0845 row: C column: 10
Seg primer: M13 Reverse
High quality sequence stop: 637
POLYA=No.
                                                                                                                                                                                                                     organism="Mus musculus"
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                                                                                                Contact: Dawood B. Dudekula
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1 (bases 1 to 667)
2 (lifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,
Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,
Waterston,B., and Wilson,R., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
WashU Xenopus EST project, 1999
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by R. Harland, PhD. (University of California,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="12" | /dev_stage=19-23" | /dev_stage="12" | /dev_host="DH10B (phage-resistant)" | /clone lib="Harland stage 19-23" | /note="Vector: pCS107 (custom); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Library constructed
                                                                                                 PheGlnLeudisAsnVallleProGlyTyrDroLysProAspMetAspAlaMetGluPro
                                                                                                                                                                                                   SerTyrGluLeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerlle
61 AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly
                          LeuGlyValGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe
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WashU Xenopus EST project, 1999
Washington University School of Medicine
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Xenopus laevis
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/organism="Xenopus laevis"
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/clone="IMAGE:3200137"
/tissue_type="neurula"
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/clone liber GREQCHN24"
/clone liber GREQCHN24"
/clone structed from limition independent clones. CDNA constructed from limilion independent clones. CDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with BCCRI size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (XS+) vector. The library was normalized in 2 pBluescript (XS+) vector. The library was normalized in 2 pBluescript and Bonaldo et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reamnealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrGlnGluTrpAspAsnSerLysSerIleLeuGlyValGlnCysGluValGlnLysGln 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 GAIGICAACAGIIGGCIACICACTIIIGGGIICCAGCIACACAAIGICAICCCIGGAIAC
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 SerProAspHisGluLeuTrpLysHisLeuSerSerSerAsnValMetProPheAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrMetPhelysAsnAsnAsnProlleSerAsnSerGlnAspIleLysCysPheMetThr
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                                                                                                                                                                                                  Science and Technology
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                  1.850
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
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                                                                                                                                                                Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute o
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                                                                                                                                                                                                                                        88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                              Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9031"
/clone="ChEST255011"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="22"
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                          Phasianinae; Gallus.
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94.15%
86.55%
75.77%
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Tel: 01612008930
Fax: 01612360409
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603341548F1 CSEQCHN24 Gallus gallus cDNA clone ChEST255011 5', mRNA
         by Dr. Francesca Mariani in the laboratory of R. Harland, Ph.D. (University of California, Berkeley). References: XBF-2 is a transcriptional repressor that converts ectoderm into neural tissue. Mariani, FV. Harland, RM., 99030283; Use of large-scale expression cloning screens in the xenopus laevis tadpole to identify gene function. Grammer TC. Liu KJ. Mariani FV. Harland RM., Dev Biol. 2000 Dec 15;228(2):197-210. PMID: 11112324; UI: 20564075; Note: This is a Xenopus Gene Collection (XGC) library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 ValThrThrAspileIleSerValAlaAsnGluAspGlyArgArgValAlaAlaIleLeu 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheAspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLys 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 ATAACCACCAATATCATCAGCGTCGCTAACGAGGATGGCAGGAGGATTGCTGCCATNGTG 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11ereuGlyValGinCysGluValGinLysGinLeuLysAlaPheValThrLeuGluArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 LeuSerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlle
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836.00
93.41%
81.87%
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BU232300
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Best Local Similarity:
Query Match:
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CCTGGTTATCCCAAACCAGACATGGATGCCATGGAACCCTCCTACGAGCTTATCCACACA 122
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525 bp mRNA linear EST 04-SEP-2003
DKFZp434E177 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434E177 5', mRNA sequence.
                                                                     108 GlnMetLysThrGlnGluTrpAspAsnSerIJysSerIleLeuGlyValGlnCysGluVal 127
                                                                                                                                                                                                          148 ilejhrSerCysGlnGlnAlaProLysThrLysLysPheAlaSerSerGlySerValPhe 167
                                                                                                                                                                                                                                           243 ATCACCAGCTGCCAGCACGCACCAACAACAACAACAACATTGCATCCAGCGCTCAGTCTTT 302
                                                                                                                                                                                                                                                                                                             German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                         128 GlniyşGlnieulyşAlaPheValThrLeuGluArgPheAspGlnieuTyrGlySerThr
                                                                                                                                                                    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2); Email s.wiemann@dKfz- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the Ger
                                                                                                                                                                                                                                                                               168 GlyLysGlyValLysPheAlaLeuLysAspGlyArgValThrThrAspIle1leSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No s1 sequence available.
This clone (DKFZp434E177) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 525) "Ilmaces, carafinini; Hominidae; Homo. Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann, Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="testis"
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/clone_lib="434 (synonym: htes3)"
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                                                                                                                                                                                                                                                                                                                                                     188 AlaAsnGluAspGlyArgArgValAlaAlaIleLeuAsnHis 201
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/clone="DKFZp434E177"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL046228.1 GI:5434312
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AL046228
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ): Email s.wiemann@dkfz-heidelberg.de,
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                           EST 04-SEP-2003
                  LeuLysAlaPheValThrLeuGluArgPheAspGlnLeuTyrGlySerThrIleThrSer 150
                                                                   CysGlnGlnAlaProLysThrLysLysPheAlaSerSerGlySerValPheGlyLysGly 170
                                                                                                                                     171 VallyysPheAlaLeuLysAspGlyArgValThrThrAspIleIleSerValAlaAsnGlu 190
                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 718)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 ProGlyTyrProLysProAspMetAspAlaMetGluProSerTyrGlubeuIleHisThr 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 PheMetThrAspValAsnSerTrpLeuLeuThrPheGlyPheGlnLeuHisAsnVallle 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sl Sequence also available.
This clone (DKFZp434F206) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
1. 718
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/ clone="DKFZp434F206"
/ tissue="type="testis"
                                                                                           367 IGCCAACAGGTCAAGAACAAGAACTICGCCTCCGGAGGGCTCTATCTTCGGCAAAGGT
                                                                                                                                                                                                                                                                                                                  ALU45768
DKFZp434F206_r1 434 (synonym: htes3) Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
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                                                                                                                                                                                                        191 AspGlyArgArgValAlaAlaIleLeuAsnHis 201
                                                                                                                                                                                                                              Conservative:
Mismatches:
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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AL045768
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Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:Al30060L24 product:odd Oz/ten-m homolog 1 DKOSOPhila), full insert sequence.

AK037897.1 GI:2633225
Pollowing this first strand reaction, double-stranded CDNA was blunted, ligated to NotI adapters, digested with EcoRI. size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the DBLuescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheGlnLeuHisAsnVallleProGlyTyrProLysProAspMetAspAlaMetGluPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGlyValGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 AATGCTGTC---CCACACCATTCAATCTCTACTCATTTGAAAATAACTACCCAGTTGGC 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 ASDIYrASDVAlLeuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLySHisLeu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SeriyrdluleulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerlle
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118
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Conservative:
Mismatches:
Indels:
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/note="Organ: heads; Vector: pBluescript II KS(+); Site_I:
/note="Organ: heads; Vector: pBluescript II KS(+); Site_I:
/note="Organ: heads; Vector: pBluescript II KS(+); Site_I:
/note="Organ: heads; Vector: pBluescript II KS(+); Site_I:
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167
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                                                                                                                                                                                                                                                                                   GlnMetLysThrGlnGluTrpAspAsnSerLysSerIleLeuGlyValGlnCysGluVal 127
                                                                                                                                                                                  ProGlyTyrProLysProAspMetAspAlaMetGluProSerTyrGluLeulleHisThr 107
                                                                                                              11eThrSerCysGlnGlnAlaProLysThrLysLysPheAlaSerSerGlySerValPhe
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                                                                                 PheMetThrAspValAsnSerTrpLeuLeuThrPheGlyPheGlnLeuHisAsnValIle
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Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bute
Archosauria; Avee; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
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                                    US-10-029-020-14_COPY_2400_2600 (1-201) x AL046228 (1-525)
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/strain="White Leghorn, Hisex"
/strain="White Leghorn, Hisex"
/clone="ChEST321d19"
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603408474F1 CSEQCHN24 Gallus gallus
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/organism="Gallus gallus"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
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/lab_host="DH10B"
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KEYWORDS
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KONVSAFERRILAHNINILSIDEDHATRICKIYDDIRKFTIRILYDOGGRETIMGEVOK

RYNEVNITYSPSGLVTFIQRGTWNERGREYDQSGKIISRTWADGKINSYTLEKSVNLI

LISQRRYIETEVDOGSDCLLSVTTRESMYRHSLOTMLSFYRIYTPPDSSTSFIQDYSR

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DGRILQTIHLGTGRRVLYXYTTKQARLSEILYDTTQVTLYTRESSGVIXTIHMHDGFI

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YDNMGRRVIDDIRVGVDANITRYFYBVDADGCLQTVSVNDKIQWRYSYDLMONINLLS

GGNTVQYYDGLGRRYASKSSLGQHLQFFYADLANFIRVTHYNHTSAEITSLYYDGG

HIJAMELSSGEEYYVACDNGTPLAFFSRRQVIXELITYPYGTTHTTGYTTYTYDGY

FNGGLYDFLTKLVHGQRDYDVAGRWTTPHHIRVQLNLLPRFFNLYSFENNY PVGK

ILGIQCELQKQLRNFISLELEGGCLHNVLPGFFREENWELTYPHGTTHTTYTYTYTYTTGBRIYGEN

FNGGLYDGTALLEGGCLHNVLPGFFREENWELTYPYGGGGTKTATRY

GUTADIIGYNNEDSRRLAAILNNAAFYLENLHFTIEGROTHYFIKGSLEEDLVLIGN

TGGRRILGRGYNYTYTOGGTRAFTRYBNITRYTHTGRGNTYFYTKGSLEEDLVLIGN

TGGRRILGRGYNYTYTOGGTRAFTRYBNITRYTHTGRGNTYFYTKGSLEEDLVLIGN

TGGRRILBGRGYNYTYSGWTSVLNGRTRRFADIQLGGGGGALCTRIRGSLEEDLVLIGN

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                                                                         /mol_type="mRNA"
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/db_xref="FANYOM_D337"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Fujiwake, S., Inoue, K., Togawa, Y., Ikegami, T., Kashimagi, K., Yonded, Y., Ishikawa, T., Ogawa, Y., Izawa, M., Ohara, E., Matahiki, M., Ookazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, URL:http://genome.gsc.riken.go.jp, Fax:81.45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The RIKEN Genome Exploration Research Group Phase II Team and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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                                                                                                                                                               High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                     Carninci, P. and Hayashizaki, Y.
                               (house mouse)
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukamalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 506)
Dias Neto,B., Garcia Correa,R., Verjovski.Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., Brunstein,A., Goares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              506 bp mRNA linear EST 21-SEP-2000 MR3-BN0163-150800-006-c07 BN0363 Homo sapiens cDNA, mRNA sequence. BEB19779 BEB19779.1 GI:10252013 BST.
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                                                                                                                                                                                                                                                                  141 AspGlnLeuTyrGlySerThr1leThrSerCysGlnGlnAlaProLysThrLysLysPhe
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reannealing hybridization was used."
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/clone_lib="CSERCCHN73"
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/note pBluescript (KS+) vector: The library was normalized in 2
/conds using conditions adapted from Soares et al., PNAS
/(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
/(1995): 791, except that a significantly longer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (chicken)

Gallus gallus

Gallus gallus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Plassianinae; Gallus.

1 chases 1 to 929

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                            BU371366 929 bp mRNA linear EST 28-NOV-2002
603598013F1 CSEQCHN73 Gallus gallus cDNA clone ChEST56814 5', mRNA
                                                                                                                                                                                                          2399
                                  2220 ATGATCCTGGGCATTCAGTGTGAGCTCCAGAAACAAACTAAGGAATTTCATTTCCTTGGAT 2279
                                                                                        139 ArgPheAspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLys 158
              119 SerIleLeuGlyValGlnCygGluValGlnLyBGlnLeuLyBAlaPheValThrLeuGlu 138
                                                                                                                                                                  2280 CAGCTICCIAIGACICCICAGIACAAIGAGGGGAGGIGICITGAAGGAGGGAAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biomolecular Sciences University of Manchester Institute of (UMIST)
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/organism="Gallus gallus"
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/strain="Compton_Line 151"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:9031"
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BU371366.1 GI:25879367
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EST 03-APR-2003
                                    (10850) Rattus norvegicus cDNA clone
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GTTGCTGGCAGATGGACACGCCTAATCATCACATATGGAAACAGTTG-----AAC 111
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172 CAAGACGTIGCAAAGTATACCACAGACATIGGCAGTIGGCTGGAGCTCTITGGTITCCAA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 ValGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPheAspGln 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 LeualaglyargTrpThrSerProAspHisGluLeuTrpLysHisLeuSerSerSerAsn 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 LeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLysPheAlaSer 162
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                          linear
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                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
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One Amgen Center Drive, Thousand Oaks,
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                                                                                                                                                                                                                                                                                                                                                                                        organism="Rattus norvegicus"
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                    CB578819
AMGNNUC:NRHY7-00034-D3-A nrhy7 (
                                                                                                                                                                                                                                                                                                                                    Plate: 00034 row: d column: 3.
Location/Qualifiers
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Amgen EST Program.
Amgen Rat EST Program.
Unpublished (2003)
Contact: Dan Fitzpatrick
                                                                                 CB578819.1 GI:29522860
EST.
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74.87$
57.29$
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                                                                                VERSION
KEYWORDS
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ORGANISM
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                                                                                                                                                              Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR3-BN0363-150
Seq primer: puc 18 forward
High quality sequence stop: 377.
                                                                                                                                                                                                                                                                                                                                    /mol_type="mana" apriess
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Site_2: Smal; A mini-library was made by cloning products
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 AspMetAspAlaMetGluProSerTyrGluLeuIleHisThrGlnMetLysThrGlnGlu 113
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                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 TTTGTCACCTTAGAACGGTTTGACCAGCTCTATGGCTCCACCATCACCAGCTGCAGCAG
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     97 (7), 3491-3496 (2000)
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Mismatches:
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Matches:
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/organism="Homo sapiens"
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96.06%
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//oclone_lib=HR85 islet"
//oclone_Torgan: Pancreas; Vector: pBluescript SK(-); Site_1:
//ocle="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Size_selected on agarose gel. Average insert size ~lkb. 5'
Size-selected on agarose gel. Average insert size ~lkb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Buclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                            CA777388 776 bp mRNA linear EST 03-DEC-2002 ip19c06.xl HR85 islet Homo sapiens cDNA clone IMAGE:6217715 3' similar to TR:Q9WTS6 Q9WTS6 TEN-M3. ;, mRNA sequence. CA777388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Barvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Library was constructed by Dr. Hiroshi Inoue DNA sequencing obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 439.
  SerGlySerValPheGlyLygGlyValLysPheAlaLeuLysAspGlyArgValThrThr 182
                      472 GTCCCTTCTGTCTTTGGCAAGGTATAAAATTTGCCATCAAGGAGGCCATAGTGACGAGCT 531
                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 776)
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Endocrine Pancreas Consortium
Unpublished (2000)
                                                                                                  AspileileSerValAlaAsnGluAspGlyArgArgValAlaAlaileLeuAsnHis
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Fax: 617-495-8557
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121 LeuGlyvalGlnCysGluvalGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe 140
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                 21 AspTyrAspValLeualaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu 40
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1 IleGlyTyTHisGlyGlyLeuTyTAspProLeuThrLysLeuValHisMetGlyArgArg
                                                                                    61 AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly
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BCU0205A BCU0205B Human FCT Human FCT Human FCT

Human

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Human pol Drosophil Drosophil Lung canc Probe #46

foe #47 bre #45 bon

Human Probe Human

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Drosophil Human Ig4

pneumo Streptoco

OM protein

Run on:

Seguence:

Searched:

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Human, NOVX, NOVX-associated disorder; cardiomyopathy; atherosclerosis; KW deal signal processing; metabolic pathway modulation; metabolic disorder; My obesity; diabetes; infectious disease; neurodegenerative disorder; acne; My Alzheimer's disease; Parkinson's disease; immune disorder; cancer; My mamory defect; infertility; congenical heart defect; hair growth; Wy ignmentation disorder; endocrine disorder; respiratory disease; health; Wy pignmentation disorder; endocrine disorder; respiratory disease; health; My memory disease; nencentation; RW pone marrow transplantation; endocrine disease; allergy; inflammation; My nephrological disorder; EGF-related protein; SCUBEL; TEN-M4; adiporyte complement-related of qtumour necrosis factor; out at first; My beta adrenergic receptor kinase; BphA6/ehc2; glucose transporter; Wy beta adrenergic receptor kinase; BphA6/ehc2; glucose transporter; Wy type la membrane sushi-containing domain; butyrophilin; containing containing; SNP; gene; ds;
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ABS52100;
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Abs78652 F
Abn85378 F
Aak51828 F
Abk92230
Aah14696 F
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Aah14696 F
     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                        nucleic search, using frame_plus_p2n model
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Database :

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LeuGlyvalGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLysPhe GACCAGCTCTATGGCTCCACAATCACCAGCTGCCAGCAGCTCCAAAGACCAAGAAGTTT 161 AlaSerSerGlyServalPheGlyLysGlyValLysPheAlaLeuLysAspGlyArgVal

141 7652

R; Liu X;

7411

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40

21 AspIyrAspValLeuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu

SerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer 61 AsnSerGlnAspileLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly

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81 PheGlnLeuHisAsnValileProGlyTyrProLysProAspMetAspAlaMetGluPro 7472 TTCCAGCTACACATGATCCCTGGTTATCCCAAACCAGACATGGATGCCATGGAACCC SerTyrGlubeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerlle 

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ThrThrAspIleIleSerValAlaAsnGluAspGlyArgArgValAlaAlaIleLeuAsn 200

7772 ACCACAGACATCATCAGTGTGGCCAATGAGGATGGGCGAAGGGTTGCTGCCATCTTGAAC

ABS78652 standard; cDNA; 8645 BP

ABS78652 RESULT

ABS78652;

7832 CAT 7834

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201 His 201

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GCATCCAGCGCTCAGTCTTTGGCAAGGGGGTTCAGTTTGCCTTGAAGGATGGCCGAGTG

7712

181

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The present invention relates to new NOVX polypeptides. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, or fight by thuman. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), immune disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, cefects, acne, hair growth, pigmentation disorders, endocrine disorders, cepiratory disease, gastro-intestinal diseases, reproductive, health, respiratory disease, bone marrow transplantation, endocrine diseases, allersy and inflammation, nephrological disorders, urinary system disorders, neuropsychiatric disorders and age-related disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease or
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                                                            "Single nucleotide polymorphism (SNP)"
/standard name= "Single nucleotide polymorphism (SNP) ^{\rm t} replace(225,C) ^{\prime} *tag= \stackrel{.}{b}
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nderson D, Shimkets RA, Burgess CE, Zerhusen BD,
Casman SJ, Boldog FL, Smithson G, Li L, Ji W;
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                                                              /standard_name= "replace(260,A)
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2000US-0257314P.
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2001US-0315617P.
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P-PSDB; ABG70388
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10-AUG-2001;
29-AUG-2001;
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29-MAY-2001;
24-JUL-2001;
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20-DEC-2000;
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                                                                                        variation
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Human; ss; gene; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thrombocytopaenia; developmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; ALDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma; inflammatory disorder; infertility; autoimmune disorder; acquired immunodeficiency syndrome; uveitis; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; diabetes mellitus; glomerulonephritis; irritable bowell syndrome; milting mental neghritis; irritable bowell syndrome;
                                                                                                                                                                                                                                                                                                                    sclerosis; ostecarthritis; ostecporosis; pancreatitis;
                                                                                                  Human cDNA encoding CGDD10, INCYTE 7488573CB1.
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                                                                     16-DEC-2002 (first entry)
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09-FEB-2001; 2001US-0268111P

7232.ATAGGCTACCATGGTGGCCTCTATGATCCACTACCAAGCTTGTCCACATGGCCGGGGA 7291

1 IleGlyTyrHisGlyGlyLeuTyrAspProLeuThrLysLeuValHisMetGlyArgArg

US-10-029-020-14\_COPY\_2400\_2600 (1-201) x ABS52100 (1-8354)

201

Length:
Matches:
Conservative:
Mismatches:
Indels:

6.8e-122 1077.00 100.00% 100.00%

Best Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

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The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to CGDD, a biologically active or acid sequence at least 90% identical to CGDD, a biologically active of fragment or an immunogenic fragment. Also included are the polymucleotides encoding CGDD1-12, a recombinant polymucleotide comprising a promoter sequence operably linked to the CGDD polymucleotides, a cell transformed with the recombinant polymucleotide, an antical transgenic organism comprising the recombinant polymucleotide, an antical antibody, screening for compounds which bind to/modulate or are captured and antagonists and encoding to compounds which bind to/modulate or are comprised and antagonists are useful for diagnosing, treating or compounds which bind to/modulate or are composited and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of CGDD, polymucleotides, paroxysmal nocturnal haemoglobinuria, polycythaemia of asorders (e.g. renal tubular acidosis, anaemia or mental retardation), curthosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia cidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer disease, parkinson's disease or the mensitual Oyle), or autoinmune/inflammatory disorders (e.g. Alzheimer disease, parkinson's disease or the mensitual Oyle), or autoinmune/inflammatory disorders (e.g. Alzheimer disease, parkinson's disease or thyroiditis, contact dermatitis, contact dermatitis, contact dermatitis, parasitic, protozoal or helmintic osteorosis, panceatitis, rumanamia, and archinic ancoders of costeorosis, panceatitis, rumanamia and and amino and costeorosis, panceatitis, rumanamia and and amino and archinic second or the expression of mucleic acid and amino accoders of costeorosis and and amino and and anion accoders and and amino accoders and an amino accoders and an amino accoders and an amino accoders and an amino acc
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                                                                                                                                                                         Burford N;
                                                                                                                                                    Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ileGlyTyrHisGlyGlyLeuTyrAspProLeuThrLysLeuValHisMetGlyArgArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7281 ATAGGCTACCATGGTGGCCTCTATGATCCACTACCAAGCTTGTCCACATGGGCCGGCA
                                                                                                                                                                                                                                                                                              New human proteins associated with cell growth, differentiation death, useful for diagnosing, treating or preventing aucoimmune inflammatory disorders (e.g. AIDS, allergy or anemia), cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8645 BP; 2060 A; 2494 C; 2319 G; 1771 T; 0 U; 1 Other;
                                                                                                                                             JY, Warren BA, Elliott VS,
Tang TY, Lal PG, Duggan BM,
DUK, Khare R, Walia NK;
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 175-178; 181pp; English.
                                                                                                                                        Fao MG, Ison CH, Lu Y,
Xu Y, Gietzen KJ, Tang
Richardson TW, Tran UK,
23-FEB-2001; 2001US-0271175P.
08-MAR-2001; 2001US-0274503P.
09-MAR-2001; 2001US-0274552P.
                                                                                                                                                                                                                                                                                                                                                                        atherosclerosis or hepatitis.
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1077.00
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Pred. No.:
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Lu DAM,
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                                                                                                                                                                                                       AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLysPhe 160
                                                                                                                                                                                                                                                          161 AlaSerSerGlySerValPheGlyLysGlyValLysPheAlaLeuLysAspGlyArgVal 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; NOV1; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive; Antiallergic; Heemostatic; Anti-HIV; Antidiabetic; Anorectic; Antiasthmatic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic; Antibacterial; Virucide; Antiparastic; Relaxant; Anticonvulsant; Gene Therapy; NOV; cancer; heart disease; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; asthma; IGA nephropathy; cirrhosis; arthritis; AIDS; diabetes; obesity; inflection; stroke; muscular dystrophy; epilepsy; wasting disorder; TEN-M4 like protein; chromosome 11; gene; ds.
                 61 AspSerglnAspIleLysCysPheMetThrAspValAspSerTrpLeuLeuThrPheGly
                                                 PheGlnLeuHisAsnValIleProGlyTyrProLysProAspMetAspAlaMetGluPro
                                                                                                   SerTyrGluLeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerIle
                                                                                                                                                     LeuGlyValGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe
                                                                                                                                                                  /trans_except= (pos: 1138. .1147, aa:Met)
/product= "NOV1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human NOV1, TEN-M4 like protein, coding sequence.
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2001US-0272338P.
2001US-0274876P.
2001US-0284704P.
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28-FEB-2001;
29-MAR-2001;
18-APR-2001;
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The invention relates to polynuclectides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are vacful in gene therapy, vaccines or peptide therapy. The polypeptides are vacful in gene therapy, vaccines or cell growth factor activity, hemmatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
(AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
                                                                                                   7739 CAGGCTCCAAAGACCAAGAAGTTTGCATCCAGGGCTCAGTCTTTGGCAAGGGGGTCAAG
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GlnAlaProLysThrLysLysPheAlaSerSerGlySerValPheGlyLysGlyValLys 172
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                             PheAlaLeuLysAspGlyArgValThrThrAspIleIleSerValAlaAsnGluAspGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Asundi V, Zhou P, Xu C, Cao
Wang D, Wang J, Zhang J, Ren F, Chen R,
Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1414-1426; 6221pp; English.
                                                                                                                                                             193 ArgArgValAlaAlaIleLeuAsnHis 201
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                                                                                                                                                                                   Human polynucleotide SEQ ID NO 373.
                                                                                                                                                                                                                                                                                 AAK51828 standard; cDNA; 13202 BP
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27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
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15-SEP-2000; 2000US-00663561.
20-OCT-2000; 2000US-00693235.
30-NOV-2000; 2000US-00728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-FEB-2001; 2001WO-US004098
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Ma Y, Zhao QA, W
Xue AJ, Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a coding sequence for a NOV protein. The NOV proteins and coding sequences are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma, IGA nephropathy, cirrhosis, arthritis, AIDS diabetes, obesity, asthma, (e.g. bacterial, viral, parasitio), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. NoV1 is a TEN-M4 like protein and the NOV1 gene is localised to chromosome 11
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                                                  Padigaru M, Li L, Zerhusen BD, Casman SJ, Shenoy S, Spytek KA, Zhong M, Gangolli EA, Burgess CE, Patturajan M, Vernet CAM: Taylor S, Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse WM, Alsobrook JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman K, Gunther E, Stone DJ; Smillet I, Peyman J, Smithson G;
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Mismatches:
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Matches:
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98.70%
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The present invention relates to methods of detecting a prostate cancersasociated transcript in a cell from a patient. The method comprises
contacting a biological sample from the patient with prostate cancerassociated polynucleotides (designated PC genes) that selectively
bybridise to a sequence that is at least 80% identical to them. The
prostate cancer-associated polynucleotide sequences are differentially
expressed in prostate tumour tissue or in prostate cancer and are derived
from the tissues of various organisms such as humans or other mammals
(e.g. mice, sheep and dogs). The methods of the invention are useful for
diagnosing and treating prostate cancer in mammals. The prostate canceras well as for identifying modulators of prostate cancer or agents that
inhibit prostate cancer. The nucleic acid sequences are particularly
useful in gene therapy, as a vaccine or in antisense applications.

Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a

Claim 22; Page 394-397; 436pp; English.

prostate tissue.

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Hevezi

Afar D,

Gish KC, Mack DH, Wilson KE, (EOSB-) EOS BIOTECHNOLOGY INC

2002-471335/50.

P-PSDB; ABG61913

13-OCT-2000; 2000US-006B7576. 08-DEC-2000; 2000US-00733288. 08-DEC-2000; 2000US-0073742. 24-OAN-2001; 2001US-0263957P. 16-MAR-2001; 2001US-0276791P.

12-OCT-2001; 2001WO-US032045

16-MAR-2001; 2001US-027688BP. 06-APR-2001; 2001US-0281922P. 24-APR-2001; 2001US-0286214P.

30-APR-2001; 2001US-00847046.

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Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

gene therapy; gene; ds

WO200230268-A2

18-APR-2002

Prostate cancer-associated DNA sequence #116

(first entry)

15-AUG-2002

ABK92230;

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GAATTAACTTACGAGCTTCTACGGCTTCAGACAAAACTCAAGAGTGGGATCCTGGAAAG
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, Otsuki
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A, Nagai K,
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Wakamatsu
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27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAX-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00183767.
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the

Claim 8; SEQ ID NO 11265; 2537pp + Sequence Listing; English.

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oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a conjuncteotide which comprises a 1'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence of in the comprises a 1'-end sequence in the comprises a 1'-end sequence in the comprises a 1'-end sequence in a selected from those defined in the specification. The primer sets can be useful for synthesising polynucleotides, comparationarly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the AMH13628 and AMH13633 to AMH18742 represent human cDNA sequences; AAMH3634 to AAMH3628 and coligonucleotides, all of which are used in the exemplification of the
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length cDNAs defined in the specification. Where a primer set comprises:

(a) an olgo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 oligonucleotide sequences defined in the specification, where the mucleotide sequences defined in the specification, where the mucleotide comprises at least 15 nucleotides; or (b) a combination of a no oligonucleotide comprising a sequence complementary to the comprises at least 15 nucleotides; or (c) a complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the complementary to a polynucleotide comprises a 3'-end sequence, where the complementary to a coligonucleotide comprises a 1 east 15 nucleotides and the combination of the 5'-end sequence)3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gardicularly full-length cDNAs. The primers are useful for synthesising polynucleotides, detection and/or diagnosis of the abnormality of the proteins encoded by cDNAs easily without any specialised methods. AAH13632 represent consent human amino acid sequences; and AAH13629 to AAH13622 represent consent immentation of the consent immentation of the consent immentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention describes primer sets for synthesising 5602 full-
                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID NO 12354; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3270 BP; 867 A; 821 C; 852 G; 730 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashi K, S
A, Nagai K,
                                                                                                                              Human cDNA sequence SEQ ID NO:12354.
                    AAH14671 standard; cDNA; 3270 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishikawa T,
1 T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                    99JP-00248036.
99JP-00300253.
                                                                                                                                                                                                                                                                                                                28-JUL-2000; 2000EP-00116126
                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34
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27-AUG-1999;
                                                                                                                                                                                                      Homo sapiens
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                                                                                            26-JUN-2001
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                                                        AAH14671;
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107 38 47 12

Indels: Gaps:

Length: Matches: Conservative: Mismatches:

3.49e-59 566.00 71.08% 52.45% 52.55%

Alignment Scores:

Percent Similarity: Best Local Similarity:

Query Match:

Yamamoto J;

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2084
                                                                                                                         2253 GCCGAGGTGCAG-----GTGAGCCGGGGGCGCGCGCGCGCGCAGTGCTGG 2300
                                                                                                                                                                                                                                                                                                                                                                                            2301 CTGTGGTTCGCCACGGTCAAGTCGCTGATCGGCAAGGGCGTCATGCTGGCCGCTCAGCCAG 2360
                                                                                                                                                                                               81 PheGlnLeuHisAsnVallleProGlyTyrProLysProAspMetAspAlaMetGluPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                  2361 GGCCGCGTGCAGACCAACGTGCTCAACATCGCCAACGAGGAGTGCATCAAGGTGGCGGCC 2420
                                                                                                                                                                                                                                           SerTyrGluLeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerlle 120
                      1 ileGlyTyrHisGlyGlyLeuTyrAspProLeuThrLysLeuValHisMetGlyArgArg 20
                                                                                                                                                                                                                                                                                    121 LeuGlyvalGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe 140
                                                                         40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                21 AsplyraspValieuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu
                                                                                                                                                                   41 SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer
                                                                                                                                                     61 AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuThrPheGly
                                                                                                                                                                                                                                                        160 ------pheAlaSerSerGlySerValPheGlyLysGlyValLysPheAlaLeuLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                  178 GlyArgValThrThrAspIleIleSerValAlaAsnGluAspGlyArgArgValAlaAla
                                                                                                                                                                                                                                                                                                                              141 AspGlnLeuTyrGlySerThr1leThrSerCysGlnGlnAlaProLysThrLysLys-
US-10-029-020-14_COPY_2400_2600 (1-201) x AAH14671 (1-3270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA sequence SEQ ID NO:11430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 IleLeuAsnHis 201
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11-JAN-2000;
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Yamamoto J;

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The present invention describes primer sets for synthesising 5602 full-
corplementary strand of a polynucleotide complementary to the
complementary strand of a polynucleotide which comprises one of the 5602
complementary strand of a polynucleotide which comprises one of the 5602
complementary strand of a polynucleotide where the
nucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 1'-end sequence complementary to a
polynucleotide comprises a 1 least 15 nucleotides and the combination of
coligonucleotide comprises a 1 least 15 nucleotides and the combination of
coligonucleotide comprises a 1 least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in the
specification. The primer sets can be used in antisense therapy and in
specification. The primers allow of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the proteins
connas assily without any specialised methods. AAH03166 to AAH13628 and
connas assily without any specialised methods. AAH03166 to AAH13628 and
consern thuman amino acid sequences; and AAH3629 to AAH13628 corpresent
coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                               primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                            Claim 8; SBQ ID NO 11430; 2537pp + Sequence Listing; English.
                                       oogai T, Nishikawa T, Hayashi K, Saito K, Y.
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
(HELI-) HELIX RES INST.
                                                                                                                              WPI; 2001-318749/34.
                                                  Isogai T,
                                                                                 s,
                                                                                 ſshii
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Sequence 3614 BP; 967 A; 898 C; 928 G; 821 T; 0 U; 0 Other; Conservative: Mismatches: Indels: Length: Matches: 4.03e-59 566.00 71.08% 52.45% 52.55% present invention Alignment Scores: No.:

2429 Triccarcrigiacia artecrigia procedente de la recensión de 1488 2192 ATTGGATTTCATGGGCCTGTATGACCCACTCACCAATTAATCCACTTTGGAAAAAA 2251 GATTATGACATTTTGGCAGGACGGTGGACAACACCTGACATAGAAATCTGGAAAGAATT 2311 AspTyrAspValLeuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu 40 PheGlnLeuHisAsnValIleProGlyTyrProLysProAspMetAspAlaMetGluPro SerTyrGluLeuIleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerIle IleGlyTyrHisGlyGlyLeuTyrAspProLeuThrLysLeuValHisMetGlyArgArg 41 SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer ::: ---gggaaggacccagctccttttaacttgtacatgtttaggaataacaacctgcaagc 61 AsnSerGlnAspIleLysCysPheMetThrAspValAspSerTrpLeuLeuThrPheGly US-10-029-020-14\_COPY\_2400\_2600 (1-201) x AAH14183 (1-3614) Percent Similarity: Best Local Similarity: 2252 2312 81 101 Н 21 Query Match: Score: qq ŏ qq ð g à 엄 ð g ð ò

04-JAN-2001; 2001US-0259785P. 20-FBB-2001; 2001US-0269B14P. 09-MAR-2001; 2001US-0279863P. 29-MAR-2001; 2001US-0279832P. 29-WAR-2001; 2001US-0279833P.

2001US-0259415P. 2001US-0259785P.

29-DEC-2000;

13-APR-2001; 2001US-0283889P. 18-APR-2001; 2001US-0284447P. 25-APR-2001; 2001US-0286683P.

25-APR-2001; 29-MAY-2001;

2428

80

16-AUG-2001;

17-AUG-2001;

2001US-0312915P. 2001US-0313325P. 2001US-0322699P. 2001US-0333350P.

CURAGEN CORP

(CURA-)

26-NOV-2001;

120

2001US-0294080P

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Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antialergic; virucide; antianaemic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy; pick's disease; vesicular transport disease; cystic fibrosis; goltre; dibbetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.
                                                                                                                                2645 CTGTGGTTCGCCACGGTCAAGTCGGCAAGGCGTCATGCTGGCCGTCAGCCAG 2704
                                                                                                                                                                                       2705 GGCCGCGTGCAGACCAACGTGCTCAACATCGCCAACGAGGACTGCATCAAGGTGGCGGCC 2764
                          2537 TTCGGAGTCCAGCAGCAAGTGGCGCGGCAAGGCCAAGGCCTTCCTGTCGCTGGGGAAGATG 2596
                                                                                                              -----pheAlaSerSerGlySerValPheGlyLysGlyValLysPheAlaLeuLysAsp 177
                                                                                                                                                                     GlyArgyalThrThrAspIlelleSerValAlaAsnGluAspGlyArgArgValAlaAla 197
121 LeuglyvalGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe 140
                                                                           141 AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLys---
                                                                                                                                                                                                                                                                                                                                                                                                       Human NOV15c encoding cDNA SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "NOV15c"
                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                       ABQ82345 standard; cDNA; 8473
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                                                                                  2597 GCCGAGGTGCAG----
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ABQ82345
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v VT, Spaderna SK, Gorman L,
Gangolli EA, Guo X, Shenoy S;
Burgess CE, Edinger S, Ellerman K;
Macdougall JR,
                          Liu X;
                         Eisen A,
                      Vernet CAM,
          Wolenc AR, Vells
Pa Tchernev VT,
Gange
Spytek KA, Li L, Wolenc ...,
Malyankar U, Shimkets RA, Tchernev v
Kekuda R, Patturajan M, Gusev V, Ga
'--11i L, Casman SJ, Boldog F, Bi
                                                          L L, Casman
E, Smithson G,
                                                                                                      2002-732706/79
                                                                                                                    P-PSDB; ABP53588
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disorders New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, diso of vesicular transport, gastrointestinal disorders, and autoimmune diseases

Claim 8; Page 119-121; 444pp; English

The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, cyrostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, antidiabetic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the numan disease selected from NOVX-associated disorder, such as cancers covary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or Pick's disease), disorders of vesicular transport (e.g. epilepsy, stroke, disease), disorders of vesicular transport (e.g. epilepsy, stroke, disease), disorders of vesicular transport (e.g. epilepsy, stroke, disease), disorders of ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX proteins from minute content of an incompose and as vaccines. The NOVX proteins from minute coloquical samples (tissue typing), and in forensic identification of a longical sample. The present sequence encodes human NOVISC, which is 

Sequence 8473 BP; 2301 A; 2017 C; 2145 G; 2006 T; 0 U; 4 Other;

8473 107 38 47 12 Length:
Matches:
Conservative:
Mismatches: Indels: Gaps: 1.39e-58 566.00 71.08% 52.45% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match .. No.:

US-10-029-020-14\_COPY\_2400\_2600 (1-201) x ABQ82345 (1-8473)

9 1170 ---GGGAAGGACCCAGCTCCTTTAACTTGTACATGTTTAGGAATAACAACCCTGCAAGC SerSerSerAsnValMetProPheAsnLeuTyrWetPheLysAsnAsnAsnProIleSer 41

> a à g à g ð a

- 61 AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly 80
- PheGlnLeuHisAsnValileProGlyTyrProLysProAspMetAspAlaMetGluPro 100 7287 81
  - 101 SerTyrGlubeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerIle 120

---AAGAGTCAGCAGTGGGATGATATACCGCCCATC 7394 ----GTGAGCCGCCGCGCGCGCGCGCAGTCCTGG 7502 121 LeuGlyValGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe 140 141 AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLys--- 159 178 GlyArgValThrThrAspIleIleSerValAlaAsnGluAspGlyArgArgValAlaAla 197 Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide; antianaemic; antibacterial; protozoacide; antihelminthic; gene therapy; 160 -----PheAlaSerSerGlySerValPheGlyLygGlyValLysPheAlaLeuLysAsp 7503 crgredriceccacegreaagreecrgareecaaeecareareergeecae Human NOV15d encoding cDNA SEQ ID NO:41. ABQ82346 standard; cDNA; 8487 BP. 7347 TCTTACGAACTTGTG--1623 GTGCTCAACAAC 7634 (first entry) 198 IleLeuAsnHis 201 7455 GCCGAGGTGCAG-17-DEC-2002 ABQ82346; RESULT 10 ABQ82346 ð g à 셤 à d g ò 8 임

cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; etroke; ischaemic cerebrovascular disease, Alzheimer's disease; epilepsy; pick's disease; vesicular transport disease; cystic fibrosis; goitre; diabetes mellitus; Grave's disease; especial disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.

Homo sapiens.

Location/Qualifiers 299. .8140 /\*tag= a /product= "NOV15d" WO200262999-A2

15-AUG-2002

2001US-0279863P. 2001US-0279832P. 2001US-0279833P. 2001US-0283889P. 2001US-0284447P. 2001US-0286683P. 2001US-0294080P. 2001US-0259415P. 31-DEC-2001; 2001WO-US049976 2001US-0269814P 20-FEB-2001; 09-MAR-2001; 29-MAR-2001; 13-APR-2001; 04-JAN-2001; 29-MAR-2001; 18-APR-2001; 25-APR-2001;

2001US-0312915P. 2001US-0313325P. 2001US-0322699P. 2001US-0333350P. 29-MAY-2001; 16-AUG-2001; 17-SEP-2001; 26-NOV-2001;

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Wolenc AR, Vernet CAM, Elsen A, L.C., Gorman L;
kets RA, Tchernev VT, Spaderna SK, Gorman L;
jan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
n SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
             Spytek KA, Li L, Wolch, Tone...
Malyankar U, Shimkets RA, Tone...
Walyankar U, Shimkets RA, Gusev V, Ga'
Walida R, Patturajan M, Boldog F, Bu
Casman SJ, Millet I, M
(CURA-) CURAGEN CORP.
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WPI; 2002-732706/79. P-PSDB; ABP53589 New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune diseases.

Claim 8; Page 123-125; 444pp; English.

The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, noticopic, candidovascular, cytostatic, anticallergic, anticalmanator, anticarbrittic, virucide, immunosuppressive, anticallergic, anticanaemic, antibacterial, tungicide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the human disease selected from NOVX-associated disorder, such as cancers human disease selected from NOVX-associated disorder, such as cancers covary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or pick's ischaemic cerebrovascular tiasese, Alzheimer's disease or pick's disease, or goitte), gastrointestinal disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be produce antibodies and as vaccines. The NOVX nucleotide sequences may be biological sample. The present sequence encodes human NoV15d, which is ocated on chromosome

Sequence 8487 BP; 2306 A; 2029 C; 2148 G; 2001 T; 0 U; 3 Other;

8487 107 38 47 12 Matches: Conservative: Mismatches: Indels: Length: 1.4e-58 566.00 71.08% 52.45% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Score:

US-10-029-020-14\_COPY\_2400\_2600 (1-201) x ABQ82346 (1-8487)

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7222
                                                              7282
              PheGlnLeuHisAsnValIleProGlyTyrProLysProAspMetAspAlaMetGluPro 100
                                                                                                                                                    80
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                                                                                                                                                                  41 SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer
                                                                                                                           7166 ---GGGAAGGACCCAGCTCCTTTTAACTTGTACATGTTTAGGAATAACAACCTGCAAGC
                                                                                                                                                    61 AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly
1 IleglyTyzHisGlyGlyLeuTyzAspProLeuThrLysLeuValHisMetGlyArgArg
                                                 21 AsplyrAspValLeuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu
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2001US-0284447P. 2001US-0286683P. 2001US-0294080P. 2001US-0312915P.

25-APR-2001; 2 29-MAY-2001; 2 16-AUG-2001; 2 13-APR-2001; 18-APR-2001;

2001US-0283889P

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Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide; antianematic; antibacterial; protozoacide; antihelminthic; gene therapy; earner; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy; Pick's disease; vesicular transport disease; castic fibrosis; goitre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; vaccine; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.
                                                                                              7283 ITCCAICTGCACAAIGCTAITCCIGGAITCCCIGITCCCAAAITTGAITTAACAGAACCI 7342
                                                                              140
                                                                                                                                 141 AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLys--- 159
                                                                                                                                                                                  GlyargvalThrThrAspIlelleSerValAlaAsnGluAspGlyArgArgValAlaAla 197
                           SerlyrGluLeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerlle
                                          121 LeuGlyvalGinCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NOV15b encoding cDNA SEQ ID NO:37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "NOV15b"
                                                                                                                                                                                                                                                                                                                                                                              ABQ82344 standard; cDNA; 8645 BP.
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09-MAR-2001; 2001US-0279863P.
29-MAR-2001; 2001US-0279832P.
29-MAR-2001; 2001US-0279833P.
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2001US-0259785P.
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                                                                                                                                                                                                                                                                                                 198 IleLeuAsnHis 201
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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, nocitropic, cardiovascular, antidiabetic, antidinflammatory, antichematic, antiabacterial, funciode, immunosuppressive, antiallergic, antiahaemic, virucide, protozoacide and antihabaminhic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a contract of a medicament for treating a syndrome associated with a contract of a medicament for treating a syndrome associated with a contract of a leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, discase), disorders of vesicular transport (e.g. cystic fibrosis, discase), disorders of vesicular transport (e.g. cystic fibrosis, discase), discases (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune haemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic conduce antibodies and as vaccines. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX proteins from minute cological samples (tissue typing), and in forensic identification of a located on chromosome mapping, and in forensic identification of a located on chromosome and processes in the present sequence encodes human NOVISb, which is
                                                                                                        Wolenc AR, Vernet CAM, Eisen A, Liu A;
kets RA, Tchernev VT, Spaderna SK, Gorman L;
jan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
n SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
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                                                                                                                                                                                                                                                                                           New NOVX polypeptides and polymucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 SerSerSerasnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7222 ATTGGATTTCATGGTGGCCTGTATGACCCACTCACCAATTAATCCACTTTGGAGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GGGAAGGACCCAGCTCCTTTTAACTTGTACATGTTTAGGAATAACAACCTGCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AsmSerGlnAspIleLysCysPheMetThrAspValAsmSerTrpLeuLeuThrPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8645 BP; 2343 A; 2060 C; 2200 G; 2038 T; 0 U; 4 Other;
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Mismatches:
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                                                                                       Spytek KA, Li L, Wolenc L, Malyankar U, Shimkets RA, Tchernev v Kekuda R, Patturajan M, Gusev V, Gr L) L, Casman SJ, Boldog F, B
                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 114-117; 444pp; English
17-AUG-2001; 2001US-0313325P.
17-SEP-2001; 2001US-0322699P.
26-NOV-2001; 2001US-0333350P.
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566.00
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                                                                             (CURA-) CURAGEN CORP.
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Query Match:
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7627 GCCGAGGTGCAG-----GTGAGCCGGCGCCGGCCGGCGCGCGCGCGCTCCTGG 7674
PheGlnLeuHisAsnVallleProGlyTyrProLysProAspMetAspAlaMetGluPro 100
                                                                                                       121 LeuGlyValGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe 140
                                                                                                                                                                                                                                 141 AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLysLys--- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide; antirhematic; antiathritic; immunosuppressive; antiallergic; virucide; antianemic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; proke; schaemic cerebrovascular disease; Alzheimer's disease; allergy; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ducerative colitis; gastric disorder; dudenal disorder; vaccine; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia;
                                                   SerfyrGlubeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerlle
                                                                          |||-----AAGAGTCAGCAGTGGGATGATATACCGCCCATC
                                                                                                                        Trccarcriccacaargcrarrccragarrccrarrccaaarrrdarrraacagaaccr
                                                                                                                                                                                                                -----PhealaSerSerGlySerValPheGlyLysGlyValLysPheAlaLeuLysAsp
                                                                                                                                                                                                                                                                    GlyArgValThrThrAspIleIleSerValAlaAsnGluAspGlyArgArgValAlaAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOV15a encoding cDNA SEQ ID NO:35.
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/*tag= a
/product= "NOV15a"
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                                                                              7519 rcrracgaacrrgrg----
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20010S-0259785P
20010S-025984P
20010S-0279863P
20010S-0279832P
20010S-0279832P
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20-FEB-2001;
09-MAR-2001;
29-MAR-2001;
29-MAR-2001;
13-APR-2001;
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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, noticately, cardiovascular, contidabetic, anticallergic, anticalmentic, varioside, immunosuppressive, anticallergic, anticalmentic, varioside, protozoacide and antibelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the therapy. The NOVX proteins, nucleotides or antibodies can be used in the human disease selected from NOVX-associated disorder, such as cancers continged and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or pick's ischaemic cerebrovascular transport (e.g. cystic fibrosis, ciabaetes mellitus, Grave's disease, or goitre), gastrointestinal disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune haemolytic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be produce antibodies and as vaccines. The NOVX nucleotide sequences may be biological sample. The present sequence encodes human NOVISa, which is
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kets RA, Tchernev VT, Spaderna SK, Gorman L;
jan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
nn SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
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Matches:
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566.00
71.08%
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18-APR-2001; 2001US-0284447P.
25-APR-2001; 2001US-0286683P.
29-MAX-2001; 2001US-0294080P.
                                                   16-AUG-2001; 2001US-0312915P.
17-AUG-2001; 2001US-0313325P.
17-SEP-2001; 2001US-0322699P.
26-NOV-2001; 2001US-0333350P.
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Kekuda R, Partun
Rastelli L, Casman SJ,
                                                                                                                                              (CURA-) CURAGEN CORP.
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Best Local Similarity:
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Malyankar U,
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7806
                                                                                                                                                                                    Six hundred and twenty five polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders.
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                                                                                                             101 SerTyrGluLeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerIle 120
                                                     PheGlnLeuHisAsnVallleProGlyTyrProLysProAspMetAspAlaMetGluPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ss, gene; secreted protein; immune deficiency; viral infection; bacterial infection; fungal infection; autoimmune disorder; burn; rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis; diabetes; allergy; asthms; neurodegenerative disease; Crohn's disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour; coagulation disorder; haemophilia; inflammatory disorder; ulcer; tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;
                                                                                                                                                                    121 LeuglyvalginCysGluvalGlnLysGlnLeutysAlaPheValThrLeuGluArgPhe
                                                                                                                                                                                                                                                      7639 GCCGAGGTGCAG-----GTGAGCCGGCGCCGGGCCGCGCGCGCCGCAGTCCTCG
                                                                                                                                                                                                                                                                                   ----PheAlaSerSerGlySerValPheGlyLySGlyValLySPheAlaLeuLySASP
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7687 CTGTGGTTCGCCACGGTCAAGTCGCTGAAGGCGTCATGCTGGCCGTCAGCCAG
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                                                                                   <u>rrccarctigcacaatecratrcctiggarrcccrigrrcccaaarrrgarraacagaaccr</u>
61 AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLhrPheGly
                          SH,
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JR;
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The invention relates to 625 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins, their complements and sequences that hybridise to them. Also included are a vector comprising the polynucleotide, a host cell antibodies that him to the proteins encoded by the polynucleotides, antibodies that bind to the proteins and identification of modulators of the proteins or the expression of the polynucleotide. The polynucleotides can be used as probes for the identification and isolation of full length as nutritional supplements. The protein is useful in the treatment of various immune defliciencies and disorders such as viral infections,
                                                                                                                                                                                                                                                                                                                                   Dacterial infections, fungal infections, autoimmune disorders (e.g., theumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are disease, parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for tissue regeneration, for wound healing also useful for reatment of burns, incisions and ulcers. The proteins are lymphoid cell deficiencies. The present sequence is one of the 625 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences encoding a secreted protein
Claim 1; Page 91-92; 339pp; English
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Sequence 791 BP; 200 A; 195 C; 209 G; 183 T; 0 U; 4 Other;

for wound healing

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791
106
37
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          Length:
Matches:
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Indels:
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          7.66e-59
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                                                                                  PheGlnLeuHisAsnVallleProGlyTyrProLysProAspMetAspAlaMetGluPro
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1 IleGlyTyrHisGlyGlyLeuTyrAspProLeuThrLysLeuValHisMetGlyArgArg 20

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9058 103 38 49 15

Length:
Matches:
Conservative:
Mismatches:
Indels:

5.1e-54 529.50 68.78% 50.24%

Percent Similarity: Best Local Similarity:

Query Match:

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623 CAGACCAACGTGCTCAACAACGAGGACTGCATCAAGGTGGCGGCCGTGCTCAAC 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotides which are differentially-regulated in breast cancer. The methods and compositions of the present invention are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and/or treating diseases and conditions relating to breast cancer, and may be used in gene therapy or antisense therapy. They can also be used in research, drug discovery, clinical medicine and forensic medicine. Sequences given in records ACC72012-ACC72074 represent polynucleotides of the invention that are differentially-regulated in breast cancer. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPD at
                                                                                                                                                                                                                                                                                          Durest cancer; cytostatic; gene therapy; antisense therapy; regulated; drug discovery; clinical medicine; forensic medicine; gene; chromosome 5q33.3; ds.
181 ThrThrAspIleIleSerValAlaAsnGluAspGlyArgArgValAlaAlaIleLeuAsn
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                                                                                                                                                                 ACC72051 standard; DNA; 9058 BP
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14-MAY-2002; 2002US-00144194.
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14-MAY-2002; 2002US-00144194.
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Conservative: Mismatches: Indels: Gaps:

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Length: Matches:

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The invention relates to isolated polynucleotides which are differentially-regulated in breast cancer. The methods and compositions of the present invention are useful for detecting diagnosing, staging, monitoring, prognosticating, preventing and/or treating diseases and conditions relating to breast cancer, and may be used in gene therapy or antisense therapy and forensic medicine. Sequences given in records ACC72012-ACC72074 represent polynucleotides of the invention that are differentially-regulated in breast cancer. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                          New isolated human differentially-regulated breast cancer polynucleotide and polypeptide, useful for diagnosing, staging, prognosticating, preventing and/or treating diseases and conditions relating to breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other;
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P-PSDB; ABR58318
                                                                                                                                                                                                                                                                                                           Claim 2;
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7742 7412 7532 7355 ------PheAlaSerSerGlySerValPheGlyLysGlyValLysPheAlaLeuLys 176 100 9 80 40 61 AsnSerGlnAspIleLysCysPheMetThrAspValAsnSerTrpLeuLeuThrPheGly PheGlnLeuHisAsnValIleProGlyTyrProLysProAspMetAspAlaMetGluPro 7473 TITICAGCITAGCAACATCATICCTGGCTTCCCGAGAGCCAAAATGTATTTCGTGCCTCCT SerTyrGluLeulleHisThrGlnMetLysThrGlnGluTrpAspAsnSerLysSerlle ---GAGAATGGACAGCTCATT LeuGlyvalGlnCysGluValGlnLysGlnLeuLysAlaPheValThrLeuGluArgPhe 141 AspGlnLeuTyrGlySerThrIleThrSerCysGlnGlnAlaProLysThrLySLys---41 SerSerSerAsnValMetProPheAsnLeuTyrMetPheLysAsnAsnAsnProlleSer AspTyrAspValleuAlaGlyArgTrpThrSerProAspHisGluLeuTrpLysHisLeu lleglyTyrHisGlyGlyLeuTyrAspProLeuThrLysLeuValHisMetGlyArgArg 7533 CCCTATGAATTGTCAGAGAGTCAAGCAAGT-----US-10-029-020-14\_COPY\_2400\_2600 (1-201) x ACC72052 81 101 121 160 21

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177 AspGlyArgValThrThrAspIleIleSerValAlaAsnGluAspGlyArgArgValAla 

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197 AlalleLeuAsnHis 201 ::::::||||||:: 7803 TCTGTGCTGAACAAC 7817

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    Sequence 43, Application US/10383201
    Publication No. US20040029226A1
    CBNERL INFORMATION:
    APPLICANT: Alsobrook II, John et al.
    TITLE OF INVENTION:
    FILE REFERENCE: 21402-568A

                                                                                                                                                                                                                                                                                                                                             Sequence 65, Appl
Sequence 79, Appl
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Sequence 41, Appl
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Sequence 77, Appl
Sequence 62, Appl
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Sequence 17002, A
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Sequence 33231, Ap
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          4 13 US-10-383-201-43

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4 13 US-10-382-201-55

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18 US-09-808-602-74

19 US-09-808-602-77

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11 US-09-864-751-2133

12 US-10-198-846-13376

13 US-10-198-846-1330

14 US-10-029-386-1332

15 US-10-029-386-1332

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19 US-01-282-122A-32058
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CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: US/2020
PRIOR APPLICATION NUMBER: 0/029020
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2002-03-20
PRIOR FILING DATE: 2002-03-20
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR PLING DATE: 2002-06-14
PRIOR PLING DATE: 2002-06-14
PRIOR PLING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/391,79
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               RESULT 1
US-10-383-201-43
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                                                           Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/CQm121/USTPTO spool/USION09020/runat 06082004 112218_29331/app_query.fasta_1.3519
-Q=/CQm21_L/USTPTO spool/USION09020/runat 06082004 112218_29331/app_query.fasta_1.3519
-DB=Published Applications_NA -QFMT=fastap -SUFFIX=p2n.rmpb -MINMATCH=0.1
-LOOPCI=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LCOAL -UNITFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIRN=200000000 -USER=US10029020 @CGN 1 1 2156 @runat_06082004 112218_29331
-NOPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-NOFU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DBY TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                          August 14, 2004, 01:33:47; Search time 1084.27 Seconds (without alignments) 2448.158 Million cell updates/sec
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1. /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2. /cgn2_6/ptodata/2/pubpna/DETNEW PUB.seq:*
3. /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
4. /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5. /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*
6. cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*
7. /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
8. /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
9. /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
10. /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/US09_NEW PUB.seq:*
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14. /cgn2_6/ptodata/2/pubpna/US09_NEW PUB.seq:*
15. /cgn2_6/ptodata/2/pubpna/US10_NEW PUB.seq:*
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19. /cgn2_6/ptodata/2/pubpna/US10_NEW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                       OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3225727 seqs, 2453303834 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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CAGCCCCCTAAGGGCAATGCCTCAGTCATACAGGACTTCACTGAGGATGGGCACCTCCTT
                                                  6032 CACACCTTCTACCTGGGCACTGGCCGCAGGGTGATATACAAGTATGGGAAACTGTCAAAG
                                                                                 LeuAlaGluThrLeuTyrASpThrThrLysValSerPheThrTyrASpGluThrAlaGly
                                                                                               6092 CTGGCAGAGACGCTCTATGACACCACCAGGTCAGTTTCACCTATGACGAGACGGCAGGC
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Publication No. US20040033971A1
GENERAL INFORMATION:
APPLICANT: Gangolli et al.
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Mismatches:
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Matches:
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Gaps:
          PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 10/051,874
PRIOR FILING DATE: 2002-01-16
PRIOR PILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-03-22
PRIOR PILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SOFTWARE: CHASSEGLIST VETSION 0.1
SEQ ID NO 43
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100.00%
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                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                               , NAME/KEY: CDS
, LOCATION: (35)..(8341)
US-10-383-201-43
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Best Local Similarity:
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Pred. No.:
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                                                                                                        GlnArgGlnTyrIlePheGluPheAspLysAsnAspArgLeuSerSerValThrMetPro
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TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE REPERENCE: 21402-225

CURRENT APPLICATION NUMBER: US/10/029,020

PRIOR APPLICATION NUMBER: 60/256,704

PRIOR FILING DATE: 2000-12-19

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                                                      LeuGlnThrGluProHisLeuLeuAlaGlyThrValAsnProThrValGlyLySArgAsn
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APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Gunther, Exik
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APPLICANT: Gunther, Exik
APPLICANT: Gunther, Exik
APPLICANT: Stone, David
ITTLE OF INVENTION: Using the Same
FILE OF INVENTION: UNMERR: US/10/042,865
CURRENT FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/250,831
PRIOR APPLICATION NUMBER: 60/272,38
PRIOR PLING DATE: 2001-01-01-09
PRIOR PLING DATE: 2001-01-03-09
PRIOR PLING DATE: 2001-03-09
PRIOR PLING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SEQ ID NO 1
FRIGHT: 8438
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Publication No. US20040029216A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
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Boldog, Ference L
Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothemberg, Mark E
Ellerman, Karen
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Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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Malyankar, Uriel M
Millet, Isabelle
Peyman, John
Smithson, Glennda
Gunther, Brik
Stone, David
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Zerhusen, Bryan D
Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                          Tchernev, Velizar
Miller, Charles E
Guo, Xiaojia
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                     2751.00
97.24%
97.06%
96.70%
             ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(8325)
US-10-383-201-55
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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PRIOR PILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
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NUMBER OF SEQ ID NOS: 2699
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APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Van (* Veer, Laura Johanna
APPLICANT: Van (* Vijer, Marc J.
APPLICANT: Bernards, Reme
TITLE (* NVENTION: Diagnosis and Prognosis of Bre
FURRENT APPLICANTON NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Lauxa Johanna
APPLICANT: Van de Vijver, Marc J.
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  APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Bre;
FILE REFERENCE: 3301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT APPLICATION NUMBER: 60/380,770
PRIOR PILING DATE: 2002-05-14
NUMBER OF ENQ ID NOS: 2699
SEQ ID NO 1743
LENGTH: 3614
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DATABASE ACCESSION NUMBER: NM 018104
DATABASE ENTRY DATE: 2001-06-18
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Publication No. US20030224374A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongrue
APPLICANT: He, Yudong
APPLICANT: Linaley, Peter
APPLICANT: Roberts, Chris
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APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
ATILLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
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CURRENT APPLICATION NUMBER: 05/10/038,854
CURRENT PILING DATE: 2003-01-22
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR APPLICATION NUMBER: 60/259,814
PRIOR APPLICATION NUMBER: 60/259,814
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
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Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
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Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
Burgess, Catherine E
Ellerman, Karen
Gunther, Erik
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Gangolli, Esha A
Guo, Xiaojia S
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                                Vernet, Corine
Eisen, Andrew J
Liu, Xiaohong
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Kekuda, Ramesh
                Volenc, Adam R
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ORGANISM: Homo sapiens
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US-10-038-854-39
Sequence 39, Application US/10038854
Publication No. US20040022781A1
PUBLICATION:
PUBLICANT: Spytek, Kimberly A
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PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
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SOFTWARE: Patentin Ver. 2.1
LENGIH: 8645
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
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CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 06/258,928
PRIOR FILING DATE: 2000-01-29
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR APPLICATION NUMBER: 60/259,832
PRIOR PILING DATE: 2001-03-29
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PRIOR FILING DATE: 2001-04-13
                                                                              Sequence 37, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
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Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
Smithson, Glennda
Millet, Isabelle
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Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
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APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
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Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
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Gusev, Vladimir Y
Gangolli, Esha A
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Shenoy, Suresh G
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Eisen, Andrew J
Liu, Xiaohong
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RESULT 9
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LeudsnGlyvalasnValThrTyrSerProGlyGlyTyrIleAlaGly1leGlnArgGly 140
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                                                                                                        PRIOR APPLICATION NUMBER: 60/258,928

PRIOR FILING DATE: 2001-12-29

PRIOR FILING DATE: 2001-12-29

PRIOR FILING DATE: 2001-01-02

PRIOR FILING DATE: 2001-01-02

PRIOR FILING DATE: 2001-01-04

PRIOR PELICATION NUMBER: 60/259,785

PRIOR FILING DATE: 2001-01-02-0

PRIOR PELING DATE: 2001-03-29

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          APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
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CURRENT FILING DATE: 2003-01-22
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US-10-038-854-35
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GluThrProLeuProIleAspLeuTyrArgTyrAspAspValSerGlyLysThrGluGln
                                                                                                                                                                                    PheGlyLysPheGlyValIleTyrTyrAspIleAsnGlnIleIleThrThrAlaValMet
                                                                                                  TITGGAAAGTITGGAGTTATATATATTATGATATTAACCAGATCATTTCTACAGCTGTAATG
                                                                                                                                                             ThrHisThrLysHisPheAspAlaTyrGlyArgMetLysGluValGlnTyrGlullePhe
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Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
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Gorman, Linda
Kekuda, Ramesh
Patturajan, Meera
Gusev, Vladimir Y
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Tchernev, Velizar
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Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
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APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Vernet, Corine
APPLICANT: Elsen, Andrew J
APPLICANT: Liu, Xiaohong
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Gangolli, Esha A
Guo, Xiaojia S
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APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Herrman, John L
APPLICANT: Herrman, John L
APPLICANT: Mishra, John L
APPLICANT: Mishra, Vishnu
APPLICANT: Machae, Feter S
APPLICANT: Machael Feter S
APPLICANT: Machael John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same;
TITLE OF INVENTION: NUMBER: US/09/808,602
CURRENT APPLICATION NUMBER: 09/800,198
FRIOR FILING DATE: 2001-03-14
FRIOR FILING DATE: 2001-03-05
FRIOR FILING DATE: 2000-03-05
NUMBER OF SEQ ID NOS: 114
SEQ ID NOS: 114
SEQ ID NO 74
SEQ ID NO 74
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                               US-10-029-020-14\_COPY\_1760\_2300~(1-541) x US-09-808-602-74~(1-8797)
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                    Sequence 74, Application US/09808602; Sequence 74, Application US/09808602; Patent No. US20020155115A1; APPLICANT: Vernet, Corine A APPLICANT: Fernandes, Elma APPLICANT: Shimkets, Richard A APPLICANT: Majumder, Kumud; APPLICANT: Mishra, Vishnud; APPLICANT: Mishra, Vishnud; APPLICANT: Mishra, Vishnud; APPLICANT: Mezes, Peter S
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GENERAL INFORMATION:

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APPLICANT: Fernandes, Elma
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APPLICANT: Majumder, Kumud
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APPLICANT: Majumder, Vannu
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: MacDougall, John
TITLE OF INVENTION: NO. US20020155115Alel Proteins and Nuclec Acids Encoding Same
CURRENT APPLICATION NUMBER: US/09/808,602
TITLE OF INVENTION: NOWBER: 00/800,198
PRIOR FILING DATE: 2001-03-04
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VOS: 114
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US-09-808-602-77
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US-09-808-602-77
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                                                                       GlnProProGluGlyAsnAlaSerValIleGlnAspPheThrGluAspGlyHisLeuLeu
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                                    LeuAsnGlyAsnLeuHisLeuLeuSerProGlyAsnSerAlaArgLeuThrProLeuArg
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APPLICANT: Vernet, Cornie AM
APPLICANT: Vernet, Enandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Herrmann, John L
APPLICANT: Herrmann, John L
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishna
APPLICANT: Mishra, Vishna
APPLICANT: Masse, Peter S
APPLICANT: Rastelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
CURRENT APPLICATION NUMBER: 60/186,596
FRIOR APPLICATION NUMBER: 60/186,596
FRIOR APPLICATION NUMBER: 60/186,596
FRIOR PILLING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE PATENTING DATE: 2000-03-03
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                               AspGlyGlnLeuGlnThrValSerIleAsnAspLysProLeuTrpArgTyrSerTyrAsp
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Sequence 65, Application US/09800198

Publication No. US20030087816A1

SEMERAL INFORMATION:
APPLICANT: Shinkets, Richard A

APPLICANT: Shinkets, Richard A

APPLICANT: Majumder, Rundd
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Rundd
APPLICANT: Majumder, School
APPLICANT: Mazes, Peter S

APPLICANT: Mazes, Peter S

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 1596-6-697

CURRENT APPLICATION NUMBER: US/09/800,198

CURRENT APPLICATION NUMBER: G0/186,596

PRIOR FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 98

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 65
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|GACGGGAAAGTCTGGAGTTATTCCTATCTTGACAAGTCCATGGTCCTTCTGCTACAGAGC
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APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Herman, John L
APPLICANT: Mishra, Vishnu
APPLICANT: Mishra, Vishnu
APPLICANT: Machae, Peter S
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same; FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: 09/800,198
FRIOR FLING DATE: 2001-03-14
PRIOR FLING DATE: 2001-03-05
PRIOR FLING DATE: 2001-03-05
PRIOR FLING DATE: 2001-03-05
NUMBER OF SEQ ID NUMBER: 60/186,596
PRIOR FLING DATE: 2000-03-03
NUMBER OF SEQ ID NUMBER: 60/186,596
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                        6824 TATGACCTCCGTGACCGGATAACCAGGCTAGGGGACGTGCAGTACAAAATCGATGACGAT 6883
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Patent No. US20020155115A1
GENERAL INFORMATION:
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APPLICANT: Fernandes, Blna
APPLICANT: Shimkets, Richard A
APPLICANT: Herrman, John L
APPLICANT: Mishra, Kumud
APPLICANT: Mishra, Vishnu
APPLICANT: Meshra, Vishnu
APPLICANT: Meses, Peter S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 HisThrPheTyrLeuGlyThrGlyArgArgVallleTyrLysTyrGlyLysLeuSerLys
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                    AlaArgGlyGlnValThrValPheGlyArgArgLeuArgValHisAsnArgAsnLeuLeu
                                                                                                      SerLeuAspPheAspArgValThrArgThrGluLysIleTyrAspAspHisArgLysPhe
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TTTCACAGCGAACCTCATGTCCTGGGTGGACAGTAACTCCCACCATAGGACGATGTAAT ValThrLeuproileAspAsnGlyLeuAsnLeuValGluTrpArgGlnArgLysGluGln ::::::		TrpSerProser.	hrSerArgile       :::  arcGCGCATG	LeuLeuLeuHisser            CTACTGCTTCAGAGC SerValThrMetPro	CTGTTACT  YFARGASH  TTAGGAAT	spglyhis;       Argggagg	Lysteu       AAGCTA	AAACTI SAAACTI NIGTYEI GCTAT	tval      GGTC	Nla CC	`a — ĕ	- X	
GCTGG Leuas       TTGAA	GlyargargleuargVa        ::	AladlyArgProSerLeu	IICIICAACGGGCGCCTGG AspGlnAlaGlyArgIleTl   :::          GACAAGCAAGGATCA:	TyrLeuGluLysSerMetVal 		valileginAspPheThrGluA:        grgattttgAttaCGTGATG	ArgArgvallleTyrLysTyrGly    :::    CGACAGTCTTTACAGTATGGA ThrLysValSerPheThtTyTASp		IleglyProLeuileAspArgGlnilePheArgPheThrGluGluGlyMetValAsnAla 	ArgPheAspTyrAsnTyrAspAsnSerPheArgValThrSerMetGlnAlaVallle 	AsnGluThrProLeuProIleAspLeuTyrArgTyrAspAspValSerGlyLysThrGlu  :::	GlnPheGlyLysPheGlyVallleTyrTyrAsplleAsnGlnIleIleThrThrAlaVal 	tThrHisThrLysHisPheAspAlaTyrGlyArgMetLysGluValGlnTyrGluIle      :::             :::  GACACTGAGTAAGCACTTTGATACCCACGGACGCATTAAAGAAGTTCAATATGAGATG
TTTCACAGCGAACCTCATGTCCTGG ValThrLeuProlleAspAsnGlyL ::::::      :::::        ATTCTCTACCAATGGAGAATGGTI	alaargGlyGlnValThrValPheGlyArgArgLeuArgValHisAsnArgAsnLeuLeu	H-4 1-0	b closeliecteltakteleiteltariitiitaktosseetelisseetisseetilekseetseetsa 1 IlemetSerGluargmetGluTyrAspGlnalaGlyArgIleThrSerArgIlePheAla 1	1 AspGlyLysThrTrpSerTyrThrTyrLeuGluLysSerMetValLeuLeuLeuHi.	6 CAGCGGCAGTACATCTTGAGTATGATTCTTCAGACCGGCTCCATGCTGTTACTATGCCT 1 ASNVAlAlaArgGInThrLeuGluThrIleArgSerValGlyTyrTyrTxArgAsnIleTyr 1 :::	1 GlnProProGluGlyAsnAlaSerValIleGlnAspPheThrGluAspGlyHisLeuLeu 	241 HisThrPheTyrLeuGlyThrGlyArgArgVallleTyrLysTyrGlyLysLeuSerLys 6106 AAACATCATTTTAGGTACTGGTCGACAAGTTTTACAAGTATGGAAAGCTATCCAAA 261 LeuAlaGluThrLeuTyrAspThrThrLysValSerPheThrTyrAspGluThrlaGly		IleglyProLeuIleAspargGlnI 	1 ArgpheaspTyrasnTyraspA 	0 AsnGluThrProLeuProlleAspl 	G1 CA	0 MetThrHisThrLysHisPheAspA         6 ATGACACTGAGTAAGCACTTTGATA

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6886 GGATTCCTGTGTCACGAGGCTCAGATGTATTTGAGTACAATTCCAAAGGACTTTTAACA 6945 6586 TTCCGATCCCTGATGTACTGGATGACTGTGCAATATGACAGCATGGGAAGAGTAACTAAA 6645 419 LysGluLeuLysValGlyProTyrAlaAsnThrThrArgTyrSerTyrGluTyrAspAla 439 500 GlyPheLeuArgGlnArgGlyGlyAspIlePheGluTyrAsnSerAlaGlyLeuLeuIle 519 PheArgSerLeuMetTyrTrpMetThrValGlnTyrAspAsnMetGlyArgValValLys 7006 AGG 7008 540 Arg 540 420 400 > Q ≱ વૃ  $\approx$ Ф > Д ≈ Q. <u>ب</u> <u>ک</u> ۾ ≿

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Sequence Sequence

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7125, Ap 3388, Ap 42, Appli 1, Ap

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Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

Sequence Sequence

Sequence 5, Sequence 5,

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Sequence 7234, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICATUS MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7224
LENGTH: 4881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GlySerLeuArgLeuLeuAlaAsnGlyMetGluValAlaLeuGlnThrGluProHis
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US-09-222-991A-11787
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US-09-252-991A-1898
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1 US-08-462-949-1
1 US-08-023-7649-1
4 US-09-03-7628-256
4 US-09-134-001C-1976
1 US-08-480-604A-5
2 US-08-496A-5
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Pseudomonas aeruginosa
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32.17%
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 Percent Similarity:
Best Local Similarity:
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176.5
173.5
169.5
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162.5
146.5
125.5
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-DG-Ggn2_1/USPTO_spool/US10029020/runat_b2n.rni -MINNARCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits NA -OFMT=tastap -SUFFIX=p2n.rni -MINNARCH=0.1 -LOOPCL=0
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MINS=human40.cdi
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-DELEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7234, Ap
Sequence 304, App
Sequence 1157, Ap
Sequence 296, App
Sequence 14461, Ap
Sequence 1416, Ap
Sequence 111, App
Sequence 111, App
Sequence 1419, Ap
Sequence 90, Appl
Sequence 11853, A
                                                                                            August 14, 2004, 01:16:21; Search time 160.054 Seconds (without alignments) 1875.793 Million cell updates/sec
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTus
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                   nucleic search, using frame plus p2n model
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US-09-543-681A-304
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US-09-711-164-295
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US-09-352-991A-14461
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US-09-453-702B-11
US-09-453-702B-00
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2845
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Score

Result No.

Database :

	I   I   I   I   I   I   I   I   I   I	465 SLeuLeu	1801 GGTCACCGAATACAGCTACCCAACACCGCCTGATCGGCGTCCGGACGG  527 rTrpserValArgTyrArgTyrAspGlyLeuGlyArgArgVal 541  2861 GCGCCAGGTCGTCTACCGCTTACGACGCCTTCGGCCGACGCTTCGGCCGACGCATC 3903  1 2 43 eBab 304 Application US/09543681A  1
	33A 2336 33A 2336 7G1 132 CG6 2387 aG1 152 GG 2447 LLY 172 CGG 2507 TCC 2567	2627 2687 208 2742 223 2783 243 2843 255	258 DE 2963 DE 2963 DE 278 DE 3017 RE 298 US 316 SE 298 SE
27 LeuleualaciyThrvalasnProThrvalGlyLysArgAsnValThrLeuProlleAsp	TyraspasphisarglysPheThrLeuargile-Lerisical Hilling GGGAACGATCGGAGTACGGAGACGATCGGAGACGATCGGAGACGATCGGAGACGATCGGAGACCCGGAGACCCGGAGACCCGGAGAGAGA	2568 GCTCGGCCAGTTGATAGAACAGCTTTCCGGACGGTGCGCCCCTATCGTACCAGACGTGCGCCCCCTATCGTACCAGACGTGCGCCCCCTATCGTACCAGACGTGCGCCCCTATCGTACCAGACGTACCCTACAGACGTACCCTACAGACGCTACCAGATCACCCCCCAGAGCGCCCATCCCAGATCACCCCTAGACGCCCAGTCCCAGATCACCCTACCCTGCCCGGTGCGCCCAGATCACCCTGCCCGGTGCGCCCAGATCACCCTGCCCGGTGGCGCCAGCGCCGCAGTCCATCACAGATCACCCTGCCCGGTGGCGCCAGCGCCGCATG  208 uThr1leArgSerValglyTyTTyTATGASn1leTyrGlnProPr 2143TACCGCTACAACGCTTACGGCAAGGTCCAGCGATGCCA 223 GGLuGlyAsnAlaSerVallleGlnAspPheThrGluAspGlyHisLeuLeuHisThrPh 2784 CGACAGGGCCGGATGACCCGCTACCAACGCTTACGACCTGCTCAGTCAG	256GlyLysLe 2904 CGAGATCGAGAACGAGCGAACGCTATCGCCTCGATTACCACGGCAACGGCTGAT 258 uSerLysLeualaGluThrLeuTyrAspThrThrLysValSerPheThrTyrAspGluTh 2964 CAGCCAGGAAACCGGCTTCGACGCCGCCGCCCCTTCGCTACGCTCTCA 278 ralaGlyMetLeuLysThrIleAsnLeuGlnAsnGluGlyPheThrCysThrIleArgTY 278 ralaGlyMetCGAGAAACCGGCTCGGCGCGCCCTACGCCTCCAA 298 rargGlnIleGlyProLeuIleAspArgGlnIlePheArgPheThrGluGluGl
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	223 ProGluGlyAsnAlaSerValIleGlnAspPheThrGluAspGlyHisLeuLeuHisThr 242 2278 CTT	306AsphrgGlnIlePheArgPheThrGluGluGlyMetValAsnAlaArgPhe 322   2590 GCCGGAGGCCCATATCTGTGCGCCGTAACCGTCGGCCAGAGGCGCGACGC 2649
8 8 8 8 8 8 8 8 8 8 8		5     6
Db 3739 ACACAATACAGTCCACAATGGGGTAATCAGGACGAAAGTTCCAGTATGATAACAACTCT 3798  463 AsileuHisleuleuSerProGlyAsnSer	RESULT 3  US-09-543-681A-1157  Sequence 1157, Application US/09543681A  Partent No. 6605709  GENERAL INFORMATION: APPLICANT: GARY BRETON TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS FILE REFERENCE: 2709-1002-001 CURRENT PILLING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR PILLING DATE: 1999-04-09 NUMBER OF SCO ID NOS: 8344 SEQ ID NO 1157 LENGTH: 4761 TYPE: DNA ORGANISM: Proteus mirabilis FEATURE: NAME/KEY: unsure LOCATION: (4726) CTHER INFORMATION: Identity of nucleotide at the above locations are unknown. US-09-543-681A-1157	Alignment Scores:  Scores:  Scores:  Scores:  Scores:  Scores:  207.00  Best Local Similarity:  32.66\$  Conservative:  Best Local Similarity:  17.28\$  Mismatches:  18  Best Local Similarity:  17.28\$  Mismatches:  18  Decent Similarity:  17.28\$  Mismatches:  18  Indeplay:  17.28\$  Mismatches:  18  Indeplay:  17.28\$  Mismatches:  18  Indeplay:  17.28\$  Mismatches:  18  Indeplay:  17.28\$  Mismatches:  18  Indeplay:  17.28\$  Mismatches:  18  Indeplay:  17.28\$  Mismatches:  18  Indeplay:  17.28\$  Mismatches:  18  Indeplay:  17.28\$  Mismatches:  18  Indeplay:

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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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                        ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1).
US-09-711-164-296
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Sequence 206, Application US/09711164

Sequence 206, Application US/09711164

Sequence 206, Application US/09711164

GENERAL INFORMATION:
APPLICANT: Porsyth, R. Allyn
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, CENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
FILE OF INVENTION: UNMBER: US 60/164415

PRIOR FILING DATE: 10999-11-9

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 4134

TYPE: DNA
8872 CCCTTATCCCCGCAGGTGACCACCTTCGGTTACGATAAAGTGGGACGGTTGCTGTTTCGA 2931
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GAAAACGCCGATTATCGCACGGAATACCTTTATCAACCTTTGAGTGTGACGTTACGCCGA 2991
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3454 GTCAGTTATGGTCAAACGGGGGAGGTTTTTACGGCGGACATTGGTACTACCACAGTTAT
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CAGTTAACGTCAGCCACCGGCCTGGAATTGCGCCGGGAATATGATGAATTG
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                                         GlyLysLeuSerLysLeuAlaGluThrLeuTyrAspThrThrLysValSerPheThrTyr
                                                               1477 GGCCGTCTG-----ATTCAGGAAACTGCCCCTGACGGCGATATCACCGCTATAT
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US-09-252-991A-14461
; Sequence 14461, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION;
; APPLICANT: Marc J. Rubenfield et al.
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TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR PILING DATE: 1999-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 SEQ ID NO 14461 SEQ ID NOS: 33142 SEQ ID NO 14461 LENGTH: 3387
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Best Local Similarity:
Query Match:
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      1320 GGGCTGAAGCGGGTGGTGAAAAAGGAACGCGGACGGCAGCGTCACGCAGAGTCAGTTT
                                                               GACGCGGTGGGCAGGCTCAGGCCACAGACGACGACGACAACAGAA
                                                                                                   ThrIleArgSerValGlyTyrTyrArgAsnIleTyrGlnProProGluGlyAsnAlaSer
                                      AspLysAsnAspArgLeuSerSerValThrMetProAsnValAlaArgGlnThrLeuGlu
                                                                                                                                      ----TACAGCCCGGATGTGGTGACGGGCCTC
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---GAATACGATGCTGCCGGACGGGTCATCCGCCTGACCAGT
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133
78
227
170
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Matches:
Conservative:
Mismatches:
Indels:
                                                                          NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REGISTRATION NUMBER: 960296.95017
TELECOMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEPHONE: (608) 251-9166
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGAATTTACCTGCCGCCGCTGGTGCGC----
                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-09-453-702B-226
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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34.70%
21.88%
6.75%
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Query Match:
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on 512 myrbenGerblaglyfenfentlefwsklaffvrksnkrdklaglyserTroserValkrd 531	qa	TACCGCTTTGAGTACGGGCAGGACCGTGTGACCATCACGGACAGCCTGAACCGGCGGGAG
2289ATCAGGCATATCAGGGACGGAGGGTGACGATG	λ Q	126 ValthrTyrSerFroGlyGlyTyrIleAleGlyTleGlhArgGlyTleMetSerGlu 144
Oy 532 TyrargTyraspGlyLeuGlyArg 539	ð	145ArgMetGluTyrAspGlnAlaGlyArg1leThrSerArg1le 158
	qa	26803 GCGGACGGGAGCATCACCCGCAGCGAGTATGATGAGGCGGGGGGGG
NESULT 8 US-09-453-702B-11	λ̈	159 PheAla
; Sequence 11, Application US/US453/UZB ; Patent No. 635723	qu	26863 GATHCHGGCGGGACGGACGGACGGACACTGCATATGGCGTCGGGTGCGGTGACAGCG 26922
tner, Fre	ζÖ	161
; Burland, Valerie ; Perna, Nicole T.	αα	26923 GTGACGGGGCCGGACGGCGGGGGGGGGTATGGCTAT
Plunkett, Guy Welch, Rod	<i>\</i> 0	177 LeuLeuHisSerGlnArgGlnTyrIlePheGluPheAspLysAsnAspArgLeuSerSer 196
; TITLE OF INVENTION: No. 6365723el Sequences of E. coll 0157; NUMBER OF SEQUENCES: 265	qa	26962AACAGCCAGCGGCAG
; CORRESPONDENCE ADDRESS: ; ADDRESSES: Quartles & Brady cmptpm: 1 court binchmay Great	à	euGluThrIleArgSerValGlyTyrTyr 216
: I south Finchiey Madison	qa	26986 didakidiracididakongongidikacago 27015
; STATE: WI ; COUNTRY: US	ò	217 ArgAsnIleTyrGlnProProGluGlyAsnAlaSerValIleGlnAspPheThrGluAsp 236
; ZIP: 53701-2113 ; COMPUTER READABLE FORM:	qu	27016CGGGAGTATGATGAAG 27033
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible	λ	237 GlyHisLeuLeuHisThrPheTyrLeuGlyThrGlyArgArgVallleTyrLysTyrGly 256
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0	qu	27034 GGAAGCTG 27042
CURRENT APPLICATION DATA:	ò	257 LysLeuSerLysLeuAlaGluThrLeuTyrAspThrThrLysValSerPheThrTyrAsp 276
; FILING DATE: 03-Dec-1999 ; CLASSIFICATION: <unknown></unknown>	qa	27043GCGGCGGGGAGACCTCGCGCAGCGGAGAGACGACGCGGTACAGCTATGAT 27090
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 60/110,955	ò	277 GluThrAlaGlyMetLeuLygThrIleAsnLeuGlnAsnGluGlyPheThrCysThrIle 296
; FILING DATE: 04-DEC-1998 ; ATTORNEY/AGENT INFORMATION:	q	27091 GACCCGGCGAGTGAGCTGCCGACAGGATACAGGACGCGACGGGCAGTACAAAACAGATG 27150
; NAME: Seay, Nicholas J. ; REGISTRATION NUMBER: 2786 ; REGISTRATION NUMBER: 2786	ò	ProLeulleAspArgGlnIlePheArgPheThrGluGluGly
REFERENCE/DOCKET NUMBER: 960296.9501/ TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 1000000000000000000000000000000000000	qa	27
TELEFACINE: (008) 251-9100	ζ	<pre>yrAspAsnSerPheArgValThrSerMetGln    </pre>
; INFORMATION FOR SEQ ID NOT II: ; SEQUENCE PERROTERISTICS:	đ	CGGTACGGTCAACAATC
TYPE: nucleic acid ; ;TRANDEDNESS: double	8	337 AlaValileAsnGluThrProLeuProlle
) MOLECULE TYPE: DNA (genomic) ; SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-09-453-702B-11	8 8 8	349 TyrargTyrAspAspValSerGlyLysThrGluGlnPheGlyLysPheGlyVal 366
.1 Length:	8 8	ou .
188.50 Matches: 33.47% Conservative:	qa	27358GACCTCACCGCTATCGTTGCCCCGGACGCCGCAGTGAGATACAGTAT 27408
	<i>∂</i> 8	387 AspalaTyrGlyArgMetLysGluValGlnTyrGluIlePheArgSerLeuMetTyr 405
US-10-029-020-14_COPY_1760_2300 (1-541) x US-09-453-702B-11 (1-31960)	}	406 TrDMetThrValGlnTyrAspAsnMetGlyArgValValLysLysGluLeuLysValGly 425
103 ArgileLeuTyrAspGlnAladlyArgProSerLeuTrpSerPro 117	දු අ	
Db 26629 CGCTACCGGTATGATGATGATGCCGGGTGACGGAGTCACCCGGAGGGGGGTGACC 26688 Ov 118	<i>à</i>	426 ProTyrAlaAsnThrThrArgTyrSerTyrGluTyrAspAlaAspGlyGlnLeuGlnThr 445
	Ωρ	27496 ACCAACGAGAACGGCAGCCAGTCCACGTTCCGGTATGACCCGGTGGACAGGCTGACTGA

y 140 Gly 144	y 145ArgMetGluTyrAspGlnAlaGlyArglleThrSerArg 157 b 616 AACTCTAATAAGTATGATATTTGGAAACTGATATTTAAATCCAATCCTGGTTTTAGT 675	y 158 IlePheAlaAspGlyLysThrTpSerTyrThrTyrLeuGluLysSerMetValLeuleu 177	y 178 LeuHisSerGlnArgGlnTyrIlePheGluPheAspLysAsnAspArgLeuSerSerVal 197	Y 198 ThrMetProAsnValAlaArgGlnThrLeuGluThrIleArgSer 212	y 213 ValGlyTyrTyrArgAsnIleTyrGlnProProGluGlyAsnAlaSerValIleGlnAsp 232	233	Y 251 Valile 252     0 904 GTCTTTCAGACACAACTGAATTTGAAAACGCACTTTTAAAACCAAAAGTTGCTGTATCG 963	253TyrLysTyrGlyLysLeuSerLysLeuAlaGluThrLeuTyr 	267 AspThrThrLysValSerPheThrTyrAspGluThrAlaGlyMetLeuLys	284 ThrileAsnLeuGlnAsnGluGlyPheThrCysThrileArgTyrArgGlnIleGlyPro :::	304	1135	324 TyrAsnTyrAspAsnSerPheArgValThrSerMetGlnAlaValileAsnGluThr 342    :::    :::        :::    :::    :::	/ 343 ProLeuProIleAspLeuTyrArgTyrAspAspValSerGlyLysThrGluGlnPheGly 362	363	373 GlnIleIleThrThralaValMetThrHisThrLySHiSPheAspAla 388 	389 TyrGlyargMetLysGluValGlnTyrGluIlePheArgSerLeuMetTyr405 1399 TyrGgGGAAGTAACAATACCAAATGTAATACAAAGTTTGAATTATAATACAGG 1455	406TrpMetThrValGln
do Db	VQ QQ	da da	ζς O	ζ. Op	Oy Dp	QY ACINETOBACTER Db	<b>∂</b> 8	QV qu	Qy Bb	<i>₹</i> ∂	oy.	<b>q</b> 0	Sy da	ζς Q	da ag	Kō	QY du	ò a ò
ValSerIleAsnAspLysProLeuTrpArgTyrSerTyrAspLeuAsnG1yAsnLeuHis 465 	sparg       accec			AsnargalaglySerTrpSerValargTyrargTyrasgGlyLeuGlyArg 539		D AMINO ACID SEQUENCES RELATING TO	VERWICH: BAGREAULI FOR DIAGNOSTICS AND THEKAFEUTICS  LICATION NUMBER: US/09/328,352  NOTE: 1009-016.04	NUMBER OF SEQ ID NOS: 8252 SEQ ID NO 1419 LENGTH: 2415 TYPE: DAA	OKGANISM: Acinetobacter baumannii 9-328-352-1419	1.27e-12 Length: 24 185.50 Matches: 14 33.79\$ Constraive: 78	6.52% 4.52%	14_COPY_1760_2300 (1-541) x US-09-328-352-1419 (1-2415)	33 AsnProThrValGlyLysArgAsnValThrLeuProlleAspAsnGly 48		alThr ::		12	13
Qy 446 Db 27556	Oy 466 Db 27610	Qy 486 Db 27670	Qy 501 Db 27730	Oy 521 Db 27772	RESULT 9 US-09-328-352 ; Sequence 14	; Patent No. 6562958 ; GENERAL INFORMATION: ; APPLICANT: Gary L. ; TITLE OF INVENTION: right of information:			) ORGANISM: Acin US-09-328-352-1419	Alignment Scores: Pred. No.: Score: Score: Best Local Similarity:	Query Match: DB:	US-10-029-020-14_COPY	Qy 33 Db 220	Oy 49 Db 280	Qy 69 Db 340		Oy 109 Db 436	

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1197 AATACGCAGGTGCGCGTTTCACGTATAACGCGCAGCATCCGGGCCGGATGGTGGCGCAC 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgilePheAlaAspGlyLysThrTrpSerTyrThrTyrLeuGluLysSerMetValLeu 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 LeuLeuHisSerGlnArgGlnTyrIlePheGluPheAspLysAsnAspArgLeuSerSer 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 IleGlnArgGlyIleMetSerGluArgMetGluTyrAspGlnAlaGlyArgIleThrSer
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|GTGGTGAAAAAAAAGAACTGGCGACGGCAGCGTCACGCACAGCGGCTATGACGCGGCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 783 TATAACGACGGGAACCAGCTGACGGCGGTGGTGTCCCCGGACGGGCTGGAGAGCCGCCGG
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116
68
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137
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Mismatches:
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                                                                                                                                                                                                 Length:
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                                                                    TOPOLGGY: Inhear MOLECULE TYPE: DAA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: US-09-453-7028-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 ValThrMetProAsnValAla-
                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                3.55e-12
185.50
34.01%
21.44%
6.52%
                  SEQUENCE CHARACTERISTICS
INFORMATION FOR SEQ ID NO:
                                     LENGTH: 4453
                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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GGTAATGAGACCTATCTTTATAATGCTGATGGACTAAGAGTCCGTGCTGTAAGGGATGAT 1983
                      .516 AGCGGGTTGCTGAATAATATCTCTGCTACAAGTCTGGAAAAGTGTGTCCTCAATGTTGAT 1575
                                                                                                                                                                 AACGCTACAATTGACCGTTATGGTACAGGTTTGATGAGTACTGTTGAGTTAGATTAGATCAAGCA 1695
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                                                         -----TyrAspAsnMetGlyArgValValLysLysGluLeuLysValGlyProTyrAla
                                                                                                                                                                                                  ArgTyrSerTyrGluTyrAspAlaAspGlyGlnLeuGlnThrValSerIleAsnAspLys
                                                                                                                                                                                                                                                                       -----ProbeuTrpArgTyrSerTyrAspbeuAsnGlyAsnLeuHis
                                                                                                                                                                                                                                                                                                                                            LeuLeuSerProGlyAsnSerAlaArgLeuThrProLeuArgTyrAsp1leArgAspArg
                                                                                          1576 TATGGTTACGATAAATTGAACCGAGTTAATAAGCTTTCGGACAAATGTGGATCAGTTTAT
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MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb stc
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Welch, Rod
OF INVENTION: No. 6365723el Sequences of
OF SEQUENCES: 265
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REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlySerTrpSerValArgTyrArgTyrAspGly 536
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STREET: 1 South Pinckney Street
CITY: Madison
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FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 90, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burland,
Turna, Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: WI
COUNTRY: US
ZIP: 53701-2113
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                                                                                               Pseudomonas aeruginosa
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184.00
37.14%
22.15%
           1998-07-27
     PRIOR FILING DATE: 1996
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 11853
LENGTH: 2997
TYPE: DNA
                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
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US-09-252-991A-11853
                                                                                                                                                                                                     Percent Similarity:
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Patent No. 6557795

GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: AERGIGANOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGIGANOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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                                                    ValSerPheThrTyrAspGluThrAlaGlyMetLeuLysThrIleAsnLeuGlnAsnGlu 290
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564 GCGTTCACTGACTGCTCGGGCTACCAGACCGGTTATGAATACGACCGCTTCGGCCAGATG 505
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---GTATCGGAGACATCGCGCTGTGGGGACGTC
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669 ATCCGGTATGCTTATGATAATCCGCACGGTGAATTACCGGCCACGACAACAGATGCGACG
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TATGACGAGCGCGGCAGCAGCATCACCGATGCC-----AACGGCGTCACC 543
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Conservative:
Mismatches:
Indels:
       CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,786
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 IleArgSerValGly-----
                                                                                                                                                                                      TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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US-09-252-991A-7069
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TITLE OF INVENTION: NUCLEIC ACID AND AMING TITLE OF INVENTION: BAUNANNII FOR DIAGNOST FILE REFERENCE: GTC99-03PA CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 EQ ID NO 2478 LENGTH: 4884
                                                                                                    TYPE: DNA; CRCANISM: Acinetobacter baumannii US-09-328-352-2478
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                                      SerPheArgValThrSerMetGlnAlaVallleAsnGluThrProLeuProIleAspLeu 348
                                                                                                                                          --IleAsnGlnIle 374
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US-09-328-352-2478
; Sequence 2478, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
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Search completed: August 14, 2004, 21:39:25 Job time: 275.054 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

August 14, 2004, 01:13:26; Search time 6344.74 Seconds (without alignments) 2546.273 Million cell updates/sec 1 YYIGADGSLRLLLANGMEVA.....YNRAGSWSVRYRYDGLGRRV 541 55026578 27513289 seqs, 14931090276 residues Total number of hits satisfying chosen parameters: US-10-029-020-14\_COPY\_1760\_2300 2845 0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Title: Perfect score: Scoring table: Sequence: Searched: Run on:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0%
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Listing first 45 summaries

Command line parameters:
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-Q=/Cqn2\_1/USTPTO spool/USIOS0200f/runat 06082004\_112216\_29287/app query.fasta\_1.3519
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=bluman40.cdi -LIST=45
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNTWT=pto -NORM=ext -HEAPSIZE=560 -MINLEN=0 -MAXLEN=200000000
-USRTS=STSOORS=00 -GCGN 1 1.13135\_@TUNATE 06082004\_112215\_29287 -NCPU=6 -ICPU=3
-NO NWARP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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#### ALIGNMENTS

AY413475 6246 bp DNA linear GSS 12-DEC-2003 Homo sapiens HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. AY413475.1 GI:39769437 DEFINITION ORGANISM AY413475 LOCUS ACCESSION VERSION KEYWORDS SOURCE

RESULT 1

Homo sapiens
Homo sapiens
Bukaryota; Metacaa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6246)

REFERENCE

179   HisSerGlnArgGlnTyrllePheGluPheAspLysAsnAspArgLeuSerSerValThr		299 ArgGlnIleGlyProLeuIleAspArgGlnIlePheArgPheThrGluGluGludlyMetVal 318	4228 ATCAACGAGACCCCACTGACTCTTTTTTTTTTTTTTTTT	Greateaccecatactaritiearecatarideacatareacatarasea   Greateacecatareacecatarea   Greateacecatareacatarea   Greateacecatareacatareacatarea   Greateacecatecatareac	STTYF 45        CCLEU 47        ACTA 46	
6 6 6 6 6 6	3 8 8 8 8	8 8 8 8 8	8 8 8	8 8 8 8 8	8 8 8 8	6 8 6 8 6 8
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  JOURNAL Science 302 (5652), 1960-1963 (2003)  REFERENCE 2 (bases I to 6246)  REFERENCE 2 (bases I to 6246)  AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,	Adams, M. D. and Cargill, M.  TITLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, ROCKVILLe, MD 20850, USA COMMENT This sequence was made by sequencing genomic exons and ordering FERTURES Location/Qualifiers Location/Qualifiers   Location/Qualifiers   Location/Qualifiers     Norganism="Homo sapiens"     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location     Application   Location   Location   Location     Application   Location   Location   Location     Application   Location   Location   Location     Application   Location   Location   Location     Application   Location   Location   Location     Application   Location   Location   Location   Location     Application   Location   Location   Location   Location   Location     Application   Location	gene (1>6246  ORIGIN Alignment Scores: 0 Length: 6246 Score: 2834.00 Matches: 541  Percent Similarity: 99.63\$ Mismatches: 0 Best Local Similarity: 99.63\$ Mismatches: 0 Query Match: 2 Namatches: 0	Gaps: 1	Tedes IIIIII	SerLeubspPheaspArgValThrArgThrGluLys11eTyrAspAspHisArgI 	OY 121 LeuAsnGlyValAsnValThrTyrSerProGlyGlyTyrIlealaGlyIleGlnArgGly 140

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                         121 LeuAsnGlyValAsnValThrTyrSerProGlyGlyTyrlleAlaGlyIleGlnArgGly
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                                                       Pan troglodytes HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence, AX413476
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on allgament.
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Matches:
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Indels:
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
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381 ThrHisThrLysHisPheAspAlaTyrGlyArgMetLysGluValGlnTyrGluIlePhe 400
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               2441 TACCAAACAGAGCCGCACGTTCTGGCTGGCACCGCTAATCCGACGGTTGCCAAAAGAAAC
                                                       ValThrLeuProlleAspAsnGlyLeuAsnLeuValGluTrpArgGlnArgLysGluGln
                                                                         AlaArgGlyGlnValThrValPheGlyArgArgLeuArgValHisAsnArgAsnLeuLeu
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21 LeuGlnThrGluProHisLeuLeuAlaGlyThrValAsnProThrValGlyLysArgAsn
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                                                                                                            AspolyPheLeuArgGlnArgGlyGlyAspilePheGluTyrAsnSerAlaGlyLeuLeu 518
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Fockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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TRANSCRIPT, partial sequence,
                                                    | IlelysalaTyrasnArgAlaGlySerTrpSerValArgTyrArgTyrAspGlyLeuGly
                                                                                                                                                                                       l (bases 1 to 5094)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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Matches:
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Homo sapiens HCM2218 gene, VIRTUAL
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/db_xref="taxon:9606"
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AY405420.1 GI:39761394
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221 GlnProProGluGlyAsnAlaSerValIleGlnAspPheThrGluAspGlyHisLeuLeu 240
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-00V-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2434 TACCAGACAGAGCCCCACGTTCTGGCTGGCAGCGAATCCCACAGTAGCCAAAAGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerLeuAspPheAspArgValThrArgThrGluLysIleTyrAspAspHisArgLysPhe
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/organism="Mus musculus"
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D. M., Civello, D. R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X. H., White, T. J., Sninsky, J., Adams, M.D. and Cargill, M.
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase 1 & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length CDNAs

Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length CDNAs

Nature 420, 563-573 (2020)

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                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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High-efficiency full-length cDNA cloning
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JRL:http://genome.gsc.riken.go.jp/

AK037897

Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:Al30060L24 product:odd Oz/ten-m homolog 1 (Drosophila), full insert sequence.

LOCUS DEFINITION

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378 AlayalMetThrHisThrLysHisPheAspAlaTyrGlyArgMetLysGlyyalGlnTyr 397
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KGNVSAFERRLRAHNRALLSIDEDHWYRTGKT YDDIRKFTIRILYDDYGRFILWSPVS
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                                                                                                                                                                                                                   note="unnamed protein product; odd Oz/ten-m
(Drosophila) (MGD|MG1:1345185, GB|NM_011855,
3LASTN, 99%, match=3037)
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371
77
75
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Matches:
Conservative:
Mismatches:
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                                                       organism="Mus musculus"
                           Location/Qualifiers
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85.50%
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             URL:http://fantom.
                                        . .3038
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Best Local Similarity:
Query Match:
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Pred. No.:
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379

399 362 422

459

542

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
This clone was contributed by the Brain Molecular Anatomy Project
                 BU610605

BU610605

ULM-FCO-caq-f-07-0-UI.rl NIH BMAP FCO Mus musculus cDNA clone
ULM-FCO-caq-f-07-0-UI 5', mRNA sequence.
AlaArgPheAspTyrAsnTyrAspAsnSerPheArgValThrSerMetGlnAlaVallle 339
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                                                                                                                                                     243 CAGTITGGAAAATICGGAGTGATATACTACGACATCAACCAAATCATTCCACGGCCGTG 302
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TITLE
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ResGen, Invitrogen Corp. Note: this is a NH_MGC Library."
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             517
                                                                                537
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
      GluAspGlyPheLeuArgGlnArgGlyGlyAspIlePheGluTyrAsnSerAlaGlyLeu
                                                                     518 LeulleLysAlaTyrAsnArgAlaGlySerTrpSerValArgTyrArgTyrAspGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 GlyMetLeuLysThrIleAsnLeuGlnAsnGluGlyPheThrCysThrIleArgTyrArg
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ph.D. cDNA Library Preparation: ResGen, Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution: MGC clone distribution information can thus./image.lln.gov
http://image.lln.gov
Htg://image.lln.gov
Rlate: LLAM13799 row: d column: 11
High quality sequence stop: 677.
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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79.39%
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AGENCOURT 8843351 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6329777 5', mRNA Sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="MHIOB" (phage-resistant)" /clone_lib="NIH_MGC_130" /clone_lib="NIH_MGC_130" /note="Organ: otcoysts; Vector: pCMV-SPORT6.1; Site_l: BcoRV, Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library.
                         541
                                                                                                                                            IleArgAspArglleThrArgLeuGlyAspValGlnTyrLysMetAspGluAspGlyPhe 501
                                                                                                                                                                                                                         LeuArgGlnArgGlyGlyAspilePheGluTyrAsnSerAlaGlyLeuLeuIleLysAla 521
                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I Chases 1 to 931.

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (WGC)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ph.D. and Nancy L. Freeman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       þe
542 GGAAACCTCCACTTGCTCAACCCCAGCAGCAGCGCCCGCTGACCCCTCTGCGCTTATGAC
                                                                                                                                                                   TyrasnargalaglySerTrpSerValargTyrargTyraspGlyLeuGlyArgArgVal
                                                                GlyAsnLeuHisLeuLeuSerProGlyAsnSerAlaArgLeuThrProLeuArgTyrAsp
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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Mus musculus
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                                                                                                                                                  / Strain="colored" |
/ Strain="colored" |
/ Strain="colored" |
/ Strain="colored" |
/ Strain="colored" |
/ Strain="whole brain" |
/ Gev stage="embryollo.5 dpc" |
/ Jab_host="DH10B (T1 phage resistant)" |
/ Glone="Lib="MIBMAP_FCO" |
/ Clone="Lib="MIBMAP_FCO" |
/ Site 2: Not I; The library was constructed_according to Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRna was size fractionated on a 1% agarose gel: First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYx.Asc vector. The library tag sequence located between the Not I site and the polyh tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Amatomy Project University of Iowa Mouse Brain Molecular Amatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instrutues of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator:"
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Mismatches:
Indels:
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Matches:
                                                                                                'organism="Mus musculus"
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                                                          Location/Qualifiers
                                                                                                                     /mol_type="mRNA"
/strain="C57BL/6"
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1174.00
93.85%
79.62%
41.27%
                       (BMAP)
Seg primer: pYX-5.
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/dev stage="1,5, and 15 days newborn"
/dev stage="1,5, and 15 days newborn"
/lab host="BH10B (T1 phage resistant)"
/clone lib="Will BMAP GVO"
/note="Organ: Brain; Vector: pXx- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonafo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on al% agarose
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoR I adaptor, digested with NotI and then cloned
directionally into pXx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                             Contact: Robert Strausberg, Ph.D.
Email: capaber-remail.nin.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Discribution information on be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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Mismatches:
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/clone="IMAGE:30546171"
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Location/Qualifiers
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/mol_type="mRNA"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                   LysThrTrpSerTyrThrTyrLeuGluLysSerMetValLeuLeuLeuHsSerGlnArg
                                                                                                                                AGCGAAAAGGTGGACTATGACAGCCAGGGAAGATCGTATCTCGGGTCTTTGCCGATGGG
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|GCTGGCCACACCATGCAGCATCGGTACTTGGCTACTACCGCAACATCTACAATCCC
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UI-M-GV0-cjh-j-04-0-UI.rl NIH BMAP GV0 Mus musculus cDNA clone
IMAGE:30546171 5', mRNA sequence.
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is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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/note="organ: Braim, Vector: pXX- Asc; Site_1: BcoR I;
/site_2: Not I; The library was constructed according
/site_2: Not I; The library was osnitucted according
/site_2: Not I; The library was primed with oligo-dr
/gel: First strand cDNA synthesis was primed with oligo-dr
/gel: First strand cDNA synthesis was primed with oligo-dr
/gel: First strand cDNA was
/size selected according to mRNA size fraction, ligated
/with BcoR I adaptor, digested with Not! and then cloned
/directionally into pXX-Asc vector: The library tag
/sequence located between the Not I site and the polyA tail
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Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
thttp://genome.uiowa.edu/distribution/mousefi.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 758)

11 (bases 1 to 758)

12 (harbi-/mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                       423
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                                                          GAACATCTACCAGCCCCCGGAAGGCAACGCCTCAGTCATTCAGGACTTCACTGAGGATGG
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UI-M-FYO-cez-f-24-0-UI.rl NIH_BMAP_FY0 Mus musculus CDNA clone
                                    IThrMetProAsnValAlaArgGlnThrLeuGluThrIleArgSerValGlyTYrTYrAr
                                                                                                            nAspPheThrGluAspGl
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/clone="IMAGE:6844153"
/tissue_type="whole_brain"
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Location/Qualifiers
1. 758
/ organism="Mus musculus"
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
063W14 of library G from Tetraodon nigroviridis, genomic survey
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgAspArglleThrArgLeuGlyAspValGlnTyrLysMetAspGluAspGlyPheLeu 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     681 CGAGACAGAATCACTCGACTGGTGATGTTCAATATCGGTTGGATGAAGATGCTTTCCTA 740
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Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fizames, C., Fischer, C., Bonneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                              LeuMetTyrTrpMetThrValGlnTyrAspAsnMetGlyArgValValLysLysGluLeu
                                                                                                                                                                                 CTCATGTACTGGATTACAATTCAGTATGATAACATGGGTCGGGTAACCAAGAGATT
                                                                                                                                                                                                                        LysValGlyProTyrAlaAsnThrThrArgTyrSerTyrGluTyrAspAlaAspGlyGln
                                                                                                                                                                                                                                                 AsnLeuHisLeuLeuSerProGlyAsnSerAlaArgLeuThrProLeuArgTyrAspIle
                          AAGTITGGAGTITATATATATGATATTAACCAGATCATTTCTACAGCTGTAATGACCTAT
                                                                ThrLysHisPheAspAlaTyrGlyArgMetLysGluValGlnTyrGluIlePheArgSer
                                                                                        LeuGlnThrValSerIleAsnAspLysProLeuTrpArgTyrSerTyrAspLeuAsnGly
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Nat. Genet. 25 (2), 235-238 (2000)
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/lab_host="DH10B (phage-resistant)"
/clone lib="MIH MGC 9"
/clone lib="MIH MGC 9"
/note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 GluThrLeuTyrAspThrThrLysValSerPheThrTyrAspGluThrAlaGlyMetLeu 282
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                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at: image.llnl.gov
High quality sequence start: 24
High quality sequence stop: 755.
Location/Qualifiers
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                                                                                                                                                                                                    (MGC)
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                                                                                                                                                                 A MANAGE ALTP://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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                                   BE741784.1 GI:10155776
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95.87%
82.23%
38.77%
                                                                            Homo sapiens (human)
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Best Local Similari
mRNA
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/de_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:3056758"
/tissue_type="whole brain"
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/lab host="DH10B (TI phage resistant)"
/clone lib="NIH BMAP GIO"
/note="Organ: Brain, Vector: pYX- Asc, Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCCAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                           UI-M-GIO-chg-a-23-0-UI.rl NIH BMAP_GIO Mus musculus cDNA clone
IMAGE:30536758 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contract: Robert Strausberg, Ph.D.
Contract: Robert Strausberg, Ph.D.
Contract: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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            432 ArgTyrSerTyrGluTyrAspAlaAspGly
                                              Location/Qualifiers
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/strain="C57BL/6"
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                     nucleic search, using frame_plus_p2n model
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Database

Result No.

845978

Minimum DB Maximum DB

Searched:

DNA encod

Human

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Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzhelmer's disease or
                                                        "Single nucleotide polymorphism (SNP)"
                            "Single nucleotide polymorphism (SNP)'
"Single nucleotide polymorphism (SNP)
                                                                                                                                                                                                                                                 A, Patturajan M, Vernet CAM, Malyankar UM, Kekuda
Anderson D, Shimkets RA, Burgess CE, Zerhusen BD,
Casman SJ, Boldog FL, Smithson G, Li L, Ji W;
                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 50-52; 318pp; English
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                                                  /*tag= c
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2000US-025314P.

2001US-0288153P.

2001US-0294075P.

2001US-0311590P.

2001US-0311590P.

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2001US-0315617P.
                                       replace(260,A)
/*tag= c
                                                                                                                   19-DEC-2001; 2001WO-US050331
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P-PSDB; ABG70388.
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02-MAY-2001;
29-MAY-2001;
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10-AUG-2001;
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29-AUG-2001;
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The present invention relates to new NOVX polypeptides. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, considers (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, neurodegenerative disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, contentials, learning and memory defects, infertility, congenital heart of pancreatitis, learning and memory defects, infertility, congenital heart of effects, acne, hair growth, pigmentation disorders, endocrine disorders, constroyr diseases, bone marrow transplantation, endocrine diseases, callergy and inflammatchin, nephrological disorders, urinary system callergy and inflammatchin, nephrological disorders, urinary system callergy and inflammatchin, nephrological disorders, urinary system consent nucleic acid sequence represents a NOVX gene. This sequence precedes a NOVX protein of the invention

BP; 1968 A; 2437 C; 2271 G; 1678 T; 0 U; 0 Other; Sequence 8354

2.79e-278

Alignment Scores: Pred. No.:

Score: Percent Similarity: Best Local Similarity: Query Match: DB:	2845.00 100.00% 100.00% 100.00%	Matches: Conservative: Mismatches: Indels: Gaps:	541
US-10-029-020-14_COPY_1760_2300 (1-541) x ABS52100 (1-8354)	_1760_2300 (1-541)	x ABS52100 (1-	-8354)
Oy 1 TyrTyrI]	leglyAlaAspGlySerl	LeuArgleuLeuLeu	1 TyrTyrIleGlyalaAspGlySerLeuArgLeuLeuLeuAlaAsnGlyMetGluValAla 20
Db 5312 TACTACA	rcegecceargecre	rieceecrecrecre	5312 TACTACATCGGGGCCGATGGCTCCTTGCGGCTGCTGCTGGCCAACGGCATGGAGGTGGCG 5371

6331 6451 6391 5971 6031 6091 6211 6271 5791 5851 5911 6151 360 380 5731 340 5491 240 260 280 300 320 160 100 09 GluThrProLeuProlleAspLeuTyrArgTyrAspAspValSerGlyLysThrGluGln GlnArgGlnTyrIlePheGluPheAspLysAsnAspArgLeuSerSerValThrMetPro 5912 AACGIGGCGCGGCAGACACIAGAGACCAICCGCTCAGGGGCTACTACAGAAACAICTAT MetLeuLysThrIleAsnLeuGlnAsnGluGlyPheThrCysThrIleArgTyrArgGln IleGlyProLeuIleAspArgGlnIlePheArgPheThrGluGluGlyMetValAsnAla ATTGGGCCCCTGATTGACCGACAGATCTTCCGCTTCACTGAGGAAGGCATGGTCAACGCC ArgPheAspTyrAsnTyrAspAsnSerPheArgValThrSerMetGlnAlaValIleAsn ceritidactacaactateacaacaectreegggagaccagcatgcaggctaaac AspGlyLysThrTrpSerTyrThrTyrLeuGluLysSerMetValLeuLeuLeuHisSer GATGGGAAGACATGGAGCTACACATACTTAGAGAAGTCCATGGTGCTGCTACTACACAGC cácácáciáráratctroactrocacaacaatcacceccrotrotrograccarecco GlnProProGluGlyAsnAlaSerValIleGlnAspPheThrGluAspGlyHisLeuLeu HisThrPheTyrLeuGlyThrGlyArgArgVallleTyrLysTyrGlyLysLeuSerLys cacacctrictaccredecacredececacacacataracaacraracaaacrercaaae LeuAlaGluThrLeuTyrAspThrThrLysValSerPheThrTyrAspGluThrAlaGly <u> CTGCCAGAGACGCTCTATGACACCACCAAGGTCAGTTTCACCTATGACGAGACGGCAGGC</u> SerleuAspPheAspArgValThrArgThrGluLyslleTyrAspAspHisArgLysPhe ThrieuligileleuTyrlaglinalaGlyargProSerLeuTrpSerProSerSerArg croanrecreteacereacaracrecerreessinacerrecresser | IleMetSerGluArgMetGluTyrAspGlnAlaGlyArglleThrSerArgllePheAla 41 ValThrLeuProlleAspAsnGlyLeuAsnLeuValGluTrpArgGlnArgLysGluGln 61 AlaArgGlyGlnValThrValPheGlyArgArgLeuArgValHisAsnArgAsnLeuLeu 5492 GCTCGGGGCCAGCTCACTCTTTGGGCGCCGGCTGCGGGTGCACAACCGAAATCTCCTA LeuAsnGlyValAsnValThrTyrSerProGlyGlyTyrIleAlaGlyIleGlnArgGly 21 LeuGlnThrGluProHisLeuLeuAlaGlyThrValAsnProThrValGlyLysArgAsn 301 6212 6272 6332 241 6032 261 281 6152 321 341 5852 6092 5612 121 5672 141 5732 5792 161 181 201 221 81 5552 101 Db ð g à d

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6572 GAĞCTGAAGGTAGGACCCTACGCCAATACCACTCGCTACTCCTATGAGTATGATGCTGAC 6631
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ThrHisThrLysHisPheAspAlaTyrGlyArgMetLysGluValGlnTyrGluIlePhe
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ABS78652 standard; cDNA; 8645 BP. ABS78652; RESULT 2 ABS78652 

(first entry) 16-DEC-2002

Human cDNA encoding CGDD10, INCYTE 7488573CB1.

Human; ss; gene; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; bolirhosis; hepatitis; parcxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thrombocytopania; developmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS; reproductive disorder; Alzheimer disease; Parkinson's disease; asthma; inflammatory disorder; infertility; autoimmune disorder; gout; allergy; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; multiple sclerosis; osteoarthritis; irritable bowel syndrome; whithere sclerosis; osteoarthritis; osteoporosis; pancreatitis; rheumatoid arthritis.

Homo sapiens,

WO200272830-A2

19-SEP-2002

08-FEB-2002; 2002WO-US003715

09-FEB-2001; 2001US-0268111P. 23-FEB-2001; 2001US-0271175P. 08-MAR-2001; 2001US-0274503P. 2001US-0274552P 08-MAR-2001; 09-MAR-2001;

(INCY-) INCYTE GENOMICS INC.

Baughn MR; Burford N; Yao MG, Ison CH, Lu Y, Warren BA, Elliott VS, Xu Y, Gietzen KJ, Tang TY, Lal PG, Duggan BM, Richardson TW, Tran UK, Khare R, Walia NK; Ding L, Lu DAM, Yue H,

WPI; 2002-723356/78. P-PSDB; ABG97359

differentiation and New human proteins associated with cell growth, differentiation death, useful for diagnosing, treating or preventing autoimmune inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atherosclerosis or hepatitis.

Claim 5; Page 175-178; 181pp; English.

The invention relates to an isolated polypeptide comprising GDD1-12 (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to GCDD, a biologically active fragment or an immunogenic fragment. Also included are the CGDD caid sequence at least 90% identical to GCDD, a biologically active polymucleotides encoding GCDD-12, a recombinant polymucleotide and a comprising the recombinant polymucleotide, an anti-doynmoleotides, a cell transformed with the recombinant polymucleotide, a transgenic organism comprising the recombinant polymucleotide and a antibody, screening for compounds which bind to/modulate or are companists of GCDD polymucleotide microarray. The polypeptides, polymucleotide microarray. The polypeptides, polymucleotide microarray. The polypeptides, polymucleotide and a agonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of GCDD, polymucleotide microarray. The polypeptides, polymucleotides, polymucleotide microarray engines associated with aberrant expression of GCDD, polymucleotide microarray engines, an entit of a particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, propartitis, paroxysmal nocturnal haemoglobinuria, polycythaemia disorders (e.g. renal tubular acidosis, anaemia or mental retardation) cell-popsy), reproductive disorders (e.g. Alzheimer disease, Parkinson's disease or the menstrual cycle), or autoinmune/inflammatory disorders (e.g. AlDS, thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, contact dermatitis, parasitic, proteins associated with cgdD. The present sequence encodes contact dermatitis associated with cgdD. The present sequence encodes 

Sequence 8645 BP; 2060 A; 2494 C; 2319 G; 1771 T; 0 U; 1 Other;

Matches: Conservative: Mismatches: Length: Indels: 2.93e-278 2845.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match:

US-10-029-020-14\_COPY\_1760\_2300 (1-541) x ABS78652 (1-8645)

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Human; NOVI; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive; Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic; Anorectic; Antiasthmatic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic; Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant; Gene Therapy; NOV; cancer, heart disease; inflammation; authormune disorder; allergy; blood disorder; AlloS; diabetes; obesity; asthma; IgA nephropathy; cirrhosis; arthritis; Allabetma; disease; infection; stroke; muscular dystrophy; epilepsy; wasting disorder; TEN-M4 like protein; chromosome 11; gene; ds.
                                                                                                                                                                                                                                        AlaTyrAsnArgAlaGlySerTrpSerValArgTyrArgTyrAspGlyLeuGlyArgArg
                                                                                                                                                                                                                                                                                                                                                                        6921 GCCTACAACCGGGCTGGCGGCTGTCAGGTACCGCTACGATGGCCTGGGGCGGCGC
                                                                                                                                                                                           481 ASDIIGAKGASPANGIIGTHKANGLOUGIYASPVALGINTYKLYSMELASPGIUASPGIY
                                                                  AsnGlyAsnLeuHisLeuLeuSerProGlyAsnSerAlaArgLeuThrProLeuArgTyr
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/product= "NOV1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NOV1, TEN-M4 like protein, coding sequence.
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10-JAN-2001; 2001US-0260831P.
28-FEB-2001; 2001US-0272338P.
09-MRR-2001; 2001US-0274876P.
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                                                                                                                                                                                                                                                                                    IleMetSerGluArgMetGluTyrAspGlnAlaGlyArgIleThrSerArgIlePheAla
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                                                                                                                                               5661 ACCCTCGGATTCTGTACGACCAGGCGGGCGCCCAGCCTCTGGTCACCCAGCAGGAG
                                                                                                                                                                                                                           SerLeuAspPheAspArgValThrArgThrGluLysIleTyrAspAspHisArgLysPhe
                                                           rcriciogaciticaticocitaacacacacacacatetatetateacaccaccacastic
                                                                                                        ThrLeuArg11eLeuTyrAspG1nAlaGlyArgProSerLeuTrpSerProSerArg
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pharmacogenomics. P~PSDB; ABB98401 

The present sequence is a coding sequence for a NOV protein. The NOV proteins and coding sequences are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma, IgA nephropathy, cirhosis, arthritis, AIDsheimer's disease, infections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. NOV1 is a TEN-M4 like protein and the NOV1 gene is localised to chromosome 11 NOVX polypeptides and encoding polynucleotides, useful for preventing treating NOVX-associated disorders e.g. cancer, inflammation, or Alzheimer's disease, and in chromosome mapping, tissue typing or Claim 9; Page 8-9; 358pp; English.

Sequence 8438 BP; 2001 A; 2434 C; 2268 G; 1735 T; 0 U; 0 Other;

		8438	541	į		>	7	7
(0 0 (= 00 = 1		Length:	Matches	Conservative	Mismatches.		Indels:	Gaps:
		6.95e-276	2821.50	98.72%	98.72%	1 1	37.T.8	ø
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-14_COPY_1760_2300 (1-541) x ABN85378 (1-8438)	TyrTyrileGlyalaAspGlySerLeuArgLeuLeuAlaAsnGlyMetGluValAla 20 	LeuglnThrGluProHisLeuLeuAlaglyThrValAsnProThrValGlyLysArgAsn 40 	ValThrLeuproileAspAsnGlyLeuAsnLeuValGluTrpArgGlnArgLysGluGln 60 	AlaargGlyGlnValThrValPheGlyargArgLeuargValHisasnarg 77 	AsnLeuLeuSerLeuAspPheAspArgValThrArgThrGluLysIleTyrAspAspHis 97 	ArglysPheThrLeuArg11eLeuTyrAspG1nA1aG1yArgProSerLeuTrpSerPro 117 	SerSerargleuasnglyvalasnvalthrtyrserproglyglyfyrilealaglylle 137 	GlnargGly1leMetSerGluargMetGluffyraspGlnalaglyarg1leThrSerarg 157 	lephealaaspGlyLysThrTpSerTyrThrTyrLeuGluLysSer 173 	Met Valleuleuleuhi sSerginargginfyzilePhegiuPheasplysAsnasparg 193 	LeuSerSerValThrMetProAsnValAlaArgGlnThrLeuGluThrIleArgSerVal 213
-14_COPY_176	TyrTyrIlegl	LeuGlnThrGlv            CTGCAGACTGAG	ValThrLeuPro 	AlaargGlyGlr 	AsnLeuLeuSez 	ArglysPheThr               GCAAGTTCACC	SerSerArglev                AGCAGCAGGCTG	GlnargGly1le 	IlePheAlaAsp 	MetValleuleu 	LeuSerSerVal
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전	1 2	GYYYYYYY GABILLETYICHRYCEROGIUGIYASAALASSEVAIIISGIDASDPhe 233 
Qy Db	234	ThrGluAspGlyHisLeuLeuHisThrPheTyrLeuGlyThrGlyArgArgVallleTyr 253 
ې کې	254	27.
Oy Ub	274	PheThr 293
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<b>a</b> (	6278	GAGGAAGGCATGGTCAACGCCCGTTTTGACTACAACTATGACAACAGCTTCCGGGTGACC 6337
ž A	334 6338	334 SerMetGinAlavalileAsmGluThrProLeuProlleAspLeuTyrArgTyrAspAsp 353 
λo	354	
qq	6398	GIGTCAGGCAAGACAGAGCAGITIGGGAAGTITIGGTGTCAITTACTAIGACATTAACCAG 6457
٥y	374	IlelleThrThrAlaValMetThrHisThrLySHisPheAspAlaTyrGlyArgMetLys 393
qq	6458	ATCATCACCACAGCTGTCATGACCCACACCAAGCATTTTGATGCATATGGCAGGATGAAG 6517
ò	394	GluValGlnTyrGlullePheArgSerLeuMetTyrTrpMetThrValGlnTyrAspAsn 413
qq	6518	GAAGTGCAGTATGAGATCTTCCGCTCGCTCATGTACTGGATGACCGTCCAGTATGATAAC 6577
λo	414	MetGlyArgValValLysLysGluLeuLysValGlyProTyrAlaAsnThrThrArgTyr 433
qq	6578	CTACGCCAATACCACTCGCTAC 6
<i>\delta</i>	434	SerTyrGluTyrAspAlaAspGlyGlnLeuGlnThrValSerIleAsnAspLysProLeu 453
ð	m	9
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à	474	ArgLeuThrProLeuArgTyrAsp11eArgAspArg11eThrArgLeuG1yAspVa1G1n 493
q	6758	9
λ	494	TyrLysMetAspGluAspGlyPheLeuArgGlnArgGlyGlyAspIlePheGluTyrAsn 513
අ	œ	68
λŏ	514 8	SerAlaGlyLeuLeulleLysAlaTyrAsnArgAlaGlySerTrpSerValArgTyrArg 533
۵	6878 T	
à	534 T	TyrAspGlyLeuGlyArgArgVal 541
qq	6938 T	CGATGGCCTGGGGCGCGCGTG

RESULT 4
AAH14183
ID AAH14183 standard; cDNA; 3614 BP.

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The present invention describes primer sets for synthesising 5602 full-

[ ength cDNAs defined in the specification. Where a primer set comprises:

[ al an oligo-dr primer and an oligonucleotide comprises one of the 5602 complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the nucleotide comprises at least 15 nucleotides; or (b) a combination of a nolynucleotide which complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence of polynucleotide which comprises a 1'-end sequence of polynucleotide comprises at least 15 nucleotides and the combination of configuration. The primer sets can be used in antisense therapy and in specification. The primer sets can be used in antisense therapy and in specification. The primer sets can be used in antisense therapy and in specification. The primer sets can be used in antisense therapy and in specification. The primer sets can be used in antisense therapy and in specification. The primer sets can be used in suffer the principal confides, particularly full-length cDNAs. The primers are also useful for the centric and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the AAH313633 to AAH313633 to AAH313633 to AAH313633 to AAH313632 to AAH33632 represent the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration of the configuration o
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                                                                                                                                                                          detection; diagnosis; antisense therapy; gene therapy; ss.
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Otsuki T;
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Sugiyama T, Wakamatsu A, Nagai K,
                                                                                          Human cDNA sequence SEQ ID NO:11430
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2000JP-00118776.
2000JP-00183767.
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27-AUG-1999;
11-JAN-2000;
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Matches:
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78.49%
   Sequence 3614
                                      Pred. No.:
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Conservative: Mismatches:

Indels:

Best Local Similarity: Query Match:

Percent Similarity:

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> 1 TyrTyrIleGlyAlaAspGlySerLeuArgLeuLeuLeuAlaAsnGlyMetGluValAla 20 (1-3614)US-10-029-020-14\_COPY\_1760\_2300 (1-541) x AAH14183

1291 1231 1111 1171 1051 360 380 260 ArgPheAspTyrAspAsnSerPheArgValThrSerMetGlnAlaVallleAsn 340 280 300 320 200 991 LeuAsnGlyValAsnValThrTyrSerProGlyGlyTyrIleAlaGlyIleGlnArgGly 140 141 IleMetSerGluArgMetGluTyrAspGlnAlaGlyArgileThrSerArgIlePheAla 160 180 871 101 ThrieuArgileLeuTyrAspGlnAlaGlyArgProSerLeuTrpSerProSerSerArg 120 691 811 100 272 TACCAGATTGGTTATGACGGCTCCCTCAGAATTATCTACGCCAGTGGCCTGGACTCACAC 331 332 TACCAAACAGAGCGGCACGTTCTGGCTGGCACGCTAATCCGACGGTTGCCAAAAGAAAC 391 511 80 9 GluThrProLeuProlleAspLeuTyrArgTyrAspAspValSerGlyLysThrGluGln PheGlyLysPheGlyValileTyrTyrAspileAsnGlnileIleThrThrAlaValMet AGAİTİĞACİAİAGCIAİGACAACAGCİTİTCGAGIĞACCAGCAIĞCAĞGGIĞIĞALÇAAİ GlnArgGlnTyrIlePheGluPheAspLysAsnAspArgLeuSerSerValThrMetPro 201 AsnyalAlaArgGlnThrLeuGluThrileArgSerValGlyTyrTyrArgAsnIleTyr 221 GlnProProGluGlyAsnAlaSerValileGlnAspPheThrGluAspGlyHisLeuLeu 932 AACCCCCCGGAAAGCAACGCTCCATCATCACGAGTACAACGAGGAGGGCTGCTTCTA 241 HisThrPheTyrLeuGlyThrGlyArgArgValIleTyrLysTyrGlyLysLeuSerLys LeuAlaGluThrLeuTyrAspThrThrLysValSerPheThrTyrAspGluThrAlaGly MetLeuLysThr11eAsnLeuGlnAsnGluGlyPheThrCysThr1leArgTyrArgGln IleGlyProLeuileAspArgGlnIlePheArgPheThrGluGluGlyMetValAsnAla ATTGGTCCCCTGATTGACAGGCAGATTTTCCGCTTTAGTGAAGATGGGATGGTAAATGCA cigargeccerciaiterceratricarceacadercaaarreceacarceaededede AspGlyLysThrTrpSerTyrThrTyrLeuGluLysSerMetValLeuLeuLeuHisSer GATGGTAAAACATGGAGTTACACATATTTAGAAAAGTCCATGGTTCTTCTGCTTCATAGC 41 ValThrLeuProlleAspAsnGlyLeuAsnLeuValGluTrpArgGlnArgLysGluGln 452 GCCCAAGGGAAAGTCAATGTCTTTGGCCGCAAGCTCAGGGTTAATGGCAGAAACCTCCTT SerLeuAspPheAspArgValThrArgThrGluLysIleTyrAspAspHisArgLysPhe 61 AlaArgGlyGlnValThrValPheGlyArgArgLeuArgValHisAsnArgAsnLeuLeu LeuGlnThrGluProHisLeuLeuAlaGlyThrValAsnProThrValGlyLysArgAsn 361 1052 281 1112 1172 1232 261 301 321 341 692 81 121 632 752 181 812 872 161 21

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Human NOV15c encoding cDNA SEQ ID NO:39. BP. ABQ82345 standard; cDNA; 8473 (first entry) 17-DEC-2002 ABQ82345; 

Human, NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidabetic; antiinflammatory; fungicide; antirhematic; antiathritic; immunosupressive; antiallergic; virucide; antianemic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; pick's disease; orsicular transport disease; Alzheimer's disease; allergy; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; vaccine; autoimmne disease; allergic reaction; autoimmune haemolytic anaemia; arthritis; gene; chromosome 4; ss.

Homo sapiens.

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Location/Qualifiers
                                        /product= "NOV15c"
               258. .8144
                            /*tag= a
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WO200262999-A2

15-AUG-2002

31-DEC-2001; 2001WO-US049976.

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2001US-0259415P.
2001US-0259785P.
2001US-0259814P.
2001US-0279863P.
2001US-0279833P.
2001US-027833P.
2001US-0284447P.
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2001US-0284683P.
2001US-0284683P.
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                                   18-APR-2001; 2
25-APR-2001; 2
29-MAY-2001; 2
                 09-MAR-2001; 2
29-MAR-2001; 2
29-MAR-2001; 3
        04-JAN-2001;
             20-FEB-2001;
                              13-APR-2001;
                                                 16-AUG-2001;
                                                      17-AUG-2001;
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## (CURA-) CURAGEN CORP.

Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;
J, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;
Patturajan M, Gusev V, Gangolli RA, Guo X, Shenoy S;
Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
Smithson G, Millet I, Macdougall JR; Spyter ...,
Malyankar U, Shimketb ...,
Kekuda R, Patturajan M, C
Rastelli L, Casman SJ, Br
R. Ther E, Smithson G, M Spytek KA,

2002-732706/79. P-PSDB; ABP53588. New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune

Claim 8; Page 119-121; 444pp; English.

The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvalsant, cerebroprotective, nocitopic, cardiovascular, antidiabetic, antianlergic, antiantenticic, virucide, immunosuppressive, antiallergic, antiantentic, antibatchritic, virucide, immunosuppressive, antiallergic, antinanaemic, antibacterial, fungicide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers (e.g. petitedenia, lymphoma, melanoma or cancer of the liver, lung, muscle, covary, testis and uterus), neurological disorders (e.g. epitepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or pick's disease, disorders (e.g. ulcerative colitis, or gattric and duodenal disorders), autoimmune diseases (e.g. ulcerative colitis, or gattric and duodenal disorders), autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be biological samples (tissue typing), and in forensic identification of a hiological samples (tissue typing), and inferensic identification of a hiological samples (tissue typing), and inferensic identification of a hiological samples (tissue typing), and inferensic identification of a sample. The present sequence encodes human NOV15c, which biological s located on c

Sequence 8473 BP; 2301 A; 2017 C; 2145 G; 2006 T; 0 U; 4 Other;

Conservative: Mismatches: Length: Matches: Indels: 4.98e-216 2233.00 88.91% 74.68% 78.49% Similarity: Percent Similarity: Alignment Scores: Query Match Best Local .. No.:

US-10-029-020-14\_COPY\_1760\_2300 (1-541) x ABQ82345 (1-8473)

TyrTyrIleClyAlaAspGlySerLeuArgLeuLeuLeuAlaAsnGlyMetGluValAla 20

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GTTTACAGTAAAGGCAGTGGCTGGACAGTGATCTACCGTTATGACGGCCTGGGAAGGCGT 6749
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            PheleuArgGlnArgGlyGlyAspilePheGluTyrAsnSerAlaGlyLeuLeulleLys
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                                              ArgSerLeuMetTyrTrpMetThrValGlnTyrAspAsnMetGlyArgValValLysLys
ThrHisThrLysHisPheAspAlaTyrGlyArgMetLysGluValGlnTyrGluIlePhe
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New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
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04-JAN-2001, 2001US-0259785P.
20-FEB-2001; 2001US-0269814P.
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Rastelli L, Casman SJ,
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P-PSDB; ABP53589.
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Shenoy S; S. Ellerman K;

Gorman L;

net CAM, Bisen A, Liu X;
lev VT, Spaderna SK, Gorman
Gangolli EA, Guo X, Shenc
Burgess CE, Edinger S, El

where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, nototropic, cardiovascular, antidabetic, antimilalmametory, antitheumatic, antibatchritic, virucide, immunosuppressive, antimiallergic, antianaemic, antibacterial, fungicide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers (e.g. -putkaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alabeimer's disease or pick's disease, disorders of vesicular transport (e.g. cystic fibrosis, diseases), disorders of vesicular transport (e.g. cystic fibrosis, diseases), disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), and protozoal infections. The NOVX proteins can be used as immunogens to anaemia, or theumatoid arthritis), viral, bacterial, fungal, helminthic and protozoal infections. The NOVX proteins can be used as immunogens to used in chromosome mapping, identifying individuals from minute biological samples (tissue typhng), and in forensic identification of a bological sample. The present sequence encodes human NOV15d, which is The present invention describes novel human proteins designated NOVX. on chromosome 4 biological samples biological sample. located on chromoso

Sequence 8487 BP; 2306 A; 2029 C; 2148 G; 2001 T; 0 U; 3 Other;

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	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:	x ABQ82346	enArgLeuLeuL	
	4.99e-216	2233.00	88.91\$	74.68%	78.49%		0_2300 (1-541)	1 TyrTyrileglyAlaAspGlySerLeuArgLeuLeuAlaAsnGlyMetGl	
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LeuGlnThrGluProHisLeuLeuAlaGlyThrValAsnProThrValGlyLysArgAsn 40

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41 ValThrLeuProlleAspAsnGlyLeuAsnLeuValGluTrpArgGlnArgLysGluGln
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5246 ATGACTTTGCCTGGGGGAACGGTCAAAACTTGGTGGAAATGGAGATTCCGAAAAGAGCAA
                                                                                               AlaArgGlyGlnValThrValPheGlyArgArgLeuArgValHisAsnArgAsnLeuLeu
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13-ARR-2001; 2001US-0283889P.
18-APR-2001; 2001US-0284447P.
25-APR-2001; 2001US-0286683P.
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                       ArgSerLeuMetTyrTrpMetThrValGlnTyrAspAsnMetGlyArgValValLysLys 420
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02-JAN-2001; 2001US-0259415P.
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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, noticarchitic, virucide, antidiabetic, antiallergic, antialtergic, antiarthritic, virucide, immunosuppressive, antiallergic, antiantendic, antiarthritic, virucide, continuosuppressive, antiallergic, antiantendic, antiarthritic, virucide, immunosuppressive, antiallergic, antiantendic, in gene control of an antiallergic, antiantendic, antiantendic, in gene control of a medicament for treating a syndrome associated with a mandacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder. Such as cancers (e.g. el-examin, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic crebrovascular disease, Alzheimer's disease or pick's cancer, disease, disorders (e.g. orgatic fibrosis, diseases), disorders (e.g. ulcremin diseases (e.g. ulcremin diseases), control of a disorders (e.g. ulcremin diseases) control of a cutoimmune diseases (e.g. ulcremin diseases) or gastric and quodenal disorders), cancernia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX proteins can be used as immunogens to biological samples (tissue typing), and in forensic identification of a biological samples (the present sequence encodes human NOV15b, which is
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                                                             Spytek KA, Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;
Malyankar U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;
Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
Gunther E, Smithson G, Millet I, Macdougall JR;
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P-PSDB; ABP53587.
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 ArgSerLeuMetTyrTrpMetThrValGlnTyrAspAsnMetGlyArgValValLysLys
            6502 AGGICGCICAIGIACAGATIACAAITCAGTATGAIAACAIGGGICGGGTAACAAGAGA
                                                     GluLeuiysValGlyProTyrAlaAsnThrThrArgTyrSerTyrGluTyrAspAlaAsp
                                                                                                         GlyGlnLeuGlnThrValSerIleAsnAspLysProLeuTrpArgTyrSerTyrAspLeu
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/product= "NOV15a"
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02-JAN-2001; 2001US-0259415P.
04-JAN-2001; 2001US-0259765P.
20-FEB-2001; 2001US-0259814P.
09-MAR-2001; 2001US-0279863P.
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                           5422 ATGACTTTGCCTGGCGAGAACGGTCAAAACTTGGTGGAATGGAGATTCCGAAAAAGAGCAA
  ValThrLeuProlleAspAsnGlyLeuAsnLeuValGluTrpArgGlnArgLysGluGln
                                                                         5482 GCCCAAGGGAAAGTCAATGTCTTTGGCCGCAAGCTCAGGGTTAATGGCAGAAACCTCCTT
                                                                                                                                       TCAGTTGACTTTGATCGAACAACAAGACAGAAAAGATCTATGACGACCACCGTAAATTT
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CTCTCAGAAAITITATATGATAGCACAAGAGTCAGTTTTACCTATGATGAAACAGCAGGA
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New NOVX polypeptides and polymucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
                                                                                                                   Tchernev VT, Spaderna SK, Gorman L, 1884 V, Gangolli EA, Guo X, Shenoy S; 1969 F, Burgess CE, Edinger S, Ellerman K; 1let I, Macdougall JR;
                                                                                                              Vernet CAM,
                                                                                                                                                                                                                                          Claim 8; Page 110-112; 444pp; English
                                                                                                                              Gusev V,
Boldog F,
Millet I,
    2001US-0279833P.
2001US-0283889P.
2001US-0284447P.
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                              25-APR-2001; 2001US-0286683F.
29-MAY-2001; 2001US-0294080F.
16-AUG-2001; 2001US-0312915F.
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Shimkets RA,
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--ther E, Smithson G,
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Malyankar U,
                                                            17-AUG-2001;
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Liu X;

Eisen A,

The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, noticathritic, virucide, immunosuppressive, anticallergic, antitanematic, antibacterial, fungicide, proteozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers convary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or Pick's disease, disorders of vestcular transport (e.g. epilepsy, stroke, clabetes mellitus, Grave's disease, astrointestinal disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. allergic reactions, autoimmune hamolytic and protozoal infections. The NoVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be used in chromosome mapping, identifying individuals from minute cological samples (tissue typing), and in forenatic identification of a biological sample. The present sequence encodes human NOV15a, which is

C; 2201 G; 2041 T; 0 U; 4 Other; BP; 2362 A; 2067 Sequence 8675

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5314 TACCAGATTGTTATGACGGCTCCCTCAGAATTATCTACGCCAGTGGCCTGGACTCACAC 5373
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Matches:
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41 ValīhrieuProlleAspAsnGlyLeuAsnLeuValGluTrpArgGlnArgLysGluGln
                       5434 ATGACTTTGCCTGGCGAGAACGCTCAAACTTGGTGGAATGGAGATTCCGAAAAGAGCAA
                                                 AlaArgGlyGlnValThrValPheGlyArgArgLeuArgValHisAsnArgAsnLeuLeu
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                             GluLeuLysValGlyProTyrAlaAsnThrThrArgTyrSerTyrGluTyrAspAlaAsp
                                          GlyGinLeuGlnThrValSerIleAsnAspLysProLeuTrpArgTyrSerTyrAspLeu
                                                                                                          AsnGlyAsnLeuHisLeuLeuSerProGlyAsnSerAlaArgLeuThrProLeuArgTyr
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Otsuki
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A, Nagai |
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                                                                                                                                                                                                                                                                                                                          AAH14671 standard; cDNA; 3270 BP.
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Wakamatsu
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2000JP-00118776.
2000JP-00183767.
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

Claim 8; SEQ ID NO 12354; 2537pp + Sequence Listing; English.

CDNAS.

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complementary strand of a polyuncleotide which comprises one of the s602 mucleotide sequences defined in the specification, where the nucleotide comprises at least 15 mucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polyuncleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence; where the complementary to a polyuncleotide which comprises a 5'-end sequence complementary to a coligonucleotide which comprises a 1'-end sequence, where the combination of the 5'-end sequence) are aleast 15 mucleotides and the combination of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in specification. The primer sets can be used in antisense therapy and in specification. The primers for specification in the primers are useful for synthesising polynucleotides, care therapy. The primers also useful for the fetal-length cDNAs. The primers are also useful for the count and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03166 to AAH13628 and AAH33633 to AAH13642 represent human cDNA sequences; AAB92446 to AAB95893 colligonucleotides, all of which are used in the exemplification of the
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483 TICGAAIACGAIATGIGGGACCGCCTGTCTGCCAICACCAIGCCCAGTGIGGCTCGCCAC
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antisense therapy; regulated;

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Kovacs KF,

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New isolated human differentially-regulated breast cancer polynucleotide and polypeptide, useful for diagnosing, staging, prognosticating, preventing and/or treating diseases and conditions relating to breast
   Breast cancer; cytostatic; gene therapy, antisense therapy, drug discovery; clinical medicine; forensic medicine; gene; chromosome 5q33.3; ds.
                                                                                                                                                                                                                                                 Claim 2; SEQ ID NO 79; 127pp + Sequence Listing; English.
                                                                                                                                           (ORIG-) ORIGENE TECHNOLOGIES INC
                                                                                                                03-OCT-2001; 2001US-0326526P.
14-MAY-2002; 2002US-00144194.
                                                                                                 02-OCT-2002; 2002WO-US031287
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P-PSDB; ABR58317.
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The invention relates to isolated polymucleotides which are differentially-regulated in breast cancer. The methods and compositions of the present invention are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and/or treating diseases and conditions relating to breast cancer, and may be used in gene therapy or antisense therapy. They can also be used in research, drug discovery, clinical medicine and forensic medicine. Sequences given in records ACCT2012-ACCT2074 represent polymucleotides of the invention that are differentially-regulated in breast cancer. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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LeuAsnGlyAsnLeuHisLeuLeuSerProGlyAsnSerAlaArgLeuThrProLeuArg
                             TyrAsplleArgAspArglleThrArgLeuGlyAspValGlnTyrLysMetAspGluAsp
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|TCCATTGACTATGAAAATATTCGGACTGAAAAGATCTATGATGACCACGGAAGTTC
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             U; 0 Other;
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                0;1
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Mismatches:
Indels:
                2112
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Matches:
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70.61%
75.10%
                  BP;
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                  Sequence 9695
                                              Alignment Scores:
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Reis-Bucklers corneal dystrophy, cytostatic; immunosuppressive; antiallergic; antiasthmatic; antiinfertility; antiinflammatory; antidiabetic; protozoacide; hepatotropic; virucide; ophthalmological; gynaecological; antiinfertility; immunostimulant; auditory; haemostatic; gene therapy; FCTR3a; neurestin-like protein; FCTR3f.
                                                                                     "Human FCTR3f"
                                                     Location/Qualifiers
                                                                                                                                                  2000US-0186592P.
2000US-0186718P.
2000US-0187293P.
2000US-0187294P.
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8385. .9729
                                                                                                                                     05-MAR-2001; 2001WO-US007160
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06-MAR-2000;
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# (CURA-) CURAGEN CORP

07-APR-2000; 2000US-0196018P. 03-JAN-2001; 2001US-0259548P.

ĸ Majumder Herrmann JL, Shimkets RA, Herrman Mezes PS, Rastelli L; Vernet CAM, Fernandes E, Macdougall J, Mishra V, 2001-596837/67. P-PSDB; AAU08681 Novel polypeptides designated as FCTRX polypeptides, useful in detection, prevention and treatment of a broad range of pathological states.

Claim 9; Page 37-39; 215pp; English

The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the nucleic acids encoding them. These sequences are useful for the treatment or prevention of numerous disorders including myelogenous leukaemia, carcinomas, melanomas, gliomas, astrocytomas, congenital meonatal carcinomas, melanomas, gliomas, astrocytomas, congenital meonatal carcinomas, melanomas, gliomas, astrocytomas, congenital meonatal calcinomas, familial myelodysplastic syndrome, familial myelodysplastic syndrome, mental mealth conditions, immunological calsorders, allorgy and infection, bronchial asthma, Avellino type castinophilia, lung diseases, reproductive disorders, infertility, male cosinophilia, lung diseases, reproductive disorders, infertility, male cosinophilia, lung diseases such as diabetes, Schistosoma mansoni chection Spinocerebellar ataxia, plasmodium falciparum parasitaemia, corneal dystrophy-dattice type I and Reis-Bucklers corneal dystrophy. This sequence represents DNA encoding the FCTR3a homologue FCTR3f

Sequence 9729 BP; 2548 A; 2629 C; 2438 G; 2114 T; 0 U; 0 Other;

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9729
382
89
69
           Length:
Matches:
Conservative:
Mismatches:
                                               Indels:
          3.92e-206
2136.50
87.06%
70.61%
                          Percent Similarity:
Best Local Similarity:
Alignment Scores:
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US-10-029-020-14\_COPY\_1760\_2300 (1-541) x AAS14089 (1-9729)

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|TACCAGGTCTGTAATAATGGTACCCTGAGGGTGATGCTAATGCTAATGGGATGGGTATCAGC 5420
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                                                         ValThrLeuProlleAspAsnGlyLeuAsnLeuValGluTrpArgGlnArgLysGluGln
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                                                                                                                                     61 AlaArgGlyGlnValThrValPheGlyArgArgLeuArgValHisAsnArgAsnLeuLeu
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Majumder K;

Herrmann J,

Shimkets R,

Mezes PS,

Rastelli L;

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03-MAR-2000; 2000US-0186592P.
                                                                                                                    Vermet C, Fernandes E,
Macdougall J, Mishra V,
                                    SHIMKETS R.
HERRMANN J.
MAJUMDER K.
MACDOUGALL J.
MISHRA V.
MEZES P S.
                    VERMET C.
FERNANDES E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene; ss; FCTR3f; colorectal cancer; adenomatous polyposis coli; myelogenous leukaemia; congenital neonatal autoimmune thrombocytopenia; ovarian cancer; brain tumour; breast cancer; glioma; astrocytoma; renal cell carcinoma; melanoma; clear cell carcinoma; granular cell carcinoma; neurological disorder; nerve trauma; familial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy; Gardner syndrome; mental health condition; immunological disorder; allergy; asthma; lung disease; reproductive disorder; definess; allergy; asthma; lung disease; reproductive syndrome; disorder; disorder; disorder; disorder; disbetes; schistosoma mansoni infection; spinocerebellar ataxia; plasmodium falciparum infection; Groenouw's corneal dystrophy;
                                          MetThrHisThrLysHisPheAspAlaTyrGlyArgMetLysGluValGlnTyrGlulle 399
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                                                                                            420 LysGluLeuLysValGlyProTyrAlaAsnThrThrArgTyrSerTyrGluTyrAspAla
                                                                                                                                   AspGlyGlnLeuGlnThrValSerIleAsnAspLysProLeuTrpArgTyrSerTyrAsp
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                                                                                  400 PheArgSerLeuMetTyrTrpMetThrValGlnTyrAspAsnMetGlyArgValValLys
    360 GlnPheGlyLysPheGlyValileTyrTyrAspileAsnGlnIleIleThrThrAlaVal
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The invention relates to FCTRX polypeptides and the polynucleotides encoding them. The sequences of the invention are useful for the encoding them. The sequences of the invention are useful for the encoding them. The sequences of the invention are useful for the encoding that the FCTRX polypeptide, such as colorectal cancer, associated with the FCTRX polypeptide, such as colorectal cancer, adenomatous polyposis coli, malignant varian tumours, malignant brain tumours, mammary tumours, human gliomas, astrocytomas, renal cell carcinoma, neasts adenocarcinoma, ovarian carcinoma, melanomas, clear carcinoma, pracest adenocarcinoma, ovarian carcinoma, melanomas, clear carcinoma, praces, neurological disorders, neurological disorders, curroct-Marie-Tooth neuropathy, Gardner syndrome, mental health conditions, immunological disorders, allergy and infection, asthma, lung conditions, immunological disorders, allergy and infection, asthma, lung ceficiency, deemoid tumour, turcot syndrome, liver cirrhosis, hepatitis conditions, spinocerebellar ataxia, plasmodium falciparum infection, crepresents cDNA encoding an FCTRX polypeptide of the invention.
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New FCTRX polypeptide and encoding polynucleotide, useful for preventing or treating FCTRX-related disorders, such as cancer, autoimmune, neurodegenerative, gastrointestinal, reproductive and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AlaArgGlyGlnValThrValPheGlyArgArgLeuArgValHisAsnArgAsnLeuLeu
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05-MAR-2001; 2001US-00800198

6860

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Human; FCTRX; myelogenous leukaemia; carcinoma; melanoma; glioma; ds;

KW astrocytoma; congenital neonatal alloimmune thrombocytopaenia; infection;

KW meurological disorder; neurodegenerative disorders; nerve trauma;

KW familial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy;

KW familial myelodysplastic syndrome; Charlial myelodysplastic syndrome;

KW mental health condition; immunological disorder; allergy; infertility;

KW mental health condition; immunological disorder; allergy; infertility;

KW mental health condition; immunological disorder; allergy; infertility;

KW desmoid disease; turcot syndrome; liver cirrhosis; hepatitis C; virucide;

KW desmoid disease; turcot syndrome; liver cirrhosis; hepatitis C; virucide;

KW gastric disorders; pancreatic disease; Schistosoma mansoni infection;

KW princerbellar ataxia; Plasmodium falciparum parasitemaia, diabetes;

KW corneal dystrophy-Greonouw type I; Corneal dystrophy-lattice type I;

KW antiallergic; antianthactic; antiinfertility; antiinflammatory;

M antiallergic; antiinfertility; immunostimulant; auditory; haemostatic;

KW gene therapy; FCTR3b; neurestin-like protein.
        6681 GACGGGCAGCTCCAGAGCGTGGCCGTCAATGACCGCCCGACCTGGCGCTACAGCTATGAC 6740
                                                                                                                                                                                          TyrAsplleArgAspArglleThrArgLeuGlyAspValGlnTyrLysMetAspGluAsp
                                                                                            GlyPheLeuArgGlnArgGlyGlyAspIlePheGluTyrAsnSerAlaGlyLeuLle
                               LeuAsnGlyAsnLeuHisLeuLeuSerProGlyAsnSerAlaArgLeuThrProLeuArg
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, Mishra V,
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                                                              Vernet CAM, F
Macdougall J,
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Shimkets RA, Herrmann JL, Majumder K; Mezes PS, Rastelli L;

P-PSDB; AAU08680

Novel polypeptides designated as FCTRX polypeptides, useful in detection, prevention and treatment of a broad range of pathological states.

Claim 9; Page 33-35; 215pp; English.

The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the nucleic acids encoding them. These sequences are useful for the treatment or nucleic acids encoding them. These sequences are useful for the treatment or prevention of numerous disorders including myelogenous leukaemia, carcinomas, melanomas, astrocytomas, congenital neonatal allowas encourable alloimmume thrombocytopaenia, neurological disorders, neurodegenerative disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Marie Tooth neuropathy, demyelinating Gardner syndrome, familial corders, allergy and infection, bronchial asthma, Avellino type disorders, allergy and infection, bronchial asthma, Avellino type of soinophilia, lung diseases, reproductive disorders, infertility, male cosinophilia, lung diseases, reproductive disorders, infertility, male disorders, pancreatic disorders, deafness, glycoprotein la deficiency, desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric disorders, pancreatic diseases such as diabetes, Schistosoma mansoni conference spincerebellar ataxia, plasmodium falciparum parasitaemia, corneal dystrophy-Greconow type I, Corneal dystrophy-lattice type I and correlation-like protein

Sequence 9826 BP; 2567 A; 2643 C; 2479 G; 2137 T; 0 U; 0 Other;

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LysalaTyrasnargalaGlySerTrpSerValargTyrargTyraspGlyLeuGlyarg 539
                                                                                                                                                                                                                                  Human; gene; ss; FCTR3b; colorectal cancer; adenomatous polyposis coli; welogenous leukaemia; congenital neonatal autoimmune thrombocytopenia; ovarian cancer; brain tumour; breast cancer; glioma; astrocytoma; renal cell carcinoma; melanoma; clear cell carcinoma; melanoma; clear cell carcinoma; melanoma; clear cell carcinoma; francer cell carcinoma; francer cell carcinoma; francer cell carcinoma; francer cell carcinoma; francer cell carcinoma; francer cell carcinoma; francer cell carcinoma; francer syndrome; mental health condition; immunological disorder; glardner syndrome; mental health condition; immunological disorder; glavoprotein deficiency; desmoid tumour; turcot syndrome; liver cirrhosis; hepatitis C; gastric disorder; pancreatic disease; plasmodium falciparum infection; spinocerebellar ataxia; plasmodium falciparum infection; Groenouw's corneal dystrophy;
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autoimmune thrombocytopenia, malignant ovarian tumours, malignant brain
tumours, mammary tumours, human gliomas, astrocytomas, renal cell
carcinoma, breast adenocarcinoma, ovarian carcinoma, melanomas, clear
carcinoma, breast adenocarcinoma, neurological disorders, clear
cell and granular cell carcinomas, neurological disorders, mental health
colditions, immunological disorders, allergy and infection, asthma, lung
diseases, male and female reproductive disorders, deafness, glycoprotein
conditions, immunological disorders, plasmodium fiver cirrhosis, hepatitis
cy gastric disorders, pancreatic diseases, diabetes, schistosoma mansoni
circulom, spinocerebellar ataxia, plasmodium falciparum infection,
direction, spinocerebellar ataxia, plasmodium falciparum infection,
cy cepresents cDNA encoding an FCTRX polypeptide of the invention.
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for preventing

New FCTRX polypeptide and encoding polynucleotide, useful for prevor treating FCTRX-related disorders, such as cancer, autoimmune, neurodegenerative, gastrointestinal, reproductive and inflammatory

The invention relates to FCTRX polypeptides and the polynucleotides encoding them. The sequences of the invention are useful for the manufacture of a medicament for diagnosing and treating disorders associated with the FCTRX polypeptide, such as colorectal cancer,

9; Page 29-32; 155pp; English.

diseases

Claim

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APPLICANT: Alsobrow: II, John et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS:
FILE REFERENCE: 21402-568A

CURRENT APPLICATION NUMBER: 105/10/383,201

PRIOR PLICATION NUMBER: 107029020

PRIOR FILING DATE: 2001-12-19

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PRIOR PLICATION NUMBER: 60/365,984

PRIOR FILING DATE: 2002-04-12

PRIOR PLING DATE: 2002-04-12

PRIOR PLING DATE: 2002-06-14

PRIOR PLING DATE: 2002-06-14

PRIOR PLING DATE: 2002-06-14

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PRIOR PLING DATE: 2002-06-14

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PRIOR PLING DATE: 2002-06-26

PRIOR FILING DATE: 2002-06-19

PRIOR PLING DATE: 2002-06-19

PRIOR PLING DATE: 2002-09-13

PRIOR PLING DATE: 2002-09-13
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Sequence 78, Appl
Sequence 66, Appl
Sequence 74, Appl
Sequence 77, Appl
Sequence 62, Appl
Sequence 65, Appl
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Sequence 7, Appli
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Sequence 67, Appl
Sequence 143, Appl
Sequence 1743, Appl
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Sequence 79, Appl
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Sequence 1343, Ap
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Sequence 3837, Ap
Sequence 689, App
Sequence 219, App
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Sequence 39, Appl
Sequence 41, Appl
Sequence 37, Appl
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      US-10-156-761-1
US-10-282-122A-33231
US-10-369-493-34930
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Sequence 43, Application US/10383201
Publication No. US20040029226A1
GENERAL INFORMATION:
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-MODEL=frame+_p2n.model -DEV=x1h
-Q=/Cogn21/USTO92020/Txnnat_06082004_112218_2931/app_query.fasta_1.3519
-D==Published Applications_NA -QFMT=fastap -STEFETA=DA.Tmbp_NINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_NIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US10029020 @CGN 1 1 2156 @Tunat_06082004 112218_29331
-NOFU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NG $$\infty$Correst -O WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEDUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGARPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                              August 14, 2004, 01:33:47; Search time 523.097 Seconds (without alignments) 2448.158 Million cell updates/sec
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Cgm2_6/ptodata/2/pubpna/US06_WWW_PUB.seq:*

Cgm2_6/ptodata/2/pubpna/US06_WWW_PUB.seq:*

Cgm2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

Cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

Cgm2_6/ptodata/2/pubpna/US08_WWW_PUB.seq:*

Cgm2_6/ptodata/2/pubpna/US08_WWW_PUB.seq:*

Cgm2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

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Cgm2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                       nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3225727 seqs, 2453303834 residues
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Applications NA:\*

Published

Database :

33: 44: 10: 110: 112: 113: 115:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Searched:

0.5

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

SUMMARIES

Query Match Length DB

Score

Result No.

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5222 ACCTCCAGCAAGGATGATGATGACCACCAACCTGTCTGCCTCAGGCGCCCTTCTAC 5281
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                                                                  ThrSerSerLysAspAspValThrIleThrThrAsnLeuSerAlaSerGlyAlaPheTyr
                                                                                                                                                                                                                                                                                                                                        GENERAL INVENTION: POLYPEPLIDES and Nucleic Acids Encoding Same TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE REPRENCE: 21402-225
CURRENT APPLICATION NUMBER: US/10/029,020
CURRENT APPLICATION NUMBER: US/256,704
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-07-24
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; Sequence 13, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5102 GGAIGGACAACAITITAIGAGIACGACAGCIIIGGCCGCCIGACAAAGGGACCIICCCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4742 CTCAACACCCAGAACATGTATGAGCTGTCTTCACCAATTGACCAGGAGGTCTATCTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspThrThrGlyLysHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn
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Matches:
Conservative:
Mismatches:
Indels:
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                   PRIOR FILING DATE: 2002-09-23
PRIOR PLING DATE: 2002-01-16
PRIOR PLING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 10/0366,928
PRIOR APPLICATION NUMBER: 60/366,928
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SCOFTWARE: CLIRASEQLIST VERSION 0.1
SEQ ID NO 43
LENGTH: 8354
                                                                                                                                                                                                                                                                                                                                                                                                                              1.99e-170
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, LOCATION: (35)..(8341)
US-10-383-201-43
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APPLICANT: Stone, David

TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537

CURRENT APPLICATION NUMBER: US/10/042,865

PRIOR FILING DATE: 2002-05-17

PRIOR FILING DATE: 2001-01-09

PRIOR FILING DATE: 2001-01-10

PRIOR FILING DATE: 2001-01-10

PRIOR FILING DATE: 2001-02-88

PRIOR FILING DATE: 2001-02-88

PRIOR FILING DATE: 2001-02-89

PRIOR FILING DATE: 2001-02-89

PRIOR FILING DATE: 2001-02-89

PRIOR PRILING DATE: 2001-03-09

PRIOR PRILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 264

SOFTWARE PRILING DATE: 2001-04-18
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LeuAsnThrGlnAsnMetTyrGluLeuSerSerProlleAspGlnGluLeuTyrLeuPhe 100
                                                        AspThrThrGlyLysHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn 120
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                 PheThrTyrThrGlyAspGlyAspIleThrLeulleThrAspAsnAsnGlyAsnMetVal
                                                                                                                                                                    AsnValArgArgAspSerThrGlyMetProLeuTrpLeuValValProAspGlyGlnVal
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Publication No. US20040029216A1
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Gangolli, Esha A
Burgess, Catherine E
Patturalon, Meera
Vernet, Corine A.M
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Boldog, Ference L
Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
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APPLICANT: Li, Li
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Malyankar, Uriel M
Millet, Isabelle
Peyman, John
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Zerhusen, Bryan D
Casman, Stacie J
Shenoy, Suresh G
Swrtek, Kimberly
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Miller, Charles E
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Gunther, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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4678 CICIACGIGGCCGACCTIGGGAACAICCGAAITICGGTITAICCGGAACAACAACATIT 4737
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                                                                                                                                                                                                                                                        LeuAsnThrdlnAsnMetTyrGluLeuSerSerProlleAspGlnGluLeuTyrLeuPhe
                                                                         TyrAlaLysAspAlaLysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu
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Sequence 39, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Bit, Li, Adam R
APPLICANT: Wolenc, Corine
APPLICANT: Vernet, Corine
APPLICANT: Wernet, Corine
APPLICANT: Gisen, Andrew J
APPLICANT: Applicant Halyankar, Urlel M
APPLICANT: Shimkets, Richard APPLICANT: Shimkets, Richard APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
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Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
Burgess, Catherine E
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US-10-038-854-39
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UB-10-38-201-55

1 Sequence 55, Application US/10383201

2 Sequence 55, Application US/10383201

3 Sequence 55, Application No. US20040029226A1

3 GENERAL INFORMATION:

4 THILE OF INVERTION: THERREDIT POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD TITLE OF INVERTION THERREDIT POLYPEPTICATION NUMBER: US/10/383,201

5 CURRENT FILING DATE: 2003-03-06

5 PRIOR FILING DATE: 2001-12-19

6 PRIOR PILING DATE: 2002-03-20

6 PRIOR PILING DATE: 2002-04-12

7 PRIOR PILING DATE: 2002-06-14

7 PRIOR PILING DATE: 2002-09-13

7 PRIOR FILING DATE: 2002-09-13

7 PRIOR PILING DATE: 2002-09-13

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                                        GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
                                                                         ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu
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Matches:
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                                                      141 AsnvalArgArgAspSerThrGlyMetProLeuTrpLeuValValProAspGlyGlnVal 160
                                                                                                            161 TyrīrpValīhrMetGlyThrAsnSerAlaLeuLysSerValīhrThrGlnGlyHisGlu 180
                                                                                                                                                                   LeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn 200
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APPLICANT: Smithson, Gleanda
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-112-29
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 00/259,415
PRIOR APPLICATION NUMBER: 60/259,785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 41, Application US/10038854 Publication No. US20040022781A1 GENERAL INFORMATION:
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Li, Li
Wolenc, Adam R
Vernet, Corine
Eisen, Andrew J
Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
Patrivesia
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Boldog, Ferenc
Burgess, Catherine E
Edinger, Shlomit R
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Gusev, Vladimir Y
Gangolli, Esha A
Guo, Xiaojia S
Shenoy, Suresh G
Rastelli, Luca
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Gunther, Erik
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                                                   ProSerGlyCysAspCysLysAsnAspAlaAsnCysAspCysPheSerGlyAspGly
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                                 Smithson, Glennda
Millet, Isabelle
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LENGTH: 8473
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                                       241 ThrSerSerLys---AspAspValThrIleThrThrAsnLeuSerAlaSerGlyAlaPhe 259
          GlyrrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro 220
                                                                                                          ThrglyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu 240
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APPLICANT: Gunthear, Glemada
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: 60/259,928
PRIOR APPLICATION NUMBER: 60/259,928
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
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PRIOR FILING DATE: 2001-04-13
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Shinkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
Patturajan, Meera
Gusev, Vladimir Y
Gangolli, Esha A
Gangolli, Esha A
Shenoy, Suresh G
Rastelli, Luca
Casman, Steacie J
Boldog, Ferenc
Burgess, Catherine E
Edinger, Shomit R
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APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
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Eisen, Andrew J
Liu, Xiaohong
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PRIOR FILING DATE: 2001-01-04

PRIOR APPLICATION NUMBER: 60/269,814

PRIOR FILING DATE: 2001-02-20

PRIOR PILING DATE: 2001-03-29

PRIOR PELING DATE: 2001-03-29

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Matches:
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Best Local Similarity:
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LENGTH: 8487
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APPLICANT: Smithson, Glemkd
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APPLICANT: Millet, Isabelle
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APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
TITE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-01-04
PRIOR PELING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR PELING DATE: 2001-01-02-20
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR PELING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-25
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Matches:
                                                                                               Sequence 35, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
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Vernet, Corine
Eisen, Andrew J
Liu, Xiachong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
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Gorman, Linda
Kekuda, Ramesh
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Edinger, Shlomit R
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Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
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Gangolli, Esha A
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Gunther, Erik
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               5269 TACACC 5274
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LENGTH: 8675
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Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 411
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Homo sapiens
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Best Local Similarity:
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                                                                                  LENGTH: 8645
                                                                                                                                             US-10-038-854-37
                                                            SEQ ID NO 37
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APPLICANT: Eas Blotechnology, Inc.
APPLICANT: Eas Blotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REPERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2000-09-15
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-2-14
PRIOR FILING DATE: 2001-11-2-14
PRIOR FILING DATE: 2001-11-2-14
PRIOR FILING DATE: 2001-11-2-14
PRIOR FILING DATE: 2001-01-0
PRIOR FILING DATE: 2002-01-0
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                                                                LysileAsnArgileArgGlnValThrThrSerGlyGluIleSerLeuValAlaGlyAla
                                                                                                                                          21 ProSerGlyCysAspCysLysAsnAspAlaAsnCysAspCysPheSerGlyAspAspGly
                             US-10-029-020-14_COPY_1490_1750 (1-261) x US-10-038-854-35 (1-8675)
Gaps:
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5. US20030232350A1
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GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginne, Richer C.
APPLICANT: Glynne, Richer A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
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4714 TACGCCACGGATGCCATCTTGAACTCCCCGTCCTTCTTTAGCTGTGGCTCCGGATGGCACC 4773
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1834 CITAACGCGTICAACCAGIAIGAGGCIGCGTCTCCGGGAGAACAGGAACTGTACGTGTTC 4893
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                                                  61 LeuTyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe
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APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Harrmann, John L
APPLICANT: Majumder, Kunda
APPLICANT: Majumder, Kunda
APPLICANT: Majumder, Kunda
APPLICANT: Mastealli, Luca
APPLICANT: Rastealli, Luca
APPLICANT: Rastealli, Luca
APPLICANT: Rastealli, Luca
APPLICANT: MacSa, Peter S
APPLICANT: MacSa, Peter S
APPLICANT: MacSa, Peter S
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APPLICANT: MacSa, Peter S
APPLICANT: MacSa, Peter S
APPLICATION NUMBER: 05/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
TANGTH: ACAO
; Sequence 66, Application US/09800198; Publication No. US20030087816A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Rattus norvegicus
US-09-800-198-66
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APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Vishnu
APPLICANT: Mashra, Vishnu
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
TITLE OF INVENTION: No. US/09/808,602
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT APPLICATION NUMBER: 09/800,198
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
SUPPRIOR FILING DATE: 2000-03-03
SUPPRIOR FILING DATE: 2000-03-03
SUPPRIOR FILING DATE: 2000-03-03
                             #826 CACATTCGCCGTGATGCCGGGATGCCGCTATGGCTTGTGGGGCGACAAGTA 4885
                                                                                                    5006 GGATGGACAÁCCGTTTATGAGTATGACCCCGAGGACACCTGÁCCAATGCAACGTTTCCC 5065
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APPLICANT: Vernet, Corine A
APPLICANT: Shimkets, Richard A
APPLICANT: Herrman, John L
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                                                                     US-10-029-020-14_COPY_1490_1750 (1-261) x US-09-800-198-66 (1-8689)
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Sequence 74, Application US/09808602 Patent No. US200220155115A1 GENERAL INFORMATION: APPLICANT: Vernet, Corine A

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APPLICANT: Shimkets, Richard A
APPLICANT: Herrman, John L
APPLICANT: Hajunder, Kund
APPLICANT: Majunder, Kund
APPLICANT: Majunder, Kund
APPLICANT: Mashaw, Vishnu
APPLICANT: Mascowgall, John
APPLICANT: MacSes, Peter S
APPLICANT: MacSowgall, John
TITLE OF INVENTION: No. US2020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 74
LENGTH: 8797
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; ORGANISM: Drosophila melanogaster
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APPLICANT: Pernandes, Elma
APPLICANT: Pernandes, Elma
APPLICANT: Shinkets, Richard A
APPLICANT: Herrmann, John L
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Mashra, Vishna
APPLICANT: Mastelli, Luca
APPLICANT: Rastelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-697
CURRENT APPLICATION NUMBER: US/09/800,198
FILE REFERENCE: 15966-697
CURRENT APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 62
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GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
                          5171 GGATGGACACTTTTTATGACTATGACCACGAGGCCGTCTGACCAATGTGACCCGCCC
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Matches:
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Patent No. US20020155115A1
GENERAL INFORMATION:
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CORGANISM: Mus musculus
US-09-808-602-77
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US-09-808-602-77
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5231 ACGGGCGTGGTGACCAGTCTGCACCGGGAAATGGAGAAATCTATCACATTGACATTGAG
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162
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59
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                                                                                                                                                                                                                                 Mismatches:
Indels:
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Matches:
CURRENT APPLICATION NUMBER: US/09/800,198
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
LENGTH: 8797
                                                                                                                                                                                   5.95e-102
864.50
77.10%
61.83%
62.46%
                                                                                                                     TYPE: DNA ORGANISM: Mus musculus
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                                     1 LysileAsnArgileArgGlnValThrThrSerGlyGluIleSerLeuValAlaGlyAla
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APPLICANT: Fernandes, Elma
APPLICANT: Bhimkets, Richard A
APPLICANT: Herrmann, John L
APPLICANT: Majunder, Vishna
APPLICANT: Mishra, Vishna
APPLICANT: Mazes, Peter S
APPLICANT: Raseelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-697
       US-10-029-020-14_COPY_1490_1750 (1-261) x US-09-800-198-62 (1-8797)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 65, Application US/09800198 Publication No. US20030087816A1 GENERAL INFORMATION:
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APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7234
                                                                                                      7095, Ap
2771, Ap
90, Appl
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1702, Ap
1420, Ap
401, App
                                         56, Appl
54, Appl
42, Appl
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11528, A
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39, Appl
1, Appli
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15, Appl
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Sequence 11853, A
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US-09-252-991A-14909
US-09-252-991A-14461
US-09-206-942-56
US-09-206-942-54
US-09-206-942-54
US-09-206-942-54
US-09-252-991A-7031
US-09-252-991A-7031
US-09-523-991A-7035
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US-08-252-991A-11588
US-09-252-991A-11583
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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 Percent Similarity:
Best Local Similarity:
  US-09-252-991A-7234
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-MODEL-frame+ p2n.model -DEV=x1h
-De-(cgn2 1/USPTO spool/US1029020/runat 06082004_112217_29301/app_query.fasta_1.3519
-DB-1ssued_patents_NA -OFMT-fastap -SUFFIX=p2n.rni - MINNATCH=0.1 -LOOPCL=0
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGING
-NEW TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 11, Appl
Sequence 115, Ap
Sequence 1157, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 16, Appl
Sequence 16, Appl
Sequence 11708, A
Sequence 3221, Appl
Sequence 3221, Appl
Sequence 3221, Appl
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(without alignments)
1875.793 Million cell updates/sec
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                                                                                                                                                      1 KINRIRQVTTSGEISLVAGA.....SSKDDVTITTNLSASGAFYT
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
                                                        nucleic search, using frame_plus_p2n model
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US-09-453-702B-11
US-09-328-322-1419
US-09-543-681A-1157
US-09-790-988-1
US-09-446-301A-3
US-09-446-301A-16
US-09-99-32-3
US-09-09-913-50
US-09-09-913-1708
US-09-252-991A-11708
US-09-252-991A-11708
US-09-252-991A-11508
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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26758 ACGGAAGGCAGGGCTGCTGTGTGAAGAAGGAACATGCGGACGGGAGCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 ArgAspSerThrGlyMetProLeuTrpLeuValValProAspGlyGlnValTyrTrpVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-029-020-14_COPY_1490_1750 (1-261) x US-09-453-702B-11
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                             REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                          11:
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APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
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                                                                                                                                                                                                                                                      TOPOLOGY: ucuble

MOLECTLE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-453-702B-11
                                                           NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                     TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 ThrMetGlyThrAsn-----
                                                                                                                                                       251-9166
                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   0.0169
115.00
31.73%
22.12%
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.31%
                                                                                                                                                         TELEFAX: (608)
                                                                                                                                                                                                                  LENGTH: 31960
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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                               182
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                                                                                                                                                                                                                                                                                                                123 TyrThrGlyAspGlyAspIleThrLeuIleThrAspAsnAsnGlyAsnMetValAsnVal 142
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         87
                                                                                                                                                                                                  2314 TACGACCAGGCCGGACGCTTGGAGGCACTGCTCCCGGCCGAAGGCGAGCCAACCTGCTAT
                                                                                                                                                                                                                                                                143 ArgArgAspSerThrGlyMetProLeuTrpLeuValValProAspGlyGlnValTyrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 ValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGluLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 TrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPheProThr
                                                                                                                                                                                                                                      ---HisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsnPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 MetMetThrTyr---HisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsnGly
         69 IleargileargPheileargLysAsnLysPro---PheLeuAsnThrGlnAsnMetTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COFFMARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                       88 GluLeuSerSerProIleAspGlnGluLeu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Blattner, Frederick
                                                                                                                                                                   100 PheAspThrThrGlyLys-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2787 ACAGGCCGGATGAC 2801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 53701-2113
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US-09-453-702B-11
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nucleotide at the above locations are unknown.
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2125 AATTTAACCCAATGGACCGATCCGGAACAACAATCGACTTGCTATGATTGGGACAAAGAT 2184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 AsnMetTyrGluLeuSerSerProlleAspGlnGlu---LeuTyrLeuPheAspThrThr 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ArgArgAspSerThrGlyMetProLeuTrp 152
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28
73
55
                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                         Indels:
CURRENT APPLICATION NUMBER: US/09/543,681A
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                CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1157
LENGTH: 4761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/09790988; Patent No. 6632935; GENERAL INFORMATION:
                                                                                                                                                                                                                               ; OTHER INFORMATION: Identity of US-09-543-681A-1157
                                                                                                                                  TYPE: DNA
ORGANISM: Proteus mirabilis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                             0.0143
105.50
36.00%
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Query Match:
                                                                                                                                                                                          NAME/KEY: unsure
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US-09-790-988-1
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Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL FILLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
                                                              GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BACCON ET AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1117 TATTTTCAATTAAAGGACCTCATCGCGTCCCGGACATGGCGAGAAGTTGAGACAACTTAT 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerProlleAspGlnGluLeuTyrLeuPheAspThrThrGlyLysHisLeuTyrThrGln 110
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                            Sequence 1419, Application US/09328352 Patent No. 6562958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGluLeuAlaMetMetTh 185
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                                               AND THEIR USE FOR DETECTING RESISTANCE IN A OR TO STREPTOGRAMIN B AND RELATED
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Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/09/446,301A
CURRENT FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PATCHIN VEY: 2.1
SEQ ID NO 3
                APPLICANT: EL SOLH, NEVINE
APPLICANT: ALLIGNET, JEANINE
TITLE OF INVENTION: POLYNUCLEOTIDES AN
TITLE OF INVENTION: TO STREEFOGRAMIN
TITLE OF INVENTION: COMPOUNDS
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; Sequence 3, Application US/0909932
; Patent No. 6570001
; GENERAL INFORMATION:
; APPLICANT: El Solh, Nevine
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41.45%
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Best Local Similarity:
GENERAL INFORMATION:
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                        SYMBIONT
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Conservative:
Mismatches:
Indels:
 HAPPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYNITILE REPERBENE: 08136/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: UP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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18-09-464-301A-3
; Sequence 3, Application US/09446301A
; Patent No. 6506893
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105.00
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APPLICANT: Allignet, Jeanine
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: 03495.0173-00000
CURRENT PELLON NUMBER: US/09/099,932
CURRENT FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/050,380
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATCHING DATE: 1997-06-20
SOFTWARE: PATCHING DATE: 1997-06-20
SOFTWARE: PATCHING DATE: 1997-06-20
SOFTWARE: PATCHING DATE: 1997-06-20
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Sequence 16, Application US/09446301A

Patent No. 6506893

; GENERAL INFORMATION:
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US-09-099-932-3
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Best Local Similarity:
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APPLICANT: EL SOLH, NEVINE

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TITLE OF INVENTION: POLYNUCLEGOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: TO STREPTOGRAMIN B OR TO STREPTOGRAMIN B AND RELATED
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: 03715-0059
CURRENT APPLICATION NUMBER: US/09/446,301A
CURRENT FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
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US-09-099-932-50
Sequence 50, Application US/09099932
Patent No. 6770001
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (39..923, 947..1582)
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536 GATTACAAAT-
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LENGTH: 1607
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Best Local Similarity:
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APPLICANT: El Solh, Nevine
APPLICANT: Allignet, Jeanine
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: COMPOUNDS
FILE REFRERENCE: 03495.0173-00000
CURRENT APPLICATION NUMBER: US/09/099,932
CURRENT FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/050,380
BARLIER FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO S: 50
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101.50
41.45%
25.39%
7.33%
                                                                                                                                                                                                      TYPE: DNA ORGANISM: Staphyloccocus
                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (947)...(1582)
                                                                                                                                                                                                                                                           LOCATION: (39)..(923) FEATURE:
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                                                                                                                                                                                                                                                NAME/KEY: CDS
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JARGARIA MARCO Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE CURRENT AFPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

RIOR APPLICATION NUMBER: US 60/094,190

RIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 11708

LENGTH: 1515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---cracitracceceaagacegaagetitcesetcaetegegecegegagacta 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 ACCTCGGGAGCTACCTTGATCGGCAACAGCTGCCCACTAGGGGCTGAGCTTAATAACGAG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 ACAGGAAGCIGCGGCCCCGGTTACGAAATGAATGACGCTGGCTGTAAGCTTCCA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 AAATATCAGGTCGAGCATGACTTAATAACCCCGATTCCGCTTGCCCGACACTACAATGGC 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 TyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPheLeu 81
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769 GAGGGTCGAAAGTATCGTGTAGAGCGAGGCGCTAATCTTACGATTAGCGAC--
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Sequence 11708, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT PILITIG DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15163
LENGTH: 1260
                                                                                                                                                                               3213
       3100 GGCTCTGAITATTTGTATGGTGGCTCAGGTAATGATACGTTGATTAATGGTGGTAATTCC 3159
                                                                                                                                                                                                                                                                                                         3292 GIGTCCTCTGGTGATATTTGACTTAAGGAGTGGGATTCACTCATCATAATATCATTCAAT 3351
                                                                                                                                                                                                                                                ---AAAGCATTACTTACTTCA 3231
                                                                  ----AsnPheThrTyrThrGlyAspGlyAspIleThrLeuIleThrAspAsnAsnGly 137
                                                                                                                                       AsnMetValAsnValArgArgAspSerThrGlyMetProLeuTrpLeuValValProAsp 157
                                                                                                                                                                                                          158 GlyGlnValTyrTrpValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGln 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                 212 GlyArgLeuThrAsnValThrPheProThrGlyGlnValSerSerPheArgSerAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 GlyHisGluLeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSer
                                                                                                                                                                         3160 AATGTGTATACGGCTTTACAAGGTCAAGCTGGGAATGATACTTATATTGTAGAT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 AspSerSerVal-----HisValGlnValGluThrSerSer 243
                                                                                                                                                                                                                                                                                                                                                         198 AsnGluAsnGlyTrpThrThrPheTyrGluTyrAspSerPhe---
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VS-09-252-991A-15163/c
Sequence 15163, Application US/09252991A
Patent No. 6551795
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Best Local Similarity:
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Sequence 32121, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

IENGTH: 4860

TYPE: DNA

TYPE: DNA

TYPE: DNA

ORGANISM: Acinetobacter baumannii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2880 TATGAAGATGGTGAACTATTAAAAGTAATTGCTGCGGATGCTAAAGGTAATGAAAGTTCA 2739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCAGAGTAACTGCTAAAGATCTAGCTGGGAATAGCTCTCAACCACTAACCATTATAATT 2979
GlnGlyHisGluLeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLys 196
                                           873
                                                                        SerAsnGluAsnGlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsn 216
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2860 ATTGGTGATGCTTGGGTTCAGGTAAATGTTGAGGAAAAATTCGATTGGTTGAATACAGAA 2919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnValThrSerGlyGluIleSerLeuValAlaGlyAlaProSerGlyCysAspCys 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65
                        2800 GITAGTACAGATAAAATTATTITTAATGCGCCAAGTGATAGTTATATTGTTGAGCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2740 ATTAATATAAATACACCTGATATTACAGCACCTATATTAGCTAATTTGTTTAATTATGAT
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Matches:
Conservative:
Mismatches:
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                                                                                                                                               ValThrPheProThrGlyGlnValSerSer 226
                                                                                                                                                                           934 GTAACACGAACAGATGGGCAATACAACACG 963
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Best Local Similarity:
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US-09-328-352-3221
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                                      823
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARBUINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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| Sequence 482, Application US/09221017B
| Patent No. 6444799 |
| GENERAL INFORMATION: C |
| APPLICANT: ROSS, Bruce C |
| TITLE OFF INVENTION: P GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120 |
| CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: COMPATIBLE
COMPUTER: MINIMARE
SOFTWARE: FASTERM: Windows
SOFTWARE: FASTERQ for Windows Version 2.0b
                                                                                                                  CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1999-07-27
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STREET: 755 PAGE MILL ROAD
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7.04%
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Query Match:
                 GENERAL INFORMATION:
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COUNTRY: U
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APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVERVION: NUCLBIC ACID AND NAINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVERVION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
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                                       175 ThrThrGlnGlyHisGluLeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAla 194
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US-09-252-991A-14461
; Sequence 14461, Application US/09252991A
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US-09-252-991A-14909/c
Sequence 14909, Application US/09252991A
Patent No. 6551795
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SEQ ID NO 14909
LENGTH: 2181
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Best Local Similarity:
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Matches:
Conservative:
Mismatches:
Indels:
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                          FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
APPLICATION NUMBER: PP2911
FILING DATE: 10-APR-1998
ATTORNEY, AGENT INPORMATION:
NAWE: MONICOY, GLACKS H
RESISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
                 US/09/221,017B
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 27
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
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LENGTH: 2236 base pairs
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96.50
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CURRENT APPLICATION DATA:
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STRANDEDNESS: double
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TELEFAX: 706141
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                                                                                                                                                                                                                                                                        .451 GAGAGAGAATCTCTTCGGTCAGATAGAGGTCTACGTGGCGGGAACCACCCTTTTCTAT 1392
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153 LeuValValProAspGlyGlnValTyrTrpValThrMetGlyThrAsnSerAlaLeuLys 172
                                                                               -HisGluLeuAlaMetMetThrTyrHisGly 188
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

August 14, 2004, 01:13:26; Search time 3060.96 Seconds (without alignments) 2546.273 Million cell updates/sec 1384 – – – 1384 1 KINRIRQVTTSGEISLVAGA......SSKDDVTITTNLSASGAFYT 261 US-10-029-020-14\_COPY\_1490\_1750 Perfect score: Sequence: Run on: Title:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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EST:\*

Database :

em\_esthum: \*
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em\_gss\_inv:\* em\_gss\_pln:\* gb\_est2:\*
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29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

GSS 12-DEC-2003

AY413475 6246 bp DNA linear GSS 12-DEC-2 Homo sapiens HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. AY413475.1 GI:39769437 GSS. RESULT 1 AY413475 LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE

Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 6246)

REFERENCE

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2181
                                                                                                                                                                       3118 ACCTCCAGCAAGGATGATGATCACCATAACCACCAGCTGTCTGCCTCAGGCGCCTTCTAC 3177
                                                                                                                                                                                                                                                                                                                                                                                                               AY413476 5970 bp DNA linear GSS 12-DEC-2003
Pan troglodytes HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                          ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mararyota; Metazoa; Catarrhini; Hominidae; Pan. 1 (bases 1 to 5970)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) USA Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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2 (bases 1 to 5970)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.
                                                                                                                                                                                                                        ThrSerSerLysAspAspValThrIleThrThrAsnLeuSerAlaSerGlyAlaPheTyr
181 LeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn
                   2938 TIGGCCAIGATGACATACCATGGCAATICCGGCCTTCTGGCAACCAAAGCAATGAAAAC
                                                                      201 GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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                                                                                Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                         Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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                                     Thomas, P., Kejariwal, A.
            2 (bases 1 to 3190)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A Taod,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NO-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20856, USA
This sequence was made by sequencing genomic exons and order them based on alignment.
Location/Qualifiers
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Mus musculus HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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     ProSerGlycysAspCysLysAsnAspAlaAsnCysAspCysPheSerGlyAspAspGly
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AY405422 5087 bp DNA linear GSS 12-DEC-2003
Mus musculus HCM2218 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                             PheAspThrThrGlyLySHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyr
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/ BETALL="CS-FLA" (")
/ Clone="IMAGE:6840755"
/ Liboue type="whole brain"
/ dev stage="whole brain"
/ dev stage="whole brain"
/ lab_nost="mbryo 13.5,14.5,16.5,17.5dpc"
/ lab_nost="mbryo 13.5,14.5,16.5,17.5dpc"
/ lab_nost="mbryo 13.5,14.5,16.5,17.5dpc"
/ clone lib="while MRAP GIO"
/ note="Organ: Brain: Vector: pVX- Asc; Site 1: EcoR I;
/ note="Organ: Brain: Vector: pVX- Asc; Site 1: EcoR I;
/ note="Organ: Brain: Vector: pVX- Asc; Site 1: EcoR I;
/ note="Organ: Brain: Vector: prace fractionated on a 1% agarcse
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site . Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pVX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
s ACGCAGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator: "
                                                                                                                                                       3118 ACCTCAAGAAAGATGACGTCACCATAACCACCAACCTGTCTGGCTTCGGGTGCCTTCTAC 3177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Bmail: cgapbs-r@mail.nih.gov

Trissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Educancing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousef1.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                    EST 09-JUL-2003
                                  240
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                           ThrSerSerLysAspAspValThrIleThrThrAsnLeuSerAlaSerGlyAlaPheTyr
                             ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu
                                                                                                                                                                                                                                                                                                                                                                  CB520016
UI-M-GIO-cek-i-10-0-UI.rl NIH BMAP_GIO Mus musculus CDNA clone
IMAGE:6840755 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Onpublished (1999)
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Matches:
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/mol type="mRNA"
/strain="C57BL/6"
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Location/Qualifiers
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259 486

426

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AY405420 5094 bp DNA linear GSS 12-DEC-2003 Homo sapiens HCM2218 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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Clark A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, W.A., Tanenbaum, D. M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                      sequencing genomic
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Matches:
Conservative:
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Indels:
Gaps:
                                                                               organism="Mus musculus"
                                                                                              /mol_type="genomic DNA"/db_xref="taxon:10090"
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/locus\(\tag=\)"HCM2218\(\bar{1}\)
Rockville, MD 20850, USA
This sequence was made by seq
them based on alignment.
Location/Qualifiers
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UI-M-FO0-bzr-d-20-0-UI.rl NIH BMAP_FO0 Mus musculus cDNA clone
IMAGE:6406243 5', mRNA sequence.
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Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINLat:
http://mage.llni.gov
This clone was contributed by the Brain Molecular Anatomy Project
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                   1868 GACATCAATGGTACTCACCAATATACTGTAAGTTTAGTCACTGGTGATTACCTTTACAAT
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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/strain="C57BL/6"
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/tissue_type="whole brain"
/dev stage="embryo 12.5dpc"
/lab_host="multoB (TI phage resistant)"
/clone_lib="NIH BMAP_F00"
/clone_lib="NIH BMAP_F00"
/clone_lib="NIH BMAP_F00"
/clone_lib="NIH BMAP_F00"

/note="Organ: Brain; Vector: pXX- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pXX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lemnon and Soarces, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector: The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the University
lowa Brain Anatcowy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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US-10-029-020-14_COPY_1490_1750 (1-261) x BU704133 (1-723)
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/dev stage="whole brain"
/dev stage="whole brain"
/dev stage="whole Tippage resistant)"
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//done lib="NIH1BMAP FOO"
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//done lib="NIH1BMAP FOO"
//done lib="NIH1BMAP FOO"
//done lib="NIH1BMAP FOO"
//done lib="NIH1BMAP FOO"
//done Research, 6:791-806
/done Research, 6:791-806
/done Research, 6:791-806
/done lib="Strand CDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TGAGAGAGC. This library was created for the University lows Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                   BU704133 723 bp mRNA linear BST 15-JUL-2003 UI-M-FO0-bzr-j-10-0-UI.rl NIH BMAP_FO0 Mus musculus cDNA clone IMAGE:6406377 5', mRNA sequence.
                                         240
                                                           635 GGAIGGACAACATTTTTGACTAIGACAGIGAAGGICGCCIGACGAAIGITACCTICCCC 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iowa
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Email: cgapbs-r@mail.nih.gov

Issue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Extribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                   ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Matches:
Conservative:
Mismatches:
Indels:
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61.92%
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Best Local Similarity:
Query Match:
DB:
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UI-M-GIO-cej-m-11-0-UI.rl NIH BMAP_GIO Mus musculus cDNA clone
IMAGE:6840468 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
1 LysileAsnArgileArgGlnValThrThrSerGlyGluIleSerLeuValAlaGlyAla 20
                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                              80
                                                         34 AAGATCAACCGAATAAGGCAGGTCACGACAGACGGGAGATCTCCTTAGTGGCTGGGATA 93
                                                                                                                                                                                                                                     41 TyrAlaLysAspAlaLysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 737)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 GACATCAACGGTACTCACCAGTACACGTGAGCCTGGTCACGGGTGACTACCTATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 CGAATCCGAAGGGATCCGAATCGGATGCCGGTGCGGGTGTCTCCTGATAACCAGGTG
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                                                                                                                     21 ProSerGlyCysAspCysLysAsnAspAlaAsnCysAspCysPheSerGlyAspAspGly
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcos
gel: First strand cDNA synthesis was primed with oligo-dr
gel: First strand cDNA synthesis was primed with oligo-dr
gel: First scand according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pVX-Asc vector. The library tag
sequence located between the Not I site and then cloned
directionally into pVX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
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Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
II (bases I to 797)
III-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                               240 uThrSerSerLys---AspAspValThrIleThrThrAsnLeuSerAlaSerGlyAlaPh 259
                                                                                                                                                                                                                                                                                                                                                                                                              426 ATATGGTTGACCATAGGCACCAACGGGTGTCTGAAAAGCATGACCGCTCAGGGCCTGGAA 485
                                                                                                                                                                                                CD349851
UI-M-FYO-cfr-n-12-0-UI.rl NIH_BMAP_FYO Mus musculus cDNA clone
IMAGE:6855085 5', mRNA sequence.
                                                     181 LeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn
                                                                                                486 CIGGITITIGITIACITIACCAIGGCAAACAGIGGGCITITIAGCCACCAAAAGIGACGAAACI
                                                                                                                                                                                                                                                                                                        221 ThrGlyGln-ValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGl
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/note="Organ: Brain; Vector: pYX-Asc; Site l: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soarse, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
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sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 AspThrThrGlyLysHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 GACATCAACGGTACTCACCAGTACACCGTGAGCCTGGTCACGGGTGACTACCTATATAAT 305
        Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project (BMARP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuTyrValAlaAspLeuGlyAsnIleArglleArgPheIleArgLysAsnLysProPhe 80
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Conservative:
Mismatches:
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/organism="Mus musculus"
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                                                                                                                      Seq primer: pYX-5.
Location/Qualifiers
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'strain="C57BL/6"
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61.24%
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                                                                                                                                                                                                                                                                                                                                                                                                  LeuTyrValAlaAspieuGlyAsnileArgileArgPheIleArgLysAsnLysProPhe
                                                                                                                                                                                                                                                                                                                   343 AACGCTGAIGGIATCCAICAGTACACTGTGAGTCTGGTGACTGGGGGAGTACTTGTACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
 Health (NIMH), Hemin Chin, Ph.
                                                  797
154
39
1
                                                                                                                   US-10-029-020-14_COPY_1490_1750 (1-261) x CD349851 (1-797)
                                                                      Conservative:
Mismatches:
                                                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACTCCAACCGGGATGATGACGTCACTGTG 792
                                                                                          Indels:
Institute of Mental program coordinator.
                                               4.31e-89
830.50
77.20%
61.60%
60.01%
                                                                              Best Local Similarity:
                                                                  Percent Similarity:
                                      Alignment Scores:
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Pan troglodytes HCM2218 gene, VIRTUAL TRANSCRIPT, partial sequence, AY405421

LOCUS DEFINITION

AY405421

AY405421.1 GI:39761395

ACCESSION VERSION

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1687
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Pan troglodytes
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 5069)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACATCAATGGTACTCACCAATATACTGTAAGTTTAGTCACTGGTGATTACCTTTACAAT 1927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrAlaLysAspAlaLysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu 60
                                                                                                                                                                                                                                                                                                                                                                                             This sequence was made by sequencing genomic exons and ordering
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                                                                                                                                                                                                                                                               Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                          Direct Submission Submitted (16-NOV-2003) Celera Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 5069
/organism="Pan troglodytes"
                                                                                                                                                                                                          Science 302 (5652), 1960-1963 (2003)
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Matches:
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/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus_tag="HCM2218"
                                                                                                                                                                                                                                                                                                                                                                                                                   them based on alignment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               USA
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812.50
70.99%
59.16%
58.71%
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Best Local Similarity:
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ORGANISM
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AUTHORS
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AUTHORS
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JOURNAL
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GSS 02-NOV-2001
directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACGAC. This library was created for the University Iowa Brain Anatowy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 TyrTrpValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGlu 180
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AG045907.1 GI:16582799
GSS.
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Pan troglodytes
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGATCAACCGAATAAGGCAGGTCACGACAGACGGGGAGATCTCCTTAGTGGCTGGGATA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrAlaLysAspAlaLysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu 60
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Indels:
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UI-M-FIO-byq-i-13-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone
IMAGE:6400980 5', mRNA sequence.
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Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://mage.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
           1988 AGAATTAGACGGGACCCAAATCGCATGCCAGTTCGAGTGGTGTCTCCCGATAACCAAGTG 2047
                                                                                                                                                                                                                                                                                                                                                                                              240
                                                              161 TyrTrpValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGlu 180
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 739)
                                                                                                                                                                          LeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn
                                                                                                                                                                                                                                                                                                                                        2168 NNNNNNNNNNNNNNNNNNNNNNNNCTATGACAGTGAAGGTCGTCTGACAAATGTTACGATTCCA
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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Bu (bases 1 to 764)

NHH-MGC http://mgc.nci.nih.gov/

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clond through the 1.M. Bento Soares, University of Iowa Clond through the 1.M. Bento Soares, University of Iowa Clond through the 1.M. A.G.E. Consortium/Link at:

http://image.llnl.gov
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                                                                                                                                                                                               CB244782
UI-M-FYO-cdr-1-01-0-UI.rl NIH BMAP_FYO Mus musculus cDNA clone
IMAGE:6833522 5', mRNA sequence.
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                                                                     555 AACGGATGGACAACATTTTATGAG 578
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Location/Qualifiers
            200 AsnGlyTrpThrThrPheTyrGlu
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CB244782.1 GI:28366426
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CB244782
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                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2001) Asao Pujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokchama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 PheAspThrThrGlyLysHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyr 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 GAGCICTACGIGGCCGACCIIGGGAACAICCGAATICGGITTAICCGGAAGAACAAGCCT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 AsnPheThrTyrThrGlyAspGlyAspIleThrLeuIleThrAspAsnAsnGlyAsnMet 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTTCACCTACACTGGGGACGGTGACATCACACTCATCACACAACAATGGCAACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTACTGGGTGACCATGGGCACCAACAGTGCACTCAAGAGTGTGACCACACAAGGACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 PheleuAsnThrGlnAsnMetTyrGluLeuSerSerProlleAspGlnGluLeuTyrLeu 99
                                                        Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                     Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      735
147
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-024P12.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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R.Site 1 : SacI
R.Site 2 : SacI.
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Best Local Similarity:
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                                                                                                                 TITLE
JOURNAL
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gil 4732114)[ab]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and Lransformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab host="B. Coli strain XL10-Gold, T1-resistant, F-" /clone 11b="Mouse 10kb plasmid UUGCNM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/GJ (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 CACCGACAACAATGGCAACATGGTGAACGTCCGCCGAGACTCTACCGGGATGCCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eThraspasnAsnGlyAsnMetValAsnValArgArgAspSerThrGlyMetProLeuTr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PhelleArgLysAsnLysProPheLeuAsnThrGlnAsnMetTyrGluLeuSerSer-Pr
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                                                                                          00.0
Tel: 801 585 5606
Fax: 801 585 7177
Email ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0./
Plate: 0465 row: I column: 04
Seq primer: CGTYGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 588.
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                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0465104"
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704.00
98.53%
97.06%
50.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male'
                                                                                                                                                                                                                                                                     . .588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 TyrTrpValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGlu 180
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                          96 GCCTCAGACTGTGACTGCAAAAACGATGTCAACTGCATCTGCTACTCGGGAGATGACGCT
                                                                                                                        TyralaLysAspAlaLysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu
                                                                                                                                                         LeuTyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe
                                                                                                                                                                                                                                                                                 LeuAsnThrGlnAsnMetTyrGluLeuSerSerProIleAspGlnGluLeuTyrLeuPhe
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               ProSerGlyCysAspCysLysAsnAspAlaAsnCysAspCysPheSerGlyAspAspGly
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Searched:

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Aas14089 Human FCT
Adb32028 Human FCT
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Adb29075 Drosophil
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Ab37164 Oligonucl
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Ac46865 Propionib
Ab4668530 Listeria
Ab471024 Listeria
Ab4710485 Drosophil
Ab104856 Drosophil
Ab4667876 Listeria

Oligonucl

Drosophil Drosophil

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Human, NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; KW cell signal processing; metabolic pathway modulation; metabolic disorder; obesity; diabetes; infectious disease; neurodegenerative disorder; acne; M Alzheimer's disease; parkinson's disease; immune disorder; cancer; M haematopoietic disorder; cirrhosis; pancreatitis; learning defect; KW memory defect; infertility; congenital heart defect; hair growth; W pigmentation disorder; endocrine disorder; respiratory disease; health; KW gastro-intestinal disease; reproductive; neurological disease; health; KW pone marrow transplantation; endocrine disease; allergy; inflammation; KW neuropsychiatric disorder; EGF-related protein; SCUBEI; TEN-M; M neuropsychiatric disorder; EGF-related protein; SCUBEI; TEN-M; KW dipocyte complement-related Clq tumour necrosis factor; out at first; KW beta adrenezgic receptor kinase; EphA6/ehc2; glucose transporter; KW beta adrenezgic receptor kinase; EphA6/ehc2; glucose transporter; KW beta membrane sushi-containing domain; butyrophilin; KW type la membrane sushi-containing domain; sNP; gene; ds;
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cqg12_1/USPTFO spool/VS10029020/runat_06082004_112215_29265/app_query.fasta_1.3519
-Q=/Cqg2_1/USPTFO spool/VS10029020/runat_06082004_112215_29265/app_query.fasta_1.3519
-DB=N Geneseq_29Jano4 -OFMT=fastap_SUFFIX=p2n.rng-MINMATCH=0.1 -T.00PCGL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LCOAL_-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLENE=0 -MAXLEN=200000000
-USER=US10029020_@CGN_1 1_1868 @runat_06082004_112215_29265 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                GenCore version
Copyright (c) 1993 - 2004
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Listing first 45 summaries
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Result No.

Aca52160 Prokaryot Aca52159 Prokaryot Acf72220 Photorhab Continuation (7 of

Continuation (5 of Continuation (4 of

Continuation (4 of Aca44188 Prokaryot

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The present invention relates to new NOVX polypeptides. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, considerably human. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, parkinson's disease, neurodegenerative disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, consorted its learning and memory defects, infertility, congenital heart defects, acne, hair growth, pigmentation disorders, endocrine disorders, cepiratory disease, gastro-intestinal diseases, reproductive, health, consorted disorders, neuropsychiatric disorders and age-related disorders. The consorted in the invention and disorders. The present nucleic acid sequence represents a NOVX gene. This sequence consorted in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                   . R;
Liu X;
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                                                                                                       "Single nucleotide polymorphism (SNP)"
_name= "Single nucleotide polymorphism (SNP)
                                                  "Single nucleotide polymorphism (SNP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Patturajan M, Vernet CAM, Malyankar UM, Kekuc
Anderson D, Shimkets RA, Burgess CE, Zerhusen BI
Casman SJ, Boldog FL, Smithson G, Li L, Ji W;
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Matches:
Conservative:
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Indels:
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/standard_name=
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02-MAY-2001, 2001US-0288153P.

29-MAY-2001, 2001US-0294057F.

24-UUL-2001, 2001US-0307506P.

10-AUG-2001, 2001US-0311590P.

10-AUG-2001, 2001US-0311590P.

29-AUG-2001, 2001US-0311613P.
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Best Local Similarity:
Query Match:
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                                                                                                                                             WO200257453-A2
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LysileAsnArgileArgGlnValThrThrSerGlyGluIleSerLeuValAlaGlyAla 20

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                                                                                                                                                                                                                                                                               PheThrTyrThrGlyAspGlyAspIleThrLeuIleThrAspAsnAsnGlyAsnMetVal
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                                                                                                                                                                                                                                                      GATACCACCGGCAAGCACCTGTACACCCAAAGCCTGCCCACAGGAGACTACCTGTACAAC
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                         LeuTyrValAlaAspLeuGlyAsnIleArglleArgPheIleArgFysAsnLysProPhe
                                                                                                                                                                                                ProSerGlyCysAspCysLysAsnAspAlaAsnCysAspCysPheSerGlyAspGly
                                                      TyralaLysAspAlaLysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu
                                                                                                                                                                      LeuAsnThrGlnAsnMetTyrGluLeuSerSerProIleAspGlnGluLeuTyrLeuPhe
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Human; ss; gene; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thrombocytopaenia; devalopmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma; inflammatory disorder; infertility; autoimmune disorder; gout; allergy; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; diabetes mellitus; glomerulonephritis; irritable bowel syndrome; unfection; multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
                                                                                                                                                                                         LeuTyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe
                                                                                       81 LeuAsnThrGlnAsnMetTyrGluLeuSerSerProlleAspGlnGluLeuTyrLeuPhe
                                                                                                             101 AspThrThrGlyLysHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysileAsnArgileArgGlnValThrThrSerGlyGlulleSerLeuValAlaGlyAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8438 BP; 2001 A; 2434 C; 2268 G; 1735 T; 0 U; 0 Other;
                                                                                               /trans_except= (pos: 1138. .1147,aa:Met)
/product= "NOV1 protein"
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Matches:
Conservative:
Mismatches:
Indels:
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                                      Location/Qualifiers
4. .8395
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10-JAN-2001; 2001US-0260831P.
28-FEB-2001; 2001US-027239R.
09-MAR-2001; 2001US-0274876P.
18-APR-2001; 2001US-0284704P.
                                                                                                                                                                                                                                   09-JAN-2002; 2002WO-US000554
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P-PSDB; ABB98401.
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Best Local Similarity:
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Homo sapiens
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DB:
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g ò d

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The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to GGDD, a biologically active fragment or an immunospenic fragment. Also included are the comprising a promoter sequence operably linked to the GGDD opport of the CGDD comprising a promoter sequence operably linked to the CGDD opport or a transgenic organism comprising which the recombinant polymucleotide, a cell transformed with the recombinant polymucleotide, a transgenic organism comprising the recombinant polymucleotide, a transgenic organism comprising the recombinant polymucleotide, a transgenic organism comprising the recombinant polymucleotide, an anti-cGDD polymucleotide microarray. The expression of GGDD polymucleotide of GGDD polymucleotide microarray. The polypeptides, polymucleotide and a cGDD polymucleotide microarray. The polypeptides, polymucleotide and a preventing disorders associated with aberrant expression of GGDD, polymucleotides, paroxysmal nocturnal haemoglobinuria, polycthaemia or arteriosclerosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycthaemia or enrological disorders (e.g. arteriosclerosis, desease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the mensitual oycle, or autoimmune/inflammatory disorders (e.g. Alzheimer disease, parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the mensitual oycle, or autoimmune/inflammatory disorders (e.g. Alzheimer disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, contact derm
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                                                                                                                                                                                                                                   Burford N;
                                                                                                                                                                                                                  Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                New human proteins associated with cell growth, differentiation and death, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8645 BP; 2060 A; 2494 C; 2319 G; 1771 T; 0 U; 1 Other;
                                                                                                                                                                                                               Elliott VS, B
G, Duggan BM,
Walia NK;
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Mismatches:
Indels:
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Tran UK, Khare R, W
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Matches:
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                                                                                                                                                                                                                    Lu Y,
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                                           09-FEB-2001; 2001US-0268111P.
23-FEB-2001; 2001US-0271175P.
08-MAR-2001; 2001US-0274503P.
09-MAR-2001; 2001US-0274552P.
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08-FEB-2002; 2002WO-US003715.
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Xu Y, Gietzen KJ,
Richardson TW, Tra
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P-PSDB; ABG97359.
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Ding L,
Lu DAM,
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                                                                                       ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu 240
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                            5271 ACCTCCAGCAAGAATGATGTCACCATAACCACCAACCTGTCTGCCTCAGGGGGCCTTCTAC
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                                                                                                                                   81 LeuasnThrGlnasnMetTyrGluLeuSerSerProlleaspGlnGluLeuTyrLeuPhe
                                                                                                                                                                   4791 CICAACACCCAGAACAIGIAIGAGCIGICIICACCAAIIGACCAGGAGCICIAICIGIII
                                                                                                                                                                                                     101 AspIhrThrGlyLysHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn
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                                                                                                                                                                                                                                                                                            AsnValArgArgAspSerThrGlyMetProLeuTrpLeuValValProAspGlyGlnVal
                                                                                                                                                                                                                                                                                                                                                                41 TyralaLysAspalaLysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu
                                                                 LeuTyrvalAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOV15c encoding cDNA SEQ ID NO:39.
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Location/Oualifiers

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Percent Similarity:

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4976

Human NOV15d encoding cDNA SEQ ID NO:41.

8473

Length: Matches:

2.34e-86 935.50

Alignment Scores: Pred. No.: Score:

258. .8144

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(CURA-) CURAGEN CORP.
                                                                               WPI; 2002-732706/79.
                                                                                 P-PSDB; ABP53588
         WO200262999-A2
                  31-DEC-2001;
                                                   17-AUG-2001;
                                                                                                                                                              Sequence 8473
                                                     17-SEP-2001;
                                                                     Kekuda R, P.
Rastelli L,
              15-AUG-2002
                                                                 Spytek KA,
                                                                          Gunther E,
                                                                                            diseases
CDS
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AAAATTAACCGGATAAGGCAGGTCACAACAGATGGAGAAATCTCCTTAGTGGCCGGAATA 4376
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Indels:
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v VT, Spaderna SK, Gorman L;
Gangolli EA, Guo X, Shenoy S;
Burgess CE, Edinger S, Ellerman K;
Macdougall JR;
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Iyankar U, Shimkets RA, Tcherne
Wuda R, Patturajan M, Gusev V,
stelli L, Casman SJ, Boldog F,
nther E, Smithson G, Millet I,
                               /product= "NOV15c"
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02-JAN-2001; 2001US-0259415P.
04-JAN-2001; 2001US-0259785P.
20-FEB-2001; 2001US-025914P.
09-MAR-2001; 2001US-0279863P.
29-MAR-2001; 2001US-0279832P.
29-MAR-2001; 2001US-0279833P.
13-APR-2001; 2001US-0228889P.
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29-MAY-2001; 2001US-0294080P.
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cerebroprotective, nootropic, antidiabetic, antiinflammatory; fungicide, antianaematic, antiantrinic; antidiabetic, antiinflammatory; fungicide, antianaematic, antibacterial; protozoacide; antianlaninthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic crebrovascular disease; Alzheimer's disease; allergy; pick's disease; vesicular transport disease; cystic fibrosis; goitre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss. Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular;

Homo sapiens

Location/Qualifiers /product= "NOV15d" . .8140 ಹ /\*tag=

WO200262999-A2

15-AUG-2002

31-DEC-2001; 2001WO-US049976

2001US-0259415P. 2001US-0259785P. 2000US-0258928P 09-MAR-2001; 29-MAR-2001; 29-DEC-2000; 04-JAN-2001; 20-FEB-2001;

29-MAR-2001;

2001US-0269814P. 2001US-0279863P. 2001US-0279832P. 2001US-027983P. 2001US-0281889P. 2001US-028447P. 2001US-0284683P. 2001US-0313325P. 2001US-0322699P. 2001US-0312915P. 2001US-0333350P 25-APR-2001; 29-MAY-2001; 13-APR-2001; 18-APR-2001; 26-NOV-2001; 16-AUG-2001; 17-AUG-2001; 17-SEP-2001

(CURA-) CURAGEN CORP.

Tchernev VT, Spaderna SK, Gorman L; usev V, Gangolli EA, Guo X, Shenoy S; ldog F, Burgess CE, Edinger S, Ellerman K; llet I, Macdougall JR; Liu X; Vernet CAM, Eisen A, Li L, Wolenc AR, Verne Shimkets RA, Tchernev atturajan M, Gusev V, Casman SJ, Boldog F, Smithson G, Millet I, Malyankar U, Snimweev .... Kekuda R, Patturajan M, Rastelli L, Casman SJ, Li L, Spytek KA,

WPI; 2002-732706/79. P-PSDB; ABP53589 New NOVX polypeptides and polymucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune

Claim 8; Page 123-125; 444pp; English

diseases

The present invention describes novel human proteins designated NOVK, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, carchostalic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, antidabetic, antiinflammatory, antiheumatic, antiarthritic, virucide, immunosuppressive, antiallergic, antihanemic, antibaterial, fungicide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, uncleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, discheders of vesicular transport (e.g. cystic fibrosis, disease), disease, or gostro, gastrointestinal

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4913 geangeacaacentringacrangacaegercarcraeaaanennacentricca ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu 241 ThrSerSerLys---AspAspValThr1leThrThrAsnLeuSerAlaSerGlyAlaPhe 

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            autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic and protozoal infections. The NOVY proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be used in chromosome mapping, identifying individuals from minute biological samples (tissue typing), and in forensic identification of a
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disorders (e.g. ulcerative colitis, or gastric and duodenal disorders),
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biological sample. The present sequence encodes human NOV15d, which
located on chromosome 4
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TyrThr 261

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Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular;
                                                                                                                                                   cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide; antianamic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovacular disease; Alzheimer's disease; allergy, bick's disease; vesicular transport disease; cystic fibrosis; goitte; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine;
                                                                                                                                                                                                                                     ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.
                                                                                                                  Human NOV15b encoding cDNA SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/product= "NOV15b"
                                             ABQ82344 standard; cDNA; 8645 BP
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2001US-0283889P.
2001US-0284447P.
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2001US-0259785P.
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2001US-0279863P.
2001US-0279832P.
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2001US-0312915P.
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/*tag≈ a
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5093 TACACC 5098
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29-MAR-2001;
13-APR-2001;
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20-FEB-2001;
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16-AUG-2001;
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17-SEP-2001;
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                                  ABQ82344
                       RESULT
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Shenoy S; Gorman L; Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X; U, Shimkets RA, Tchernev VT, Spaderna SK, Gorme Patturajan M, Gusev V, Gangolli EA, Guo X, She, Casman SJ, Boldog F, Burgess CE, Edinger S, Smithson G, Millet I, Macdougall JR; Rastelli L, Casman SJ, Gunther E, Smithson G, Malyankar U, Kekuda R, Spytek

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> 2002-732706/79. P-PSDB; ABP53587

New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune diseases

Claim 8; Page 114-117; 444pp; English.

The present invention describes novel human proteins designated Novx, where X is 1 to 20 e.g. NoV1. NoVX sequences can have neuroprotective, where X is 1 to 20 e.g. NoV1. NoVX sequences can have neuroprotective, where X is 1 to 20 e.g. NoV1. NoVX sequences can have neuroprotective, crytostatic, antidoctive, cardiovascular, antidiabetic, antidoctive, antidoctive, antidoctive, antidoctive, antidoctive, antidoctive, antidoctive, antidoctive, antidoctive, antidoctive, antidoctive, and can be used in gene therapy. The NoVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a therapy. The NoVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a covary, testis and uterus, neurological disorders (e.g. epilepsy, stroke, covary, testis and uterus, neurological disorders (e.g. epilepsy, stroke, covary, testis and uterus, neurological disorders or pick's diabetes mellitus, Grave's disease, Alzheimer's disease or Pick's diabetes mellitus, Grave's disease, or goitre), gastrointestinal continumume diseases (e.g. allergic reactions, autoimmume hamolytic and protozoal infections. The NoVX proteins can be used as immunogens to controinted antibodies and as vaccines. The NoVX nucleotide sequences may be used in chromosome mapping, identifying individuals from minute control or contro located on chromosome 4

Sequence 8645 BP; 2343 A; 2060 C; 2200 G; 2038 T; 0 U; 4 Other;

8645 172 35 54 Conservative: Mismatches: Indels: Length: Matches: 2.4e-86 935.50 79.01\$ 65.65\$ Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: No.: Pred.

US-10-029-020-14\_COPY\_1490\_1750 (1-261) x ABQ82344 (1-8645)

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                         5088
                                                                                                                                                                              LeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn
                                                                                                                           201 GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
                                                                       ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlu
                                                                                                                                                               ThrSerSerLys---AspAspValThrIleThrThrAsnLeuSerAlaSerGlyAlaPhe
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/*tag= a
/product= "NOV15a"
/transl_except= (pos
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04-JAN-2001; 20010S-0259415F.

20-FEB-2001, 20010S-0259785F.

09-MAR-2001, 20010S-0279863F.

29-MAR-2001, 20010S-0279832P.

29-MAR-2001, 20010S-0279833P.

13-APR-2001, 20010S-028444P.

25-APR-2001, 20010S-0286683F.

25-ARR-2001, 20010S-0286683F.

16-AUG-2001, 2001US-0312915F.

17-SEP-2001, 2001US-031332F.
                                                                                                                                                                                                                                                                                                         ABQ82343 standard; cDNA; 8675
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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, noticapic, cardiovascular, contidiabetic, antiinflammatory, antirhemmatic, antiarthritic, virucide, immunosuppressive, antiallergic, antianaemic, antiarthritic, virucide, immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide, protozoacide and antihelminhic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder. Such as cancers (e.g. elutaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, covary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzneimer's disease or pick's disease, disease, disease, or goitre), gastrointestinal disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), candennia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be biological sample. The present sequence encodes human Novisa, which is located on chromosome a
                                                                                                                                                                                                                                         New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
          Spytek KA, Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;
Malyankar U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;
Kekuda R, Patuurajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
Gunther E, Smithson G, Millet I, Macdougall JR;
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                                                          Malyum.
Kekuda R, Pattur.,
Rastelli L, Casman SJ,
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Seguence 8675 BP; 2362 A; 2067 C; 2201 G; 2041 T; 0 U; 4 Other; 8675 172 35 54 Conservative: Mismatches: Matches: Length: Indels: 2.41e-86 935.50 79.01% 65.65% 67.59% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match. Score:

US-10-029-020-14\_COPY\_1490\_1750 (1-261) x ABQ82343 (1-8675)

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	4681 CTGTATATTGCAGATCTAGGGATATCCGGATCCGGGCTGTGTCAAGAATAAGCCTTTA 4740	20 4560 40 4620 60 4680 4740	LysileAsnArglleArgGlnValThrThrSerGlyGlulleSerLeuValAlaGlyAla 20	1 4501 21 41 41 4621 61
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4681 CTGTATATTGCAGATCTAGGGAATATCCCGGGCTGTGTGTCAAAGAATAAGCCTTTA 4740		80	LeuTyrValalaAspLeuGlyAsnIleArglleArgPhelleArglysAsnLysProPhe	61
61 LeuTyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe 80	61 LeuTyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe 80	4680		4621
4621 TACGCCAAGGATGCCCAAACTCAGTGCCCCCCCCCCCCC	4621 TACGCCAAGGATGCCCAAACTCAGTGCCCCCCCCCCCCGCTGCTTCTCCAGATGGTACA 4680 61 LeutyzvalalaAspLeuGlyAsmileArgileArgPheileArgLySAsmLySProPhe 80	09	TyralaLysaspalaLysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu	41
41 TyralalysaspalalysleuasnThrProSerSerLeualavalCysalaAspGlyGlu 60	41 TyralalysaspalalysleuhsnThrProSerSerLeuhlaValCysAlaAspGlyGlu 60	4620	CTTCAGAGTGTGACTGCAAAATGATGCCAACTGTGACTGTTACCAGAGTGGAATGGC	4561
4561 CCTTCAGAGGGGCACAAAAGGGCCAACTGGGACTGTACCAGAGGGAGAGGC 4620 41 Tyralaly8aspalaly8leuAenThrProSerSerLeuAlaValCy8AlaAspGlyGlu 60 4621 TAGGCCAAGGATGCAGAACTGCCCCATCCTCCCTGGCTGCTTCTCCAGATGGTACA 4680 61 LeuTyrValalaAspLeuGlyAenIleArg1leArgPhelleArg1y8ProPhe 80 61 LeuTyrValalaAspLeuGlyAenIleArg116ArgPhelleArg1y8AsnLy8ProPhe 80 61 LeuTyrCAGAACTGGGAATATCCGGGCTGTGTCAAAGAATAAGCCTTTA 4740	4561 CCTTCGGGGGGGGGAAAAGGGCGACGGGACGGGCTGCAGGGGGGGG	40	ProSerGlyCysAspCysLysAsnAspAlaAsnCysAspCysPheSerGlyAspAspGly	21
21 ProSerGlyCyBAspCyELysAsnAspAlaAsnCyBAspCysPheSerGlyAspAspGly 40	21 ProSerGlyCyBAspCyELySAsnAspAlaAsnCyBAspCysPheSerGlyAspAspGly 40	4560		4501
		20	LysileAsnArgileArgGlnValThrThrSerGlyGluileSerLeuValAlaGlyAla	Н

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2001US-0333350P

(CURA-) CURAGEN CORP

P-PSDB; ABG61913

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4921 AGAATTAGACGGGACCCAAATCGCATGCCAGTTCGAGTGGTGTCTCCTGTAACCAAGTG 4980
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AspThrThrGlyLysHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn 120
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                   GACATCAATGGTACTCACCAATATACTGTAAGTTTAGTCACTGGTGATTACCTTTACAAT
                                     PheThrTyrThrGlyAspGlyAspIleThrLeuIleThrAspAsnAsnGlyAsnMetVal
                                                                                                                TyrTrpValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGlu
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                                                                                                                                                                  ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu
                                                                           AsnValArgArgAspSerThrGlyMetProLeuTrpLeuValValProAspGlyGlnVal
                                                                                                                                                                                           GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
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                                                                                                                                                                                                                                                                     241 ThrSerSerLys---AspAspValThrIleThrThrAsnLeuSerAlaSerGlyAlaPhe
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2000US-00733288.
2000US-00733742.
2001US-026357P.
2001US-027688P.
2001US-0276888P.
2001US-0286214P.
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24-JAN-2001;
16-MAR-2001;
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06-APR-2001;
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30-APR-2001;
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The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises contexting a bloogical sample from the patient with prostate cancerassociated polynucleotides (designated PC genes) that selectively bybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer of associated genes are useful for diagnosing or treating prostate cancer. Cas well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.
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                                Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
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|TACTGGCTGACTATAAGCAATGGAGTCCTGAAAAGAGTGTCAGCCCAAGGCTATAAT 4945
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inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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5212 TACTGGCTGACTATAAGCAGCAATGAGTCCTGAAAGAGTGTCAGCCCAAGGCTATAAT
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cacattcgccgtgaigcaggcggaatgccgctatggcttgtggtgcctggcggacaagta
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                                                          Sequence 13202 BP; 3921 A; 2764 C; 2865 G; 3652 T; 0
                                                                                                                                      Conservative:
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                                         4946 CCGGCCTTAATGACCTATCCAGGAAACACAGGCCTTCTGGCTACCAAAAGTAACGAAAAT
                                                                                  GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
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R, Wang 2
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J, Zhang J, Ren F,
Goodrich R;
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Wang D, Wang J
Wejhrman T, G
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2000US-00560875.

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20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
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, Yang Y,
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01-SEP-2000;
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4043 ATTTACATTGCAGACCTTGGAAATATTCGGATCAGGGCGGTCAGCAAGAACAAGCCTGTT 4102
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                                                AspThrThrGlyLysHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn
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                                                                                                                                                                                            161 TyrTrpValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGlu
                                 LeuAsnThrGlnAsnMetTyrGluLeuSerSerProlleAspGlnGluLeuTyrLeuPhe
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14-MAY-2002; 2002US-00144194.
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P-PSDB; ABR58318.
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                                                                                                                                                                                                                                                                                                                                New isolated human differentially-regulated breast cancer polymucleotide and polypeptide, useful for diagnosing, staging, prognosticating, preventing and/or treating diseases and conditions relating to breast cancer.
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                                                           Breast cancer; cytostatic; gene therapy; antisense therapy; regulated; drug discovery; clinical medicine; forensic medicine; gene; chromosome 5g33.3; ds.
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                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 79; 127pp + Sequence Listing; English.
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863.50
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Best Local Similarity:
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                                                                                                                                   WO2003029421-A2
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                                                                                                                                                                               02-OCT-2002;
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Sequence 9695 BP; 2567 A; 2582 C; 2434 G; 2112 T; 0 U; 0 Other;
                                                                               ftp.wipo.int/pub/published_pct_sequences
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differentially-regulated in breast cancer. The methods and compositions of the present invention are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and/or treating diseases and conditions relating to breast cancer, and may be used in gene therapy or antisense therapy. They can also be used in research, drug discovery, clinical medicine and forensic medicine. Sequences given in records differentially-regulated in breast cancer. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
New isolated human differentially-regulated breast cancer polynucleotide and polypeptide, useful for diagnosing, staging, prognosticating, preventing and/or treating diseases and conditions relating to breast
                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotides which are
                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 81; 127pp + Sequence Listing; English.
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9695 162 40 59 Conservative: Mismatches: Length: Matches: Indels: Gabs: 8.41e-79 863.50 77.10% 61.83% 62.39% Similarity: Percent Similarity: Alignment Scores: Query Match: DB: Best Local Pred

US-10-029-020-14\_COPY\_1490\_1750 (1-261) x ACC72052 (1-9695)

4980 ATCACCCTCÁCIGGIGGICÁCIÁATGGAGGCCTCÁAÁGTCGTGTCCÁCÁCÁGAACCTGGÁG 5039 4799 4859 4560 gccircioancriocoa criocoa a a a a contra de a contra de a contra de a contra de a contra de a contra de a 4620 TACGCGACTGATGCTTGAATTCCCCATCATCCTTAGCTGTAGCTCCAGATGGTACC 4679 LeualametMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn 200 TyrTrpValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGlu 180 100 120 PheThrTyrThrGlyAspGlyAspIleThrLeulleThrAspAsnAsnGlyAsnMetVal 140 141 AsnValArgArgAspSerThrGlyMetProLeuTrpLeuValValProAspGlyGlnVal 160 21 ProserGlyCysAspCysLysAsnAspAlaAsnCysAspCysPheserGlyAspAspGly 40 9 80 1 LysileAsnArglleArgGlnValThrThrSerGlyGluileSerLeuValAlaGlyAla 20 TyralalysAspalalysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu LeuTyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe LeuasnThrGlnasnMetTyrGluLeuSerSerProlleaspGlnGluLeuTyrLeuPhe 101 AspThrThrGlyLySHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn <u> AACGCTGATGGCATCCACCAATACACTGTGAGCCTGGTGACAGGGGAGTACTTGTACAAT</u> 181 4800 121 161 81 4500 41 61 ò d ਨੇ a ð g q à g  $\delta$ à d ð g ð g ð q

Majumder K;

Shimkets RA, Herrmann JL, Mezes PS, Rastelli L;

Fernandes E,

Mishra V,

Macdougall J,

Vernet CAM,

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numen; related integrated neonatal allocations, assertions, assertions, assertions, assertions, assertions, assertions, and assertion neurological disorder; neurodegenerative disorders; nerve trauma; familial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy; demyelinating dardner syndrome; familial myelodysplastic syndrome; mental health condition; immunological disorder; allergy; infertility; bronchial asthma; Avellino type eosinophilia; lung disease; deafness; reproductive disorder; glycoprotein Ia deficiency; reproductive syndrome; liver cirrhosis; hepatitis C; virucide; gastric disorders; pancreatic disease; Schistosoma mansoni infection; Spinocerebellar ataxia; Plasmodium falciparum parasitaemia; diabetes; Corneal dystrophy-Greonow type I; Corneal dystrophy-lattice type I;
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GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
                                                                                                                                                                 ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu
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The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the nucleic acids encoding them. These sequences are useful for the treatment or prevention of numerous disorders including myelogenous leukaemia, carcinomas, melanomas, giorders including myelogenous leukaemia, carcinomas, melanomas, astrocytomas, congenital neonatal alloimmune thrombocytopaenia, neurological disorders, neurodegenerative cisorders, neurodegenerative cisorders, neurodegenerative myelodysplastic syndrome, mental health conditions, immunological myelodysplastic syndrome, mental health conditions, immunological cisorders, allergy and infection, bronchial asthma, Avellino type cosinophilia, lung diseases, reproductive disorders, infertility, male desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric disorders, pancreatic diseases such as diabetes, Schistosoma mansoni infection Spinocerabellar ataxia, plasmodium falciparum parasitaemia, corneal dystrophy-dreonouw type I, corneal dystrophy-lattice type I and he remos hem mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental mental
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                                                                                                      Novel polypeptides designated as FCTRX polypeptides, useful in detection, prevention and treatment of a broad range of pathological states.
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                            WPI; 2001-596837/67.
P-PSDB; AAU08681.
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5208 ACGGGGGTGGTACCAGTCTGCACCGGGAAATGGAAAATCTATTACCATTGACATTGAG 5267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, gene, ss, FCTR3f, colorectal cancer, adenomatous polyposis coli; myelogenous leukaemia; congenital neonatal autoimmune thrombocytopenia; ovarian cancer; brain tumour; breast cancer; glioma, astrocytoma; renal call carcinoma, melanoma; clear cell carcinoma; melanoma; clear cell carcinoma; granular cell carcinoma; neurological disorder;
                           LeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn
                                             5148 GGATGGACGACTTTCTATGACTATGACCACGAAGGCCGCCTGACCAACGTGACGCGCCCCC
                                                                                                                                            221 ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu
                                                                                                                                                                                                                      5268 AACTCCAACCGTGATGACGTCACTGTCATCACCAACCTCTTCAGTAGAGGCCTCC
                                                                                    201 GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurodegenerative disorder; nerve trauma; familial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy; dardner syndrome; mental health condition; immunological disorder; dardner syndrome; mental health condition; immunological disorder; gllergy; asthma; lung disease; reproductive disorder; deafness; liver cirrbosts; hepatitis C; gastric disorder; pancreatic disease; plasmodium falciparum infection; spinocerebellar ataxia; plasmodium falciparum infection; Groenouw's corneal dystrophy;
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Rastelli L;
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Mezes PS,
                                                                                                                                                                                                                                                                                                                                                ADB32028 standard; cDNA; 9729 BP.
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Macdougall J, Mishra V,
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HERRMANN J.
MAJUMDER K.
MACDOUGALL J.
                                                                                                                                                                                                                                                                                         5328 TACACA 5333
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FERNANDES E.
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P-PSDB; ADB32029.
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MEZES P S.
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(MACD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 TyrTrpValThiMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGlu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheThrTyrThrGlyAspGlyAspIleThrLeuIleThrAspAsnAsnGlyAsnMetVal
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181 LeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn
                                                                                                                                                                                                                                                                                                            AAS14085 standard; DNA; 9826 BP
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2000US-0187294P.
2000US-0187294P.
2000US-0190400P.
2000US-0196018P.
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03-MAR-2000; 2
06-MAR-2000; 2
17-MAR-2000; 2
07-APR-2000; 2
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                                                                                        The invention relates to FCTRX polypeptides and the polynucleotides encoding them. The sequences of the invention are useful for the manufacture of a medicament for diagnosing and treating disorders associated with the FCTRX polypeptide, such as colorectal cancer, adenomatous polyposis coli, myelogenous leukaemia, congenital neonatal adenomatous polyposis coli, myelogenous leukaemia, congenital neonatal cumours, mammary tumours, human gliomas, astrocytomas, renal cell carcinoma, breast adenocarcinoma, ovarian carcinoma, melanomas, clear carcinoma, breast adenocarcinoma, neurological disorders, cell and granular cell carcinomas, neurological disorders, coll and granular electromas, neuropathy, Gardner syndrome, mental health syndrome, Charcot-Marie-Took neuropathy, Gardner syndrome, mental health conditions, immunological disorders, allergy and infection, methal health diseases, male and female reproductive disorders, dasfness, glycoprotein deficiency, desmoid tumour, turcot syndrome, liver cirrhosis, hepaticis conditions, spinocrebellar ataxia, plasmodium falciparum infection, infection, gromeal dystrophy and lattice corneal dystrophy. This sequence represents cDNA encoding an FCTRX polypeptide of the invention.
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New FCTRX polypeptide and encoding polynucleotide, useful for preventing or treating FCTRX-related disorders, such as cancer, autoimmune, neurodegenerative, gastrointestinal, reproductive and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LysileAsnArgileArgGlnValThrThrSerGlyGluileSerLeuValAlaGlyAla
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                                                                                                                                                                                                                                                                                                                                                          Sequence 9729 BP; 2548 A; 2629 C; 2438 G; 2114 T; 0 U; 0 Other;
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Mismatches:
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Matches:
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                                                                       Claim 9; Page 34-37; 155pp; English.
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77.10%
61.83%
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Best Local Similarity:
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Human; FCTRX; myelogenous leukaemia; carcinoma; melanoma; glioma; ds;

W astrocytoma; congenital neonatal alloimmune thrombocytopaenia; infection;

W astrocytoma; congenital neonatal alloimmune thrombocytopaenia; infection;

KW meurological disorder; neurodegenerative disorders; nerve trauma;

KW familial myelodysplastic syndrome; francial erroch neuropathy;

W mental health condition; immunological disorder; allergy; infertility;

KW mental health condition; immunological disorder; allergy; infertility;

KW bronchial asthma; Avellino type eosinophilia; lung disease; deaficiency;

KW desmoid disease; turcot syndrome; liver cirrhosis; hepatitis C; virucide;

KW gastric disorder; pancreatic disease; Schistosoma mansoni infection;

KW pinocerebellar ataxia; plasmodium falciparum parasitaemia; diabetes;

KW Reis-Bucklers corneal dystrophy; cytostatic; immunosupressive;

KW antiallergic; antiasthmatic; antinfertility; antiinflammatory;

KW antidiabetic; protozoacide; hepatotropic; virucide; ophthalmological;

KW gene therapy; FCTR3b; neurestin-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5268 AACTCCAACCGTGATGACGTCACTGTCACCAACCACTCTTCAGTAGAGGCTCC 5327
                                                                                                                     GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
                                                                                                                                                                                                                                                                                        221 ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu
                                                                                                                                                                                                                                                                                                                                                  241 ThrSerSerLys---AspAspValThrIleThrThrAsnLeuSerAlaSerGlyAlaPhe
5088 CTTGGTCTCATGACCTATGATGGCAACACTGGGCTCCTGGCCACCAAGAGCGATGAACA
                                                                                                                                                                                                      5148 GGATGGACGACTTTCTATGACTATGACCACGAAGGCCGCCTGACGAGGTGACGCCCC
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Majumder K;

Herrmann JL,

Shimkets RA, Herrman Mezes PS, Rastelli L;

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The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the nucleic acids encoding them. These sequences are useful for the treatment or prevention of numerous disorders including myelogenous leukaemia, carcinomas, melanomas, gliomas, astrocytomas, congenital neonatal alloimmune thrombocytopaenia, neurological disorders, neurodegenerative carcinomas, terminal myelodysplastic syndrome, familial myelodysplastic syndrome, carcinome, familial myelodysplastic syndrome, mental health conditions, immunological myelodysplastic syndrome, mental health conditions, immunological disorders, allargy and infection, bronchial asthma, Avellino type cosinophilia, lung diseases, reproductive disorders, infertility, male and female reproductive disorders, glaycoprotein la deficiency, desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric disorders, pancreatic diseases such as diabetes, Schistosoma mansoni infection Spinocerebellar ataxia, plasmodium falciparum parasitaemia, corneal dystrophy-dreconow type I, Corneal dystrophy-lattice type I and remained the corneal dystrophy. This sequence represents DNA encoding
                                                                                                                                                                                                                    polypeptides designated as FCTRX polypeptides, useful in detection,
                                                                                                                                                                                                                                          prevention and treatment of a broad range of pathological states.
                                                                                                                                                                                                                                                                                          Claim 9; Page 33-35; 215pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FCTR3b, a neurestin-like protein
                                                                         Fernandes E,
                                                                                                  Mishra V,
                           (CURA-) CURAGEN CORP.
                                                                                                                                             2001-596837/67.
                                                                                                                                                                    P-PSDB; AAU08680.
                                                                                               Macdougall J,
                                                                         Vernet
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Sequence 9826 BP; 2567 A; 2643 C; 2479 G; 2137 T; 0 U; 0 Other;

9826 162 40 59 Length:
Matches:
Conservative:
Mismatches:
Indels: 8.55e-79 863.50 77.10% 61.83% 62.39% Similarity: Percent Similarity: Alignment Scores: Query Match:

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4944
                                                              AAGATTAACCGTCTACGCCAGGTAACAACCAACGGGGAGATCTGCCTTTTAGCTGGGGGCA 4704
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|TACGCGACTGATGCCATCTTGAATTCCCCATCATCCTTAGCTGTAGCTCCAGATGGTACC 4824
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                                                                                                                                                                                                                                                                                   LeuAsnThrGlnAsnMetTyrGluLeuSerSerProIleAspGlnGluLeuTyrLeuPhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160
                                                                                                                                                                                                                                                                                                                                                101 AspThrThrGlyLysHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn 120
                                                                                                                                                                                                                                                                                                                                                                                                                      140
                                                                                                   40
                                                                                                                                                           TyrAlaLysAspAlaLysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu 60
                                                                                                                                                                                                                             80
                                1 LysileAsnArglleArgGlnValThrSerGlyGluIleSerLeuValAlaGlyAla 20
                                                                                             ProSerGlyCysAspCysLysAsnAspAlaAsnCysAspCysPheSerGlyAspAspGly
                                                                                                                                                                                                                                                   1825 ATTIACATIGCAGACCTIGGAAATATICGGATCAGGGGGGGCGCTCAGGAACAAGCCIGIT
                                                                                                                                                                                                                                                                                                       141 AsnValArgArgAspSerThrGlyMetProLeuTrpLeuValValProAspGlyGlnVal
                                                                                                                                                                                                                         LeuTyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe
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US-10-029-020-14_COPY_1490_1750 (1-261) x AAS14085 (1-9826)
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Majumder K;

Herrmann J,

Shimkets R,

Fernandes E,

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Vermet

RAST/)

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5065 AAGATCCGTCGGGACAGCAGTGCCCCGTCACCTGTCATGCCTGACAACAAC 5124
                                                                                                                                                                 5304
                                                                                                                                                                                                   220
                                                                                                                                                                                                                                                161 TyrTrpValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGlu 180
                                                                                                                                                                                   ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu 240
                                                                                     LeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene; ss; FCTR3b; colorectal cancer; adenomatous polyposis coli; myelogencous leukaemia; congenital neonatal autoimmune thrombocytopenia; ovarian cancer; brain tumour; breast cancer; glioma; astrocytoma; renal cell carcinoma; melanoma; clear cell carcinoma; granular cell carcinoma; neurological disorder; factiona; neurological disorder; familial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy; Gardner syndrome; mental health condition; immunological disorder; glarcot syndrome; lung disease; reproductive disorder; deafness; glycoprotein deficiency; desmoid tumour; turoot syndrome; liver cirrhosis; hepatitis C; gastric disorder; panoreatic disease; plasmodium falciparum infection; spinocerebellar ataxia; plasmodium falciparum infection; Groenouw's corneal dystrophy;
                                                                                                 GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro
                                                     241 ThrSerSerLys---AspAspValThrIleThrThrAsnLeuSerAlaSerGlyAlaPhe
                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                         ADB32023 standard; cDNA; 9826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33-MAR-2000; 2000US-0186592P
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lattice corneal dystrophy
                                                                                                                                                                                                                                                                                                          5425 TACACA 5430
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HERRMANN J.
MAJUMDER K.
MACDOUGALL J
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FERNANDES E.
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MEZES P S.
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(MEZE/)
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The invention relates to FCTRX polypeptides and the polynucleotides encoding them. The sequences of the invention are useful for the encoding them. The sequences of the invention are useful for the encoding them. The sequences of the invention are useful for the manufacture of a medicament for diagnosing and treating disorders associated with the FCTRX polypeptide, such as colorectal cancer, adenomatous polyposis coli, myelogenus leukaemia, congenital neonatal cautoimmune thromborytopenia, malignant ovarian tumours, malmant breast adenocarcinoma, voraian carcinoma, melanomas, clear carcinoma, breast adenocarcinoma, ovarian carcinoma, melanomas, clear carcinoma, breast adenocarcinoma, neurological disorders, coll and granula disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Marie-Tooth neuropathy, Gardner syndrome, mental health conditions, immunological disorders, allergy and infection, asthma, lung diseases, male and female reproductive disorders, dafeness, glycoprotein deficiency, desmoid tumour, turcot syndrome, liver cirrhosis, hepatitis cordition, spinocerebellar ataxia, plasmodium falciparum infection, groenouw's corneal dystrophy and lattice corneal dystrophy. This sequence corneal colling an FCTRX polypeptide of the invention.
                                                                                                                       New FCTRX polypeptide and encoding polynucleotide, useful for preventing or treating FCTRX-related disorders, such as cancer, autoimmune, neurodegenerative, gastrointestinal, reproductive and inflammatory
Mezes PS, Rastelli L;
                                                                                                                                                                                                                                                                   Claim 9; Page 29-32; 155pp; English.
Macdougall J, Mishra V,
                                                     WPI; 2003-625633/59.
                                                                           P-PSDB; ADB32024
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Sequence 9826 BP; 2567 A; 2645 C; 2476 G; 2138 T; 0 U; 0 Other;

9826 162 40 59 Length: Matches: Conservative: Mismatches: Indels: Gaps: 8.55e-79 863.50 77.10% 61.83% 62.39% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB: Score:

US-10-029-020-14\_COPY\_1490\_1750 (1-261) x ADB32023 (1-9826)

20	4704	40	4764	09	4824	80	4884	100	4944	120	5004	140	5064	160
LysIleAsnArg1leArgGlnValThrThrSerGlyGluIleSerLeuValAlaGlyAla 20	ABGATTAACCGTCTACGCCAGGTAACAACCAACGGGGAGATCTGCCTTTTAGCTGGGGCA	21 ProSerGlyCysAspCysLysAsnAspAlaAsnCysAspCysPheSerGlyAspAspGly 40	GCCTCGGACTGCGACTGCAAAACGATGTCAACTGCTATTCAGGAGATGATGCC	TyrAlaLysAspAlaLysLeuAsnThrProSerSerLeuAlaValCysAlaAspGlyGlu 60	TACGCGACTGATGCCATCTTGAATTCCCCATCATCCTTAGCTGTAGCTCCAGATGGTACC	LeuTyrValAlaAspLeuGlyAsnIleArgIleArgPheIleArgLysAsnLysProPhe 80		LeuasnThrGlnasnMetTyrGluLeuSerSerProlleAspGlnGluLeuTyrLeuPhe	CITAATGCCTTCAACCAGTATGAGGCTGCATCCCCCGGAGAGCAGGAGTTATATTTT	AspThrThrGlyLySHisLeuTyrThrGlnSerLeuProThrGlyAspTyrLeuTyrAsn	::: 4945 AACGCTGATGGCTATCCACCAATACACTGTGAGCCTGGTGACAGGGGAGTACTTGTACAAT	PheThrTyrThrGlyAspGlyAspIleThrLeuIleThrAspAspAsnGlyAspMetVal	TICACATATAGTACTGACAATGATGTCACTGAATTGATAGACAATAATGGGAAATTCCCTG	141 AsnValArgArgAspSerThrGlyMetProLeuTrpLeuValValProAspGlyGlnVal 160
н	4645	21	4705	41	4765	61	4825	81	4885	101	4945	121	5005	141
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5065 AAGATCCGTCGGGACAGCAGTGGCATGCCCCGTCACCTGCTCATGCCTGACAACCAGATC 5124	161 TyrTrpValThrMetGlyThrAsnSerAlaLeuLysSerValThrThrGlnGlyHisGlu 180	5125 ATCACCCTCACCGTGGGCACCAATGGAGGCCTCAAAGTCGTGTCCACACAAACCTGGAG 5184	181 LeuAlaMetMetThrTyrHisGlyAsnSerGlyLeuLeuAlaThrLysSerAsnGluAsn 200	5185 CTTGGTCTCATGACCTATGATGGCAACACTGGGCTCCTGGCCACCAGAGGGGTTGAAACA 5244	201 GlyTrpThrThrPheTyrGluTyrAspSerPheGlyArgLeuThrAsnValThrPhePro 220		221 ThrGlyGlnValSerSerPheArgSerAspThrAspSerSerValHisValGlnValGlu 240	5305 ACGGGGGTGGTAACCACTGCACCGGGAAATGGAGAAATCTATTACCATTGACATTGAG 5364	241 ThrSerSerLysAspAspValThrIleThrThrAsnLeuSerAlaSerGlyAlaPhe 259	5365 AACTCCAACCGTGATGACGTCACTGTCATCACCAACCTCTTTTAGAGGCCTCC 5424	260 TyrThr 261	5425 TACACA 5430	
Db 5	λΌ	9 qa	δ	g qa	δ	qa	λ	qa	۸٥	qq	λ̈	qq	

Search completed: August 14, 2004, 02:31:38 Job time : 514.726 secs

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Scoring table:

Title: Perfect score:

Run on:

Sequence:

Listing first 45 summaries

Command line parameters:

Database

Ouery Score Match Length DB

Post-processing: Minimum Match 0% Maximum Match 100%

seq length: 0 seq length: 2000000000

Minimum DB Maximum DB

Searched:

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APPLICANT: Alsobrook II, John et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE
FILE REPREBENCE: 21402-568A
FILE REPREBENCE: 21402-568A
FURENT FILING DATE: 2003-03-06
PRIOR FILING DATE: 2001-12-19
PRIOR PLICATION NUMBER: 60/365,984
PRIOR PLICATION NUMBER: 60/365,984
PRIOR PLICATION NUMBER: 60/372,022
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR PLICATION NUMBER: 60/312,022
PRIOR PLICATION NUMBER: 60/312,779
PRIOR FILING DATE: 2002-06-14
PRIOR PLICATION NUMBER: 60/391,779
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-14
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PRIOR FILING DATE: 2002-06-26
PRIOR PRIOR APPLICATION NUMBER: 60/410,755
PRIOR PRIOR APPLICATION NUMBER: 60/412,957
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Sequence 7, Appli
Sequence 7, Appli
Sequence 78, Appli
Sequence 66, Appl
Sequence 77, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 143, Appl
Sequence 1674, Appl
Sequence 1674, Appl
Sequence 1674, Appl
Sequence 16821, Sequence 160821, Sequence 160821,
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Sequence 76, Appl
Sequence 64, Appl
Sequence 79, Appl
Sequence 81, Appl
Sequence 12, Appl
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Sequence 1949, Ap
Sequence 1949, Ap
Sequence 30579, A
Sequence 30577, A
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Sequence 132367,
Sequence 11176, A
Sequence 72, Appl
Sequence 707, Appl
Sequence 13785, A
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Sequence 16526, A
Sequence 2826, Ap
                      Sequence 43, Sequence 13, Sequence 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1, Market 1
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Publication No. US20040029226A1
GENERAL INFORMATION:
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                   August 14, 2004, 01:33:47; Search time 302.635 Seconds (without alignments) 2448.158 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                        782
1 YIRRIFPSGNVTNILELRNK......LIGSNDLTSARPLSCDSVMD 151
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT NBW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NBW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NBW PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US07_NBW PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_NBW PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_NBW PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NBW PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US09_NBW PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US09_NBW PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US09_NBW PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US09_NBW PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US00_NBW PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US00_NBW PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US00_NBW PUB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US00_NBW PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US00_NBW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                     protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3225727 seqs, 2453303834 residues
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RESULT 3
US-10-583-201-55
; Sequence 55, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVERTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO)
; FILLE REFERENCE: 21402-568A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 AspPheArgHisSerHisSerProAlaHisLysTyrLeuAlaThrAspProMetSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3842 GATTTCAGACATAGTCACAGTCCAGCACACAAATACTACCTGGCCACAGACCCCATGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyalavalPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3902 GGGGCCGTCTTCCTTTCTGACAGCAACAGCCGGCGGGTCTTTAAAATCAAGTCCACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ProArgGlylleThrValAspLysPheGlyLeulleTyrPheValAspGlyThrMetile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-029-020-14_COPY_1250_1400 (1-151) x US-10-029-020-13 (1-8354)
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 AlaArgProLeuSerCysAspSerValMetAsp 151
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PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/27,314
PRIOR PAPLICATION NUMBER: 60/217,314
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-07-35
PRIOR APPLICATION NUMBER: 60/30,566
PRIOR APPLICATION NUMBER: 60/30,32,38
PRIOR PILING DATE: 2001-07-44
PRIOR PILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-05-29
PRIOR SPLICATION NUMBER: 60/294,075
PRIOR SPLICATION NUMBER: 60/294,075
PRIOR SED IN NOWBER: 60/294,075
PRIOR SED IN NOWBER: 60/286,153
PRIOR SED IN NOWBER: 60/286,153
PRIOR SED IN NOWBER: 60/286,153
PRIOR SED IN NOWS: 190
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 13
LENGTH: 8354
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DB:
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; Sequence 13, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
    APPLICANT: Gangolli et al.
; TILE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; CURRENT PILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
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Mismatches:
Indels:
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           PRIOR FILING DATE: 2002-09-23
PRIOR PELING DATE: 2002-09-24
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SOFTWARE CuraSequist version 0.1
STORYBARE CuraSequist version 0.1
STORYBARE CURASEQUIST VERSION 0.1
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; LOCATION: (35),.(8341)
US-10-383-201-43
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3764 TACATTAGAAGGATCTTCCCCTCTGGAAATGTCACCAACATCCTAGAGGTCAGGGTCAGA 3823
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                 4174 AATGATCTCACATCAGCCCGGCCACTCAGCTGTGATTCTGTCATGGAT 4221
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Conservative:
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                                                                                      Sequence 1, Application US/10042865
Publication No. US20040029216A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                     Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
                                                                                                                                               APPLICANT: Padigaru, Muralidhara
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Boldog, Ference I.
Grosse, William M.
Alsobrook II, John P.
Gerlach, Valerie I.
Edinger, Shlomit R.
Rothenberg, Mark E.
Elerman, Karen
Malyankar, Uriel M.
Malyankar, Uriel M.
Millet, Isabelle
Peyman, John
Smithson, Glennda
Gunther, Erik
                                                                                                                                                                                                                                                                                                                                                                   Tchernev, Velizar T
Miller, Charles E
                                                                                                                                                                Li, Li
Zerhusen, Bryan D
Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
                                                                                                                                                                                                                                                                                                            Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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759.50
96.79%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3874 ATGAGTGGGGCCGTCTTTCTTTTCTGACAACAGCGGCGGCGGCTCTTTAAAATCAAGTCC 3933
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Matches:
CURRENT APPLICATION NUMBER: US/10/383,201
CURRENT FILING DATE: 2003-03-06
PRIOR PAPLICATION NUMBER: U0/029020
PRIOR FILING DATE: 2001-12-19
PRIOR PILING DATE: 2002-03-20
PRIOR PILING DATE: 2002-04-12
PRIOR PILING DATE: 2002-04-12
PRIOR PILING DATE: 2002-04-12
PRIOR PILING DATE: 2002-06-14
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PRIOR PILING DATE: 2002-01-16
PRIOR PILING DATE: 2002-03-18
PRIOR PILING DATE: 2002-03-18
PRIOR PILING DATE: 2002-03-18
PRIOR FILING DATE: 2002-01-16
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PRIOR FILING DATE: 2002-01-12
PRIOR PILING DATE: 2002-01-22
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SOFTWARE: CuraSeqList version 0.1
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ORGANISM: Homo sapiens
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Best Local Similarity:
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; LOCATION: (1)
US-10-383-201-55
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                                        61 ValValLysAspLeuValLysAsnSerGluValValValAlaGlyThrGlyAspGlnCysLeu
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APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: MacDougall, John
TITLE ROF INVENTYON: NO. US20020155115A1e1 Proteins and Nuclec Acids Encoding Same
TITLE ROF INVENTY PLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3856 TACATTGGGGGAATCTTCCCATCCAGGAATGTGACTAGCATATTGGAGCTGAGAATAAA 3915
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        AsnLysAspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspPro
                                                                             59 ThrvalvalvalLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGln
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Matches:
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US-09-808-602-79
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Query Match:
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LENGTH: 8409
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  PRIOR FILING DATE: 2001-04-13
PROM APPLICATION WUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
REGOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 411
SOFTWARE: Patentin Ver. 2.1
LENGTH: 8473
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Publication No. US20040022781A1
GENERAL INFORMATION:
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Bisen, Andrew J
Liu, Xiachong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
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Kekuda, Ramesh
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ORGANISM: Homo sapiens
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3976 GGCTCCCTGTACGTATCAGACACCAACAGCCGACGGATATACAAAGTCAAATCTCTTACT 4035
                                                                                                                         ProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100
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APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
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PRIOR APPLICATION NUMBER: 60/259,928
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-02-04
PRIOR FILING DATE: 2001-02-06
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PRIOR FILING DATE: 2001-03-09
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APPLICATION NUMBER: 60/279,863
FILING DATE: 2001-03-29
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Publication No. US20040022781A1
GENERAL INFORMATION:
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Wolenc, Adam R
Vernet, Corine
Bisen, Andrew J
Liu, Xiachong
Malyankar, Uriel M
Shimkets, Richard A
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Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
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Edinger, Shlomit R
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Gusev, Vladimir Y
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Rastelli, Luca
Casman, Stacie J
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Gangolli, Esha A
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Gunther, Erik
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3896 cccaaagaarggcagrrgaraagaarggarraarcracrrgargaaggaaccargarr 3955
              81 prophedspaspthrargCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100
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APPLICANT: MacDougall, John R
ITILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT PEDICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR PLING DATE: 2000-12-29
PRIOR PLING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR PLING DATE: 2001-01-04
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-03-29
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PRIOR PLING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
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APPLICATION NUMBER: 60/284,447
FILING DATE: 201-04-18
APPLICATION NUMBER: 60/286,683
FILING DATE: 2001-04-25
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Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
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Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
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Gangolli, Esha A
Guo, Xiaojia S
Shenoy, Suresh G
Rastelli, Luca
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Gusev, Vladimir Y
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Boldog, Ferenc
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Wolenc, Adam R
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Kekuda, Ramesh
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PRIOR FILING DATE: 2001-01-02
PRIOR PELING DATE: 2001-01-02
PRIOR PELING DATE: 2001-01-02
PRIOR PELING DATE: 2001-01-02
PRIOR PELICATION NUMBER: 60/259,785
PRIOR PELICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
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APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILLEG APPLICATION NUMBER: 60/258,928
PRIOR APPLICATION NUMBER: 60/258,928
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Mismatches:
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Edinger, Shlomit R
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Patturajan, Meera
Gusev, Vladimir Y
Gangolli, Esha A
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Shenoy, Suresh G
Rastelli, Luca
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Gunther, Erik
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CRGANISM: Homo sapiens
US-10-038-854-41
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                    US-10-029-020-14_COPY_1250_1400 (1-151) x US-10-038-854-37 (1-8645)
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Matches:
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Publication No. US20040022781A1
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Eisen, Andrew J
Liu, Xiachong
Malyankar, Uriel M
Shinkets, Richard A
Tchernev, Welizar
Spaderna, Steven K
Gorman, Linda
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Gusev, Vladimir Y
Gangolli, Esha A
Guo, Xiaojia S
Shenoy, Suresh G
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Wolenc, Adam R
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                                                                             TYPE: DNA
ORGANISM: Homo
                                             SEQ ID NO 37
LENGTH: 8645
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APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
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APPLICANT: Millet, Isabelle
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: 60/258,928
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR APPLICATION NUMBER: 60/259,83
PRIOR APPLICATION NUMBER: 60/259,83
PRIOR PILING DATE: 2001-01-02-0
PRIOR PILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-03-29
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Burgess, Catherine E
Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
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                                                                                                                                                                                                          Sequence 64, Application US/09800198
Publication No. US20030087816A1
GENERAL INFORMATION:
APPLICANT: Vernet, Cornie AM
APPLICANT: Fernandes, Elma
APPLICANT: Finkers, Richard A
APPLICANT: Majumder, Richard A
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Mezes, Peter S
APPLICANT: Rastelli, Luca
ITILE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15566-697
CURRENT APPLICATION NUMBER: US/09/800,198
CURRENT FILING DATE: 2001-03-05
FRIOR APPLICATION NUMBER: 60/186,596
FRIOR PETING DATE: 2000-03-03
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
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US-09-800-198-64
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US-09-800-198-64
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APPLICANT: Vernet, Corine A
APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Richard A
APPLICANT: Herrman, John L
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: MacBougall, John
TITLE OF INVENTION: No. US20020155115A1e1 Proteins and Nuclec Acids Encoding Same
TITLE OF INVENTION: No. US20020155115A1e1 Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/806,602
CURRENT APPLICATION NUMBER: 00/108
FILE REPEATON NUMBER: 00/108
FRIOR APPLICATION NUMBER: 60/186,596
FRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
                    4144 AGGAAAGTTGACCAAAATGGAATCATATCAACTCTTCTGGGCTCTAACGATTTGACTTCA 4203
                                                                     121 ArgArglleAspGlnAsnGlyIlelleSerThrLeuLeuGlySerAsnAspLeuThrSer 140
ProArgGly1leThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMetIle 120
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Patent No. US20020155115A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-09-808-602-76
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Best Local Similarity:
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APPLICANT: Vernet, Corine A
APPLICANT: Pernandes, Elma
APPLICANT: Shinkets, Richard A
APPLICANT: Herrman, John L
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Vishnu
APPLICANT: Meses, Peter S
APPLICANT: MacDougall, John
ITILE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
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Conservative:
Mismatches:
                 APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer Genes
FILE REFERENCE: 31 103 R1
CURRENT APPLICATION NUMBER: US/10/144,194A
CURRENT FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin version 3.0
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Patent No. US20020155115A1
GENERAL INFORMATION:
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74.17%
78.39%
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; LOCATION: (435)..(8336)
US-10-144-194A-81
                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
   GENERAL INFORMATION:
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                                                                                                                                                                LENGTH: 9695
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TITLE OF INVENTION: Regulated Breast Cancer Gen; FILE REFERENCE: 30 103 R.
CURRENT APPLICATION WUMBER: US/10/144,194A; CURRENT FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin version 3.0
SEQ ID NO 79
LENGTH: 9058
                                                                                                                                        Sequence 79, Application US/10144194A Publication No. US20030215809A1 GENERAL INFORMATION:
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; Publication No. US20030215809A1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (44)..(7699)
US-10-144-194A-79
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NAME/KEY: CDS
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4131 CCGAGAGGTATTGCAGTAGACAAGAATGGGCTCATGTACTTGTCGATGCCACCACCATGATC 4190
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         CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 12
LENGTH: 9729
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FILE REFERENCE: 15966-697 CIP
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; LOCATION: (210)..(8381)
US-09-808-602-12
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Query Match:
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Sequence 2, Application US/09103840A

Sequence 2, Application US/09103840A

Patent No. 629432B

GENERAL INFORMATION:

APPLICANT: WHITE, Owen R.

APPLICANT: WHITE, Owen R.

APPLICANT: WHITE, Owen R.

APPLICANT: VENERR, John C.

ITILE OF INVENTION: THERERCULOSIS

TITLE OF INVENTION: THERERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

SOFTWARE: PatentIN Ver. 2.1

SEQUENCE: SEQUENCE: 2.1
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US-09-060-299-28

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US-09-402-923A-24

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Mismatches:
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US-09-060-299-37
US-09-402-923A-37
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      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local S.
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
      -MODEL=frame+ p2n.model -DEV=xlh
-Q=(cgn2_1)(uSPTO_spool)(uS1029020/runat_06082004_112217_29301/app_query.fasta_1.3519
-Q=(cgn2_1)(uSPTO_spool)(uS1029020/runat_06082004_112217_29301/app_query.fasta_1.3519
-DB=Lsgued_patentes NA -QFMT=fastap_-SUFFIX=p2n.rni.-MINRATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MARFAIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL_OUTFORT=pco_NOFM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USFB=US10029020_GCGN_1 1.258_Grunat_06082004_112217_29301 -NOFU=6 -ICPU=3
-NO_MMAP_LARGEQUERY -NEG_SCORES=0 -WAIT_ LOSPBLOCK=100 -LONGIGG
-NO_MMAP_LARGEQUERY -NEG_SCORES=0 -WAIT_ LOSPBLOCK=100 -LONGIGG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 80, Appli
Sequence 790, Appli
Sequence 3, Appli
Sequence 85, Appli
Sequence 89, Appli
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(without alignments)
1875.793 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                       782
1 YIRRIFPSGNVTNILELRNK.....LGGSNDLTSARPLSCDSVMD 151
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/cgn2_6/ptodata/2/ina/5B_COMB.seg:*
/cgn2_6/ptodata/2/ina/6A_COMB.seg:*
/cgn2_6/ptodata/2/ina/6B_COMB.seg:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seg:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seg:*
                     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                 nucleic search, using frame_plus_p2n model
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US-09-103-840A-1

US-09-103-840A-2

US-09-103-840A-1

US-09-103-840A-1

US-09-103-840A-1

US-09-103-840A-1

US-08-961-527-80

US-09-235-451-3

US-08-652-877-89

US-08-652-877-89

US-08-652-877-87

US-08-652-877-87

US-08-652-877-83

US-08-652-877-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                682709 seqs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                          August 14, 2004, 01:16:21
                                                                                                                                                                                                                                                                                                                                                                                                                                             Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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3953533 CACCCCTATGATGTGGGGGGGGGGGGT---GCTGGCACCGTCTACGTGACCGACGGGG 3953589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 PheGlyLeulleTyrPheValAspGlyThrMetIleArgArglleAspGlnAsnGlyIle 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                 various positions throughout the sequence t,\ c\ or\ g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 SerArgArgValPheLysIleLysSerThrValValValLysAspLeuValLysAsnSer 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluvalvalalajagjyThrGlyAspGlnCys---jeuProPheAspAspThrArgCysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 HisLysTyrTyrLeuAlaThrAspProMetSerGlyAlaValPheLeuSerAspSerAsn
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: IUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-029-020-14_COPY_1250_1400 (1-151) x US-09-103-840A-2 (1-4403765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
                                                                      APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FREISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN J.
TITLE OF INVENTION: TUBERCULOSIS
TITLE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis
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Patent No. 6294328
                            Sequence 2, Application US/09103840A
Patent No. 6294328
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represent a,
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39.81%
25.93%
10.61%
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                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
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                 JS-09-103-840A-2
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ATCACC 1038131
                            1038231 TCCGGCAACGTCTATGTCACCGACAACAACAACAAGGTTGTCAAGCTAGAGGCCGAG 1038172
                                                                                                                           1038154
                                                                                                                                                                                                            --ATCACC 1038133
                                                                                                                                                                                                                                                                                                                                                                               1038090 GTCACCGAGCACAACAAAACCAGGTGGTCAAACTCCTGGGCCGGGTCGACCACCTCGACA 1038031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuProPheAspAspThrArgCysG1yAspG1yG1yLysAlaThrG1uAlaThrLeuThr
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SerGlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThr
                                                                                                                                                                                                                                                    100 AsnProArgGlyIleThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMet
                                                                                                                                                                                                                                                                                                                                     120 IleargargileaspGlnasnGlyIleIleSerThrLeuLeuGlySerAsnAspLeuThr
                                                                                 60 ValValValLysAspLeuValLysAspSerGluValValValAlaGlyThrGlyAspGlnCys
                                                                                                                                                                  LeuProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-029-020-14_COPY_1250_1400 (1-151) x US-09-103-840A-1 (1-4411529)
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN;
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1038151 CTGCCATTCACGGAT------
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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90.50
45.00%
27.00%
11.57%
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Best Local Similarity:
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US-09-103-840A-1/c
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Sequence 790, Application US/09134000C

Sequence 770, Application US/09134000C

Patent No. 6617156

Patent No. 6617158

Patent No. 6617158

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: RYPERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1997-08-08-15

PRIOR FILING DATE: 1997-08-15
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5540 GTGATTTATCTGGCATCGCAGATGCTGCAACGTTCTAATGAACGGGGTTATTTGGTT 5599
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Mismatches:
Indels:
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Matches:
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECHMUNICATION INFORMATION:
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin version 3.1
SEQ ID NO 790
LENGTH: 978
TYPE: DNA
                                                                                                                                            LENGTH: 9607 base pairs
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                                                                                                                                                                                                                                                                                                  81.00
41.56%
25.32%
10.36%
                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Query Match:
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Sequence 80, Application US/08961527
Fatent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INTURITION: Streptococcus pneumoniae Polynucleotides and Sequences
TITLE OF INTURITION: Streptococcus pneumoniae Polynucleotides and Sequences
TITLE OF STRETE: 3410
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspGlyGlyLysAlaThrGluAlaThrLeuThrAsnProArgGlylleThrValAspLys 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                          30 HislysTyrTyrLeuAlaThrAspProMetSerGlyAlaValPheLeuSerAspSerAsn 49
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                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3961639 CTGAAGCTGGCGGCCGGCTCGAAT 3961662
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                                                                                                                          TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37RV
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3961501 CACAATCGCGTGGTGGCGTTG----
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                      1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brookes, A. Anders
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83.00
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25.93%
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                      CURRENT FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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US-08-961-527-80
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Macintosh
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                        Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Patent No. 6187548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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289 GGCAAITGCGAIGAACAIACCIGCGCCCAIICGAAITGAAGCAIIIGAIAAITCAAAI--- 345
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-----ATTATGGGAACAAATCCTGTTTTCTGCGATGGTTGTGTTTATTGAC 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GCCAAGAACGACACAAACGAGTGAACTITTATTTGGTCCA 663
                                                                                                                                                                                       GlyAsnValThrAsnIle---LeuGluLeuArgAsnLysAspPheArgHisSerHisSer 27
                                                                                                                                                                                                                                                           47
                                                                                                                                                                                                                                                                                                        48 ------SerAsnSerArgArgValPheLysIleLysSerThrValValValLys 63
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APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: NUCLBIC ACID SEQUENCES ENCODING
TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
TITLE OF INVENTION: DOLYPEPTIDES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/235,451
CURRENT APPLICATION NUMBER: 60/072,151
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR PRILING DATE: 1999-01-22
PRIOR PRILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                               28 ProAlaHisLysTyrLeuAlaThrAspProMetSerGlyAlaValPheLeuSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 TIGCCTTTTCCTGATTTAATTTTAATCGATGGTGAAGGTCAAGTCGATGTTGCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          571 GATGTGTTAGCCAALCAACTAGGAGTCGATATTCCTGTAGCTGGATTA------
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37
118
58
28
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                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Enterococcus faecalis
                                                           0.129
80.00
39.01%
26.24%
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                                                                                                   Similarity:
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                                                                                   Percent Similarity:
   ; ORGANISM: Enter
US-09-134-000C-790
                                          Alignment Scores:
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Pred. No.:
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LENGTH: 2736
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DB:
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                                                         No.
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453 CCCICIGGÁAIGGIGÁCICCAIGGGGGGGGGTICCIGCIICCCCIIGIICACCICAGCÁN 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 gCysGlyAspGlyGlyLyssAlaThrGluAlaThrLeuThrAsnProArgGlyIleThrVa 106
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                                                                                                                                                                   7 ProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLysAspPheArgHisSerHis 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 TAATGGGGCTGTGGGAACCTCCGCGCCCCGCTCCGAGCTTTCTCTGGGTCGTCACCTC 43
                                                                                                                                                                                                                                                         27 SerProAlaHisLysTyrTyrLeuAlaThrAspProMetSerGlyAlaValPheLeuSer
                                                                                                                                                                                                                                                                                                                                             47 AspSerAsnSerArgArgValPheLysIleLysSerThrValValValLysAspLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 AGGTICCTCTCTATACCĠĊĀĠĠĠGAĠĠĊTGĠCTGGĠACCĊĊĠCAGGCTGAAĠCCAĀĠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Akerstrom, Goran
APPLICANT: Whilin, Claes
APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fra
           42
18
79
                        Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/652,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 85, Application US/08652877
Patent No. 6187548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: System 7.5.1
Word 6.0 (Patentin)
79.50
41.38%
28.97%
10.17%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r---CysAspSer 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Pou
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25 SerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSerGlyAlaValPhe 44
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         APPLICANT: Akerstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Murray, Edward M.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
NUMBER OP SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
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Indels:
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Matches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/US95/15203
FILING DATE: 22-NOV-1995
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 03-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-UNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REGISTRATION NUMBER: 29,699
                                                                                                                                                                                                                                                                                                                                                          ZIP: 19426-0107
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE DOCKET NUMBER: A1355E-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
                                                                                                                                                                                                                                                                  SEE: Rhone-Poulenc Rorer Inc
: 500 Arcola Rd., 3C43
Collegeville
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TYPE: nucleic acid
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78.50
41.35%
24.06%
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ADDRESSEE: Rhone-Pou
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         GENERAL INFORMATION
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US-08-652-877-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2576 GCCGGGTATCTTCTTCACTGATTGGTTCCTGCTAAAATTATGAGAGCATGGAGT 2635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2456 AATCTCTATTGGACAGACTCTCATTACAAGAGTATCAGTGTCATGAGGCTAGCTGATAAA 2515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 GlyLysAlaThrGluAlaThr---LeuThrAsnProArgGlyIleThrValAspLysPhe 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 ---GlyLeuIleTyrPheValAsp-GlyThrMetIleArgArgIleAspGlnAsnGlyIl 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GlyThrGlyAspGlnCysLeuProPheAspAspThrArgCysGlyAspGly 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerHisSerProAlaHisLysTyrLeuAlaThrAspProMetSerGlyAlaValPhe 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-029-020-14_COPY_1250_1400 (1-151) x US-08-652-877-85 (1-14042)
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Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEX/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A3355E-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 14042 base pairs
TYPE: nucleic acid
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78.50
41.35%
24.06%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68..14035
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDN/ HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2636 G----
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US-08-652-877-85
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Query Match:

RESULT 9

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2373 TTTTCAGATATGTCAAAACACATGATTTTTAAGCAAAAGATTGATGGCACAGGAAGAAA 2432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 ---GlyLeulleTyrPheValAsp-GlyThrMetlleArgArglleAspGlnAsnGlyIl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GlyThrGlyAspGlnCysLeuProPheAspAspThrArgCysGlyAspGly 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 SerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSerGlyAlaValPhe 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 GlyLysAlaThrGluAlaThr---LeuThrAsnProArgGlyIleThrValAspLysPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments TITLE OF INVENTION: Thereof and DNA Encoding Same NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 ValvalvalLysAspLeuValLysAspSerGluValValAla-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-029-020-14_COPY_1250_1400 (1-151) x US-08-652-877-87
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Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ACGGATCTCACCTCT 2688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 LeuSerAspSerAsnSerArgArgValPheLysIleLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C
APPLICANT: Murray, Edward M.
APPLICANT: Hjalm, Goran
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APPLICANT: Akerstrom, Goran
APPLICANT: Juhlin, Claes
                        : 14080 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                   12.6
78.50
41.35%
24.06%
10.04%
SEQUENCE CHARACTERISTICS:
                                                                                                       MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapier
TISSUE TYPE: Kidney
                                                                   single
                                                                                                                                                                                                                                                                                  105..14072
                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                            STRANDEDNESS:
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US-08-476-515A-83
                                                                                     TOPOLOGY:
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US-08-652-877-87
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                                                            2333 TTTTCAGATATGTCAAAACACATGATTTTTAAGCAAAAGATTGATGGCACAGGAAGAAA 2392
                                                                                                                                                                                                                                                                                                                                                                                                           2573 GCCGGGTATCTATTCTTCACTGATTGGTTCCGTCCTGCTAAAATTATGAGAGCATGGAGT 2632
                                                                                                                                               2393 ATTCTCGCAGCTAACAGGGTGGAAAATGTTGAAAGTTTGGCTTTTGATTGGATTTCAAAG 2452
                                                                                                                                                                                                                                     2453 AATCTCTATTGGACAGACTCTCATTACAAGAGTATCAGTGTCATGAGGCTAGCTGATAAA 2512
                                                                                                                                                                                          -----GlyThrGlyAspGlnCysLeuProPheAspAspThrArgCysGlyAspGly 90
                                                                                                                                                                                                                                                                             91 GlyLysAlaThrGluAlaThr---LeuThrAsnProArgGlyIleThrValAspLysPhe
                                                                                                                                                                                                                                                                                                                        110 ---GlyLeuIleTyrPheValAsp-GlyThrMetIleArgArglleAspGlnAsnGlyIl
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APPLICANT: Rask, Lars
APPLICANT: Rask, Lars
APPLICANT: Crumled, Greeg R.
APPLICANT: Murray, Edward M.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Thereof and DNA Encoding Same
                                                                                                       60 ValValValLysAspLeuValLysAsnSerGluValValAla-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ACGGATCTCACCTCT 2648
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                      45 LeuSerAspSerAsnSerArgArgValPheLysIleLys
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ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd., 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: A1355E-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEPAX: 610-454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-UUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 87, Application US/08652877 Patent No. 6187548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29,699
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Juhlin, Claes
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Savitzky, Martin
REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 500 Arcola CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 19426-0107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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2615 GCCGGGTATCTATACTTCATTGATTGGTTCCGTCCTGCTAAAATTATGAGAGCATGGAGT 2674
110 ---GlyLeuIleTyrPheValAsp-GlyThrMetIleArgArgIleAspGlnAsnGlyIl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MAILING, Claes
APPLICANT: Rask, Lars
APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Minany, Edward M.
APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: SOO Arcola Rd., 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14086
                                                                                                                              128 elleSerThrLeuLeuGlySerAsnAspLeuThrSer 140
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION NUMBER: US 08/344,036
APPLICATION NUMBER: 23-NOV-1994
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A1355E-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/652,877 FILING DATE:
                                                                                                                                                                                                                                                                                                                                    Sequence 83, Application US/08652877 Patent No. 6187548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
                                                                                                                                                                                                                                                                                                                                    Sequence | Sequence | Patent No. 61875%**
| Patent No. 61875%**
| GENERAL INFORMATION: Goran | APPLICANT: Akerstrom, Goran | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | Total | T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
107..14074
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LOCATION:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                       ; Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2375 TTTTCAGATATGTCAAAACACATGATTTTTAAGCAAAAGATTGATGGCACAGGAAGAA 2434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2495 AATCTCTATTGGACAGACTCTCATTACAAGAGTATCAGTGTCATGAGGCTAGCTGATAAA 2554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 SerHisSerProAlaHisLysTyrLeuAlaThrAspProMetSerGlyAlaValPhe 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GlyThrGlyAspGlnCysLeuProPheAspAspThrArgCysGlyAspGly 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 LeuSerAspSerAsnSerArgArgValPheLysIleLys----
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Mismatches:
Indels:
                                                                                                                                                                                                                      OPERATING SYSTEM: Windows 95
SOFTWARE: Word 7.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00483
FILING DATE: 24-MAY-1994
PRIOR APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATPORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355D
TELEPOMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEPAK: 610-454-3808
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 14083 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                               RY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-476-515A-83
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US-09-134-001C-2101

Sequence 2101, Application US/09134001C

Sequence 2101, Application US/09134001C

GENERAL No. 6380370

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 IleThrValAsp----LysPheGlyLeuIleTyrPheValAspGlyThrMetIleArgArg 122
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TATTATACCGCAGACCCTGCTCCCGGTATGGTTTATAGCACCACCGCAAGTGGTCTTGCT 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             819 CTAAATGCGGGGTATACGGCAGTTCCTTTTGAACATGTTTCCAACCAGGCAACTACAACA 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 ASpThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsnProArgGly 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        642 Arcaccgatatrgccarrgcrgrargccaacaratccagcaccaccacgrgcrgcrggrgcgcg 583
                                                                                                                                                                                                                                                                                                                                                                                                                                           987 AATTATAGCGTTCTGTAACTGTGATTCAAAACATAGCAATGGCGCTTATCACGAAATA 928
                                                                                                                                                                                                                                                                                                                                                                                                         AsnIleLeuGluLeuArgAsnLysAspPheArgHisSerHisSerProAlaHisLysTyr 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrLeuAlaThrAspProMetSerGlyAlaValPheLeuSerAspSerAsnSerArgArg 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 ValPheLysIleLysSerThrValValValValLysAspLeuValLysAsnSerGluValVal 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SerAsnAspLeuThrSerAlaArgProLeuSerCys 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SerThrLeuLeuGly--
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867 TTTTACTATCTTAACGAATATGTCGATGTGGGAACAAAATATCT-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AlaGlyThrGlyAspGlnCysLeuProPheAsp------
                                                                                                                                                                                                                                 6943
36
23
68
31
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Mismatches:
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                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 213:
                                                                                                                                                                                                                                     ength:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 2101
LENGTH: 2073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 IleAspGlnAsnGlyIleIle----
   (608) 251-9166
                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                     INFORMATION FOR SEQ ID NO: 213 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               76.50
37.34%
22.78%
9.78%
                                                           LENGTH: 6943
                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
   TELEFAX:
                                                                                                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GlyLeulleTyrPheValAsp-GlyThrMetIleArgArgIleAspGlnAsnGlyIl 128
                                                                                                                                                       SerHisSerProAlaHisLysTyrLeuAlaThrAspProMetSerGlyAlaValPhe 44
                                                                                                                                                                                                                                   -SerThr 59
                                                                                                                                                                                             TCGGGGAATCCTTCTTTCTTTGTCGGGATTGATTTTGACGCCCAGGACAGCACTATCTTT
                                                                                                                                                                                                                                                                                                                                                                                   ------GlyThrGlyAspGlnCysLeuProPheAspAspThrArgCysGlyAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 GlyLysAlaThrGluAlaThr -- LeuThrAsnProArgGlyIleThrValAspLysPhe
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                                                                                                                 US-10-029-020-14_COPY_1250_1400 (1-151) x US-08-652-877-83 (1-14086)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: No. 6365723el Sequences of E. NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           60 ValValValLysAspLeuValLysAsnSerGluValValAla--
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                                                                                                                                                                                                                                 LeuSerAspSerAsnSerArgArgValPheLysIleLys-
                   Conservative:
Mismatches:
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REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
   Matches:
                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 213, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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Welch, Rod
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78.50
41.35%
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                                       Similarity:
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                       Percent Similarity:
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Query Match:
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-----ATTTTA 429
                                                                                                                                                                                                                                                                                                    256 CGTGAAGGTGAAGCGATTGCTTGGCATTTATCAAAATTTTAGAATTÄGAAGATÄGCAAA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 GlyGlyLysAlaThrGluAlaThrLeuThrAsnProArgGlyIleThrValAspLysPhe 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TITAAGCATCCTCGTGGTATTGAAATGGAT----- 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyLeuIleTyrPheValAspGlyThrMetIleArgArgIleAspGlnAsnGlyIleIle 129
                                                                                                                                                                                                                                    196 AAAGATTTAAAAAACATGCGAAAAAGCAAAAAAATATTTTYAGCTAGTGACCCTGAC 255
                                                                                                                                                                                                                                                                 -----MetSerGlyAlaValPheLeuSerAspSerAsn 49
                                                                                                                                                                                                                                                                                                                                     50 SerArgArgValPheLysIleLysSerThrValValValLysAspLeuValLysAsnSer 69
                                                                                                                                                                                                                                                                                                                                                                                                  GluValValAlaGlyThrGlyAspGlnCysLeuProPheAspAspThrArgCysGlyAsp 89
                                                                                                                                                                                                   LysAspPheArgHisSerHisSerProAlaHisLysTyrLeuAlaThrAspPro
                                                                                                                                                                 US-10-029-020-14_COPY_1250_1400 (1-151) x US-09-134-001C-2101 (1-2073)
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ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
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                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: 1BM PC COMPATIBLE
COMPATER: 1BM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOR'D PERFECT 8.0
CURRENT APPLICATION DATA:
FILING DATE: 03-Dec-1999
CLASSIFICATION: CHORNON:
PRIOR APPLICATION: CHORNON:
                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-453-702B-244/c
; Sequence 244, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Perra, Valerie
; Perra, Nicole T.
Plunkett, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430 GATAGACTCGTTGGTTATAAT 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                               1.52
76.00
33.86%
25.20%
9.72%
                                                                                                 Similarity:
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                                                                            Percent Similarity:
Best Local Similari
US-09-134-001C-2101
                                 Alignment Scores:
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                                                                                                                  Query Match
                                                  Pred. No.:
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1496 IGGAAAAGAITTTGTGAGACATGCGAGCCTTTTACGTTGCTCAGAAGAGTATCACTGGA 1437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --CCAAATGAGAGC 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 -----IleTyrPheValAspGlyThrMetIleArgArgIleAspGlnAsnGlyIleIle 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 LysAlaThrGluAlaThrLeuThrAsnProArgGlyIleThrValAspLysPheGlyLeu 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IleArgArgIlePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLysAsp 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 PheLysIleLysSerThrValValValLysAspLeuValLysAsnSerGluValValAla 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 GlyThrGlyAspGlnCysLeuProPheAspAspThr----ArgCysGlyAspGlyGly 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- AlaValPheLeuSerAspSerAsnSerArgArgVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-029-020-14_COPY_1250_1400 (1-151) x US-09-453-702B-244 (1-2797)
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38
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59
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                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
                 REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 244:
US-09-453-702B-244
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: August 14, 2004, 21:33:24
Job time : 5053.67 secs
REGISTRATION NUMBER: 27386
                                                     TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                              75.00
36.99%
21.97%
9.59%
                                                                                                                                           LENGTH: 2797
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Best Local Similarity:
Query Match:
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Pred. No.:
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Homo sapiens
Homo sapiens
Homo sapiens
Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6246)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AY413475 6246 bp DNA linear GSS 12-DEC-2
Homo sapiens HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence,
                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                          CNS058SZ
AQ896853
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AY413476
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AZ413372
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CB518529
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BU027852
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                                                                              Query
Match Length DB
gb gss2:*
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5069
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
AY413475
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                      Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-De_Cgnz_1/USPTO_spool/USI0029020/runat_06082004_112216_29287/app_query.fasta_1.3519
-DB_EST_2/WYE-fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bits owned? -TRANS=bitman40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=bits owned? -ALIGN=100 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bits owned? -ALIGN=15 -MODE=LOCAL
-UNITS=bits -START=1 -END=-1 -MATRIX=BITS=0 -MATRIX=100.0000000
-USER=USI0029020 @CGN 1 1.11315 @runat_06082004_112216_29287 -NCFU=6 -ICFU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSENDICK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
                                                               August 14, 2004, 01:13:26 ; Search time 1770.9 Seconds (without alignments) 2546.273 Million cell updates/sec
                                                                                                                              YIRRIFPSGNVTNILELRNK.....LLGSNDLTSARPLSCDSVMD 151
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                               nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                             27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                           US-10-029-020-14_COPY_1250_1400
                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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7.0
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Perfect score:
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AY405422 Mus muscus BU705631 UI-M-F00-BU22658 603009 UI-M-GW0-CD353029 UI-M-GW0-CD352606 UI-M-GW0-CD352609 RQENOCURT AZ040891 RPCI-23-2 BF950887 RC3-NN18 C82439 RC3-NN18 C82439 RC3-SP5087 RC3-NN18 C82439 RC3-SP5087 RC3-NN18 C82439 RC3-SP5087 RC3-NN18 C82439 RC3-SP5087 RC3-NN18 RN26427 BY26342 UI-M-GW0-RN4642 UI-M-GW0-RN4642 UI-M-GW0-RN26344 60318972 AX13476 Pan trog1.

UI-M-FY0-UI-M-GI0-UI-M-GV0-UI-M-GI0-

CF538162 CF744767

sapi

Homo

Pan trogl

CD351739 AY405421 AY405420 B

Pan trogl Tetraodon

Tetraodon

Tetraodon HS 3144 A CHZ40 23D DKFZp686G

AL3333766 AL309969 AL326348 AQ896853 BZ902852 BX504880 CB057449

tigr-gss

AG030576 AZ413372 CC289028 CB518529

CH261-170 UI-M-GH0-Pan trogl

AV191089 AV191089 BX509644 DKFZp686N AL710647 DKFZp686M

BH329569 CH230-106 BI418126 LjNEST23a BU027852 QHG8D16.Y F14403 ATTS5325 AC

GSS 12-DEC-2003

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                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (Dases 1 to 3190)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 GlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A. Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-029-020-14 COPY 1250 1400 (1-151) x AY413477 (1-3190)
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Matches:
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Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="HCM4903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                          Mus musculus (house mouse)
Mus musculus
genomic survey sequence.
                                                      GI:39769439
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Mus musculus HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                               Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submitsed on Cargill, M.
Bubmitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A. Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

DEFINITION

ACCESSION VERSION KEYWORDS

CB524534 LOCUS

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CF538162
UI-M-GIO-cho-h-21-0-UI.rl NIH BMAP_GIO Mus musculus cDNA clone
IMAGE:30536156 5', mRNA sequence.
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Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NH1BMAP_GIO"
/note="Organ: Brain, Vector: pXx- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site .Double strand cDNA was
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                      sLysTyrTyrLeuAlaThrAspProMetSerGlyAlaValPheLeuSerAspSerAsnSe
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:30536156"
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Mus musculus
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/strain="C57BL/6"
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CF538162
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                                                                                                                                                                          770 bp mRNA linear EST 09-JUL-2003
UI-M-FY0-cey-b-20-0-UI.rl NIH BMAP_FY0 Mus musculus cDNA clone
IMAGE:6843669 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapber.@mail.nih.gov
Trissue Procurement: Dr. Jim Lib. University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 770)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Matches:
Conservative:
Mismatches:
                                     2098 GCCAGGCCCTCAGCTGTGACTCCGTCATGGAG 2130
141 AlaArgProLeuSerCysAspSerValMetAsp 151
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/mol_type="mRNA"
/strain="C57BL/6"
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Location/Qualifiers
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Mus musculus
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source

FEATURES

Query Match:

셤

Pred. No.:

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with EcoR I adaptor, digested with NotI and then cloned with EcoR I adaptor, digested with NotI and then cloned directionally into pWX-Asc vector. The library tag sequence located between the Not I site and the poly tail is AGGAGACAG. This library was created for the University Iowa Brain Anatowy Project (BAMP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF744767 L1-6-11.c1 NIH BMAP_GVO Mus musculus cDNA clone IMAGE:30621740 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                           21 AspPheArgHisSerHisSerProAlaHisLysTyrLyrLeuAlaThrAspProMetSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 640)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                                                                                                                                                              623
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Conservative:
Mismatches:
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Mus musculus
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TITLE
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KEYWORDS
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CF744767
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/clone="Images:3062740"
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/dev stage="InthOB [TI phage resistant)"
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/clone_norman Brain; Vector: pXX- Asc; Site_1: BcoR I;
/clone_norman Brain; Vector: pXX- Asc; Site_1: BcoR I;
/clone_norman Brain Amages state fractionated on a 1% agarose
gel.Rirst strand cDNA was size fractionated on a 1% agarose
gel.Rirst strand cDNA was size fractionated on a 1% agarose
gel.Rirst strand cDNA was size fraction, ligated with
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousef1.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 GACCTGACTAAAAACGCTGAAGTGGTGGCAGGGACCGGGGAACAGTGCCTTCCCTTTGAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgilePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLysAspPheArg
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                              db xref="taxon:10090"
                                                                                                                                                                       Seq primer: pYX-5.
Location/Qualifiers
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DEFINITION

RESULT 6 CD351739 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

PEATURES

REFERENCE

9

40

80

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Pan troglodytes HCM2218 gene, VIRTUAL TRANSCRIPT, partial sequence, AV405421
                                                                                                                                                      .40 GAATCACTCTACCTATCAGACACCAATACTCGAAAAGTCTACAAAATCTCTCGTG 199
                                                                                                                                                                                                                                                                                             800 GAAACAAAAGATCTCTCTAAAGAATTTTGAAGTGGTAGCAGGAACAGGTGACCAGTGCCTT 259
                                                                                                                                                                                                                                                                                                                                                        81 ProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 ProArgGlyIleThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMetIle 120
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                       80 GATACCAGACATAGCCACAGCCCTGCACAAGTACTATCTGGCTATGGACCCTATGTCT
                                                                                                                                                                                                                                   61 ValValLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                260 CCCTTTGACCAAAGTCACTGCGGAGATGGTGGAAAAGCCTCTGAAGGTCTCACTGAAGCC
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AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer
                                                                                                                 41 GlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 5069)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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Mismatches:
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Location/Qualifiers
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Pred. No.:
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AUTHORS
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AUTHORS
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KEYWORDS
SOURCE
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JOURNAL
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                                                                                                                                                         CD351739 T57 bp mRNA linear EST 09-JUL-2003
UI-M-GIO-cgi-a-11-0-UI.rl NIH BMAP_GIO Mus musculus cDNA clone
IMAGE:6855540 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs=remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 757)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (Jases 1 (2 / 2))
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Conservative:
Mismatches:
Indels:
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TTAACCTGTGATACTAGCATG 441
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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Query Match:

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1091 CCGTTTGACGAGGCGAGATGTGGGGGAAGGCCGTGGAAGCCCACGACCACGT 1150
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Mus musculus HCM2218 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Clark,A.G., Glanowski,S., Nielson,R., Lu,F., Murphy,B.,
Todd,M.A., Tanembaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
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Mismatches:
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Matches:
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<l. .>5094
/locus_tag="HCM2218"
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AY405422
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                                                                                                              564.50
86.00%
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AY405422
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Homo sapiens HCM2218 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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                                                                                                                                      872 TATGTGCGGCGGATATTCCCTTCTGGAAATGTAACAAGTGTCTTAGAACTA-----
                                                                                                                                                                                                       ---AGCAGCAACCCAGCTCATAGATACTACCTTGCAACGGATCCAGTCACA
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                                                                US-10-029-020-14_COPY_1250_1400 (1-151) x AY405421 (1-5069)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
        Indels:
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UI-M-F00-cac-k-16-0-UI.x1 NIH BMAP_F00 Mus musculus cDNA clone
IIMAB:6409479 5', mRNA sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 778)
          Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
(16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                      871 TACGICCGGCGATATICCCGICTGGGAATGIGACAAGIGITTIAGAACTA-
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/organism="Mus musculus"
                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:10090"
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Email: cgapbs-r@mail.nih.gov
                                    them based on alignment.
Location/Qualifiers
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/tissue_type="whole brain"
/dev stage="whole brain"
/dev stage="whole brain"
/dev stage="whole (TI phage resistant)"
/lab_host="DH10B (TI phage resistant)"
/clone lib="NH1 BMAP FOO"
/clone lib="NH1 BMAP FOO"
/clone="Organ: Brain; Vector: pXX-Asc; Site_1: EcoR I;
Site_2: Not I: The library was constructed according
Bonaldo, Lemnon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel: First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Bcok I adaptor, digested with Not! and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGC: This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program Coordinator
Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
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/strain="C57BL/6"
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| Journal of the property of the property of a comparise of a comparise of a comparise of a comparise of a comparing the first stranded from I million independent clones. CDNA synthesis was initiated using an oligo(dT) primer, using methylated of in the first strand synthesis was initiated using an oligo(dT) primer, using methylated of in the first strand synthesis reaction. Following this first strand reaction, double-stranded CDNA was blunted, ligated to NotI adapters, digested with ECORI size-selected, and cloned into the NotI and ECORI compatible sites of a custom modified MCS of the pluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soarse et al., pNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research freamnealing hybridization was used."
                                                                                                                                                                   BU226585 820 bp mRNA linear EST 26-NOV-2002 603800545F1 CSEQCHN23 Gallus gallus cDNA clone ChEST771112 5', mRNA
                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (hases 1 to 820)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                        619
 Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                 BU226585
BU226585.1 GI:25463660
                                                                                                                                                                                                                                                                              Gallus gallus (chicken)
Gallus gallus
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TyrileargargilepheProSerGlyasnValThrasnileLeuGluLeuArgasnLys 20

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CD803099
UI-M-GVO-chm-c-06-0-UI.rl NIH_BMAP_GVO Mus musculus cDNA clone IMASE:30543317 5', mRNA sequence.
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/clone="IMAGE:30543317"
/clone="IMAGE:30543317"
/clone="type="whole brain"
/dev stage="type="whole brain"
/dev stage="type="whole from 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone lib="nH1 BMAP Gyo"
/note="organ: Brain; Vector: pxx- Asc; Site_1: EcoR I;
/note="organ: Brain; Vector: pxx- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
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Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
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                                                                                                                                                                                                                                                                                                     61 ValVallysAspieuVallysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ProArgGlyIleThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMetIle
21 AspPhcArgHisSerHisSerProAlaHisLysTyrIvLeuAlaThrAspProMetSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 GCACGACCTCTGACCTGTGATACCAGCATG 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 AlaArgProLeuSerCysAspSerValMet 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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CD803099.1 GI:32461925
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primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with ECOR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 12-SEP-2003
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 HisserproAlaHisLysTyrTyrLeuAlaThrAspproMetSerGlyAlaValPheLeu 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AACAGCCCAGGACACAAATTACTTGGCTGTGGACCCGGTGACCGGCTCACTTCTACGTC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 ValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeuProPheAspAspThr 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus I toases 1 to 692)

NIH-MGC http://wgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnGlyIleIleSerThrLeuLeuGlySerAsnAspLeuThrSerAlaArgProLeuSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerAspSerAsnSerArgArgValPheLysIleLysSerThrValValValLysAspLeu
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UI-M-GH0-cgu-g-06-0-UI.rl NIH BMAP_GH0 Mus musculus cDNA clone
IMAGE:30356597 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-029-020-14_COPY_1250_1400 (1-151) x CD803099 (1-801)
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20
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Matches:
Conservative:
Mismatches:
Indels:
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CF530821.1 GI:34582785
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87.30%
71.43%
63.81%
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                          Best Local
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JOURNAL
COMMENT
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/dev stage="1", 5, and 15 days newborn"
//dev stage="1", 5, and 15 days newborn"
//lab host="hlub (TI phage resistant)"
//clone lib="hluh (HENAP GHO"
//clone lib="lut (HENAP GHO"
//note="Organ: Brain; Vector: pXx- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not! and then cloned
directionally into pXx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTCAAT. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
                        This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 09-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 GGAGCCAAAGACCTGAATAACGCTGAAGTGGTGGCAGGGACCGGGGAACAGTGCCTT
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http://genome.uiowa.edu/distribution/mousefl.html
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                /clone="IMAGE:30356597"
/tissue_type="Whole brain"
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                                                                                                                                                          'organism="Mus musculus"
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                                                                             Seq primer: pYX-5.
Location/Qualifiers
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                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6"
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/clone="INAGE:30545857"
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/dev stage="whole brain"
/dev stage="whole brain"
/dev stage="list and 15 days newborn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD803315 T89 bp mRNA linear EST 15-JUL-2003
UI-M-GV0-chu-m-02-0-UI.rl NIH_BMAP_GV0 Mus musculus cDNA clone
IMARE:30545857 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
thtp://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                            182 gradakadakadecreargadeceaakadaargecaaredarakaaaegaacrearerak 241
                                                                                                                                       114 PhevalAspGlyThrMetileArgArglleAspGlnAsnGlyIleIleSerThrLeuLeu 133
                                                                                                                                                                                                      Mis musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 789)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                   94 ThrGluAlaThrLeuThrAsnProArgGlyIleThrValAspLysPheGlyLeuIleTyr
                                                                                                                                                                                                                                                                     789
84
23
16
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Mismatches:
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/strain="C57BL/6"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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CD803315
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
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This clone was contributed by the Brain Molecular Anatomy Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 GGGACCGGGGAACAGTGCCTTCCCTTTGACGAGGCCAGGTGTGGGGGATGGAGGCAAGGCT 181
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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UI-M-GIO-cgk-o-15-0-UI.rl NIH_BMAP_GIO Mus musculus cDNA clone
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                                    IMAGE:6856648 5', mRNA sequence.
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/strain="C57BL/6"
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Mus musculus
                                                                                                   CD352566.1 GI:31144077
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Search completed: August 14, 2004, 18:03:23 Job time : 1784.9 secs

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Sequence:

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Human, NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cell signal processing; metabolic pathway modulation; metabolic disorder; cell signal processing; metabolic pathway modulation; metabolic disorder; A besity; diabetes; infectious disease; neurodegenerative disorder; acne; Alzheimer's disease; Parkinson's disease; immune disorder; cancer; we memory defect; hair growth; memory defect; infertility; congenital heart defect; hair growth; pupmentation disorder; endocrine disorder; respiratory disease; health; who me marrow transplantation; endocrine disorder; age-related disorder; mephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBE; TEN-M4; heuropsychiatric disorder; EGF-related protein; SCUBE; TEN-M4; het adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; type la membrane sushi-containing domain; butyrophilin; type la membrane sushi-containing; SNP; gene; ds; type la membrane sushi-containing; SNP; gene; ds;
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Abn85378 Human NOV
Abs78652 Human cDN
Abq82345 Human NOV
Abq82346 Human NOV
Abq82343 Human NOV
Acc72051 BCU0205A
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                   - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                               3373863 seqs, 2124099041 residues
                                                                                                                       US-10-029-020-14_COPY_1250_1400
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ABN85378
ABS78652
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ABQ82346
ABQ82344
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ACC72051
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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geneseqn2001bs:*
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Maximum DB seq length: 2000000000
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Match Length DB
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8438
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727.5
727.5
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Jatabase :

Result

Aas55933 Streptoco Abx05900 S. pneumo Aav52213 Streptoco Abt42143 Toxicity Confinuation (2 of Aax87478 Rat vanil Aax19730 Rat VRRP-

Enterococ

Enterococ Human pla Human pla

Abs99293 Aat28774 Aax13498

Aav05995 Aat28776 Aat28775 Aav05997

Human Human

Human

Continuation (40 o

Abs67814 Human Aak82889 Human

Drosophil Drosophil Arabidops

Aac18884 Human sec

Aac39026 Arabidops Adb61918 Human cDN Abn59835 Novel hum Continuation (11 o

Human FCT Human Pc0

Adb32023 F Aal60066 E Abk92230 E

Prostate

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Aak51828 HAD129075 HAD129074 HAD104855 HAD104854 HAD104854 HAD104854 HAD11444 HAD214144 HADZ1444 HADZ1

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ValValLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu

ProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100

4022 CCCTTTGATGACACTCGCTGCGGGGATGGTGGGGAAGGCCACAAAACCACAATTCACAAT

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3902

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61

3962

81

101

121

GlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThrVal

3842 GATTTCAGACATAGTCACAGTCCAGCACACAAATACTACCTGGCCACAGACCCATGAGT

21 AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer

4082 cccadedantacadresacaagrringescrearcracriceresardscaccardarc 4141

ProArgGlyIleThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMetIle 120

4142 AGACGCATCGATCAGAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCACATCA 4201

4202 GCCCGGCCACTCCAGCTGTGATTCTGTCATGGAT 4234 AlaArgProLeuSerCysAspSerValMetAsp 151

141

ABN85378 standard; DNA; 8438

RESULT 2 ABN85378

g

(first entry)

21-OCT-2002

ABN85378;

ArgarglleAspGlnAsnGlyIleIleSerThrLeuLeuGlySerAsnAspLeuThrSer 140

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The present invention relates to new NOVX polypeptides. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, by referably human. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, parkinson's disease, neurodegenerative disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, the invention are also useful for treating or preventing cirrhosis, compared tits, learning and memory defects, infertility, congenital heart defects, acne, hair growth, pigmentation disorders, endocrine disorders, respiratory disease, gastro-intestinal diseases, reproductive, health, congration, mention, mention, endocrine diseases, allergy and inflammation, nephrological disorders, urinary system callergy and inflammation, nephrological disorders, urinary system disorders, neuropsychiatric disorders and age-related disorders. The present nucleic acid sequence represents a NOVX gene. This sequence concess a NOVX protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease or
                                                                                                                      "Single nucleotide polymorphism (SNP)"
name= "Single nucleotide polymorphism (SNP)"
                                                        "Single nucleotide polymorphism (SNP)"
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i L, Ji W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8354 BP; 1968 A; 2437 C; 2271 G; 1678 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n M, Vernet CAM, Malyankar UM,
Shimkets RA, Burgess CE, Zerh
Boldog FL, Smithson G, Li L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 50-52; 318pp; English.
                                                                                                     /*tag= c
/standard_name=
                                                                 name=
                                                                                                                                                                                                                                                                                              20-DEC-2000; 2000US-0257314P.
02-MAY-2001; 2001US-0288153P.
29-MAY-2001; 2001US-0294075P.
24-JUL-2001; 2001US-0307506P.
10-AUG-2001; 2001US-0311590P.
10-AUG-2001; 2001US-0311613P.
                      replace (225, C)
                                                                                 replace (2\overline{6}0, A)
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                                          /*tag= b
/standard_1
      /standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gangolli EA, Patturajan Stone DJ, Anderson D, S
Spytek KA, Casman SJ, B
                                                                                                     /*tag=
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P-PSDB; ABG70388
                                                                                                                                                                WO200257453-A2
                                                                                                                                                                                                                                                                              19-DEC-2000; 2
20-DEC-2000; 2
02-MAY-2001; 2
29-MAY-2001; 2
                                                                                                                                                                                                   25-JUL-2002
                            variation
                                                                                   variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer
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Human, NOV1; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive; Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic; Antiasthmatic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic; Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant;
                                                                                                                                                          Gene Therapy, NOV; cancer; heart disease; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; asthma; IGA nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy; wasting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Casman SJ, Shenoy S, Spytek KA;
E, Patturajan M, Vernet CAM;
                                                                                                                                                                                                                                                                                                                /trans except= (pos: 1138. .1147, aa:Met)
/product= "NOV1 protein"
                                                                              TEN-M4 like protein, coding sequence.
                                                                                                                                                                                                                     TEN-M4 like protein; chromosome 11; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zerhusen BD, Cas
EA, Burgess CE,
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JAN-2001; 2001US-0260417P.
10-JAN-2001; 2001US-0260831P.
28-FEB-2001; 2001US-027338P.
09-MAR-2001; 2001US-0284704P.
                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-2002; 2002WO-US000554
                                                                                                                                                                                                                                                                                         .8395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Padigaru M, Li L,
Zhong M, Gangolli
                                                                                                                                                                                                                                                                                                                                                               WO200255704-A2
                                                                                                                                                                                                                                                    Homo sapiens
                                                                              Human NOV1,
                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-2002
```

3782 TACATTAGAAGGATCTTCCCCTCTGGAAATGTCACCAACATCCTAGAGCTGAGGAATAAA 3841 TyrileArgArgIlePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLys 20

g

US-10-029-020-14\_COPY\_1250\_1400 (1-151) x ABS52100 (1-8354)

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Conservative: Mismatches: Length: Matches:

Percent Similarity: Best Local Similarity:

Score:

Query Match:

7.99e-95 782.00 100.00% 100.00% 100.00%

Alignment Scores:

[ndels:

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The present sequence is a coding sequence for a NOV protein. The NOV proteins and coding sequences are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma, plan nephropathy, cirthosis, arthritis, Alzheimer's diseases, infections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. NOVI is a TEN-M4 like protein and the NOVI gene is localised to chromosome 11
                                                                                                                                                                                      preventing or
Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse WM; JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman K; I J, Malyankar U, Millet I, Peyman J, Smithson G;
                                                                                                                                                                           NOVX polypeptides and encoding polynucleotides, useful for prever treating NOVX-associated disorders e.g. cancer, inflammation, or Alzheimer's disease, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                      Claim 9; Page 8-9; 358pp; English.
                                                                    Stone DJ;
                                                                                                             2002-590674/63
                                                                                                                                  P-PSDB; ABB98401
                                                                                                                                                                                                                                               pharmacogenomics
                                           Macdougall J,
                                                                    Gunther E,
                           Alsobrook
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Conservative: Mismatches: Length: Matches: Indels: 9.38e-92 759.50 96.79% 96.79% Similarity: Percent Similarity: Alignment Scores: Query Match: Score:

Sequence 8438 BP; 2001 A; 2434 C; 2268 G; 1735 T; 0 U; 0 Other;

US-10-029-020-14\_COPY\_1250\_1400 (1-151) x ABN85378 (1-8438)

3764 TACATTAGAAGGATCTTCCCCTCTGGAAATGTCACCAACATCCTAGAGCTGAGGGGCCAGA 3823 3824 AATAAAGATITCAGACATAGTCACAGCACACAAATACTACCTGGCCACAGACCCC 3883 3943 4003 1004 Tecerecerricareacaerecereceseareareaaaeecaeaaeeceaeaeecaeaee 1064 ACCAATCCCAGGGGTCCCCCAGGCATTACAGTGGACAAGTTTGGGCTGATCTACTTCGTG 4123 115 38 28 78 98 1 TyrileArgArgIlePheProSerGlyAsnValThrAsnIleLeuGluLeu----Arg 19 AsnlysAspPheArgHisSerHisSerProAlaHisLysTyrLeuAlaThrAspPro 3884 AIGAGIGGGCCGICITICTICACAGCAACAGCCGGCGGGTCTTIAAAATCAAGTCC 59 ThrValValValLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGln 3944 ACTGTGGTGGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGAACAGGTGACAG 79 CysLeuProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeu MetSerGlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLys1leLysSer ThrAsnProArg-----GlyIleThrValAspLysPheGlyLeuIleTyrPheVal 66 à ద ð d à g ò qq à 엄 ð g

4184 AATGATCTCACATCAGCCCGGCCACTCAGCTGTGATTCTGTCATGGAT 4231 ABS78652 ID ABS7 XX RESULT 3 d

ABS78652 standard; cDNA; 8645 BP

136 AsnAspLeuThrSerAlaArgProLeuSerCysAspSerValMetAsp 151

116 AspGlyThrMetIleArgArglleAspGlnAsnGlyIleIleSerThrLeuLeuGlySer 135

ð Dp à

16-DEC-2002

(first entry)

Human cDNA encoding CGDD10, INCYTE 7488573CB1

Human; ss; gene; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thrombocytopenia; developmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma; inflammatory disorder; infertility; autoimmune disorder; gout; allergy; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; diabetes mellitus; glomerulonephritis; irritable bowel syndrome; multiple sclerosis; osteoarthritis; osteoprosis; pancreatitis; rheumatoid arthritis.

Homo sapiens.

WO200272830-A2

19-SEP-2002.

08-FEB-2002; 2002WO-US003715.

09-FEB-2001; 2001US-0268111P. 23-FEB-2001; 2001US-0271175P. 08-MAR-2001; 2001US-0274503P. 09-MAR-2001; 2001US-0274552P.

(INCY-) INCYTE GENOMICS INC.

Burford N; Baughn MR; Warren BA, Elliott VS, TY, Lal PG, Duggan BM, Khare R, Walia NK; Yao MG, Ison CH, Lu Y, Xu Y, Gietzen KJ, Tang ' Richardson TW, Tran UK, Yue H, Ding L, Lu DAM,

WPI; 2002-723356/78. P-PSDB; ABG97359 New human proteins associated with cell growth, differentiation and death, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atherosclerosis or hepatitis.

Claim 5; Page 175-178; 181pp; English.

The invention relates to an isolated polypeptide comprising GGDD1-12 caid sequence at least 90% identical to GGDD, a biologically active acid sequence at least 90% identical to GGDD, a biologically active C acid sequence at least 90% identical to GGDD, a biologically active C fragment or an immunogenic fragment. Also included are the CGDD comprising a promoter sequence operably linked to the GGDD oblymucleotides, a cell transformed with the recombinant polymucleotide, a transgenic organism comprising the recombinant polymucleotide, an anti-off, screening for compounds which bind to/modulate or are antibody, screening for compounds which bind to/modulate or are antibody, screening for compounds which bind to/modulate or are cGDD polymucleotide microarray. The polypeptides, polymucleotides, and artagonists are useful for diagnosing treating or cGDD polymuclative (e.g. arteriosclerosis, atherosclerosis, agonists and artagonists are useful for diagnosing treating or preventing disorders associated with aberrant expression of GGDD, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, particularly cell proliferative (e.g. arteriosclerosis, and of GGD, particularly cell proliferative (e.g. arteriosclerosis, and of GGD, particularly cell proliferative (e.g. arteriosclerosis, and of GGD, particularly cell proliferative (e.g. arteriosclerosis, and of GGD, particularly cell proliferative (e.g. arteriosclerosis, and of GGD, particularly cell proliferative (e.g. arteriosclerosis, and of GGD, particularly cell proliferative (e.g. arteriosclerosis, and of GGD, particularly cell proliferative (e.g. arteriosclerosis, and of GGD, ceptiles), reproductive disorders (e.g. arteriosclerosis, and of GGD, ceptiles), reproductive disorders (e.g. arteriosclerosis, and of GGD, ceptilitis, contact demantitis, crohact demantitis, contact demantitis, contact demantitis, pour, irritable bowel syndrome, multiple sclerosis, glomerulonephritis, qout, irritable bowel syndrome, autoimmune contact demantitis, proteorosis, parase 

Location/Qualifiers 258. .8144 /\*tag= a /product= "NOV15c"

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New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                Malyankar U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L, Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S; Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K; Gunther E, Smithson G, Millet I, Macdougall JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 119-121; 444pp; English.
                                                                                                                     31-DEC-2001; 2001WO-US049976
                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-732706/79.
P-PSDB; ABP53588.
                                                                   WO200262999-A2
                                                                                                                                                                                                                                          13-APR-2001;
18-APR-2001;
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29-MAY-2001;
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20-FEB-2001;
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  Key
4131 cccaddddarracadrodacaadrrrdddcrdarcracrrcgrddardcacacardarc 4190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AGTCACAGTCCAGCACACAAATACTACCTGGCCACAGACCCCATGAGT 3950
                                                                                                                                                                                                                                                                                                                                                       3951 GGGGCCGTCTTCCTTTCTGACAGCAGCGGGCGGGTCTTTAAAATCAAGTCCACTGTG 4010
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                                                                                                                                                                                                                                1 TyrileArgargilePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLys 20
 infections. They are also useful in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of proteins associated with CGDD. The present sequence encodes a CGDD protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Argarg11eAspG1nAsnG1y11e11eSerThrLeuLeuG1ySerAsnAspLeuThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                     4011 GIGGIGAAGGACCITGICAAGAACICTGAGGIGGITGCGGGGGCACAGGIGACCAGTGCCTC
                                                                                                                                                                                                                                                                                                                                                                                             ValValLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu
                                                                                                                                                                                                                                                                                     21 AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer
                                                                                                                                                                                                                                                                                                                                       41 GlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThrVal
                                                                                                                                                                                                                                                         3852 TACATTAGAAGGATCTTCCCCTCTGGAAATGTCACCAACATCCTAGAGCTG---
                                                                 C; 2319 G; 1771 T; 0 U; 1 Other;
                                                                                                                                                                                                        (1-8645)
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                                                                                                                                       Conservative:
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                                                                                                             Length:
Matches:
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                                                                       Sequence 8645 BP; 2060 A; 2494
                                                                                                           2.21e-87
727.50
95.36%
95.36%
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                                                                                                                                       Percent Similarity:
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                                                                                                                 Pred. No.:
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Liu X;

Eisen A,

Wolenc AR, Vernet CAM, Kets RA, Tchernev VT,

ri Li

2001US-0322699P 2001US-0333350P

2001US-0279832P. 2001US-0279833P. 2001US-0283889P. 2001US-0284447P. 2001US-0286683P. 2001US-02940B0P. 2001US-0312915P. 2001US-0313325P

2001US-0269814P 2001US-0279863P

2001US-0259785P

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The present invention describes nove, indicate the result invention describes nove, indicate the care interest interest interest interest in invention describes nove the result interest in anticidabetic, anticidament, cerebroprotective, nontrathritic, virucide, immunosuppressive, anticlalergic, anticidaterial, fungicide, protozoacide and anticlalergic, anticidaterial, fungicide, protozoacide and anticlalergic, anticidate can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzhelmer's disease or Pick's ischaemic cerebrovascular transport (e.g. cystic fibrosis, disease), disorders (e.g. ulcerative colitie), or gastrointestinal disorders (e.g. ulcerative colitie), or gastrointestinal disorders (e.g. ulcerative colities, or gastrointestinal disorders (e.g. ulcerative colities), viral, bacterial fungal, helminthic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be biological samples (tissue typing), and in forensic identification of a biological sample. The present sequence encodes human NOVISC, which is
The present invention describes novel human proteins designated NOVX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T; 0 U; 4 Other;
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Alignment Scores: Pred. No.:

Human, NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antiinflammatory; fungicide; antiarhemmatic; antiarhritic; immunosuppressive; antialprafic; virucide; antianaemic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy; diabetes mellitus; Grave's disease; cystic fibrosis; goitre; ulcerative colitis; gastric disorder; duodenal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergy reaction; autoimmune haemolytic anaemia;

Human NOV15c encoding cDNA SEQ ID NO:39.

(first entry)

17-DEC-2002

ABQ82345;

ABQ82345 standard; cDNA; 8473 BP

g

rheumatoid arthritis; gene; chromosome 4; ss.

Homo sapiens

Length:

1.27e-72

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Page

31-DEC-2001; 2001WO-US049976

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3600 TACGTGCGGCGGATATTCCCTTCTGGAAATGTAACAAGTGTCTTAGAACTAAGAAATAAA 3659
                                                                                                                                                                                                                                                                           3779
                                                                                                                                                                                               CCCAAAGGAATGGCAGTTGATAAGAATGGATTAATCTACTTTGTTGATGGAACCATGATT 3959
                                                                                                                                                                                                                                                                                                                                                             ProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                      101 ProArgGlyIleThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMetIle 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ArgarglleaspGlnAsnGlyllelleSerThrLeuLeuGlySerAsnAspLeuThrSer 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular;
cerebroprotective; nootropic; antidiabetic; antinflammatory; fungicide;
antirheumatic; antiarthritic; immunosuppressive; antiallergic; virucide;
antianaemic; antibacterial; protozoacide; antihelminthic; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy;
                                                                                                                                                                                                                                        41 GlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThrVal
                                                                                                                                                                                                                                                          61 ValValLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu
                                                                                                                 TyrIleArgArgIlePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLys
                                                                                                                                                                              AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer
                                                                                      US-10-029-020-14_COPY_1250_1400 (1-151) x ABQ82345 (1-8473)
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14
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Matches:
Conservative:
Mismatches:
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                                                Indels:
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/product= "NOV15d"
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619.00
90.67%
74.00%
79.16%
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                          Best Local Similarity:
            Percent Similarity:
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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, cyfostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, antidiabetic, anticonvulsant, cerebroprotective, notropic, cardiovascular, cantidiabetic, antianflammatory, antinheamatic, antiarthritic, virucide, immunosuppressive, antiallergic, antianematic, antiarthritic, virucide, immunosuppressive, antiallergic, antianematic, antiarthritic, virucide, corporaced conditions and antihelminhic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a converse selected from NOVX-associated disorder, such as cancers (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, cischaemic cerebrovascular disease, Alzheimer's disease or pick's disease), disorders of vesicular transport (e.g. cystic fibrosis, cischaemia, or intermatoid arthritis), viral, bacterial, fungal, helminthic and protozoal linfections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines 'neukaenia' cusequences may be produce antibodies and as vaccines. The NOVX nucleotide sequences may be biological samples (tissue typing), and in foorential eremic entering can entered contactions and and infortations from minute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                       Shenoy S;
5, Ellerman K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes human NOV15d, which is
                                                                                                                                                                                                                                                                                                                                                                         Liu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8487 BP; 2306 A; 2029 C; 2148 G; 2001 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                  Wolenc AR, Vernet CAM, Eisen A, Liu X, kets RA, Tchernev VT, Spaderna SK, Gormanjan M, Gusev V, Gangolli EA, Guo X, Sh.
                                                                                                                                                                                                                                                                                                                                                                                                                         Burgess CE, Ed
Macdougall JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
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Patturajan M, Gusev v,
T. Casman SJ, Boldog F, B
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                                                                                                       09-WAR-2001, 2001US-0279853P
29-WAR-2001, 2001US-0279832P
29-MAR-2001, 2001US-0279833P
13-APR-2001, 2001US-0284849P
18-APR-2001, 2001US-0284447P
                                                                                                                                                                                                   25-APR-2001; 2001US-0286683P.
29-MAY-2001; 2001US-0294080P.
                                                                      2001US-0259785P.
2001US-0269814P.
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2001US-0322699P.
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74.00%
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J, Shimkets RA,
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Rekuda R, Patturu, ...
Rastelli L, Casman SJ, ...
...ber E, Smithson G,
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Best Local Similarity:
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                                                                                                                                                                                                                                     16-AUG-2001;
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                                    29-DEC-2000;
02-JAN-2001;
                                                                      04-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                   Spytek KA,
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1 TyrileArgArgilePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLys 20

US-10-029-020-14\_COPY\_1250\_1400 (1-151) x ABQ82346 (1-8487)

15-AUG-2002.

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The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, includies, antidiabetic, antidiabetic, antidiabetic, includies, and can be used in gene protozoacide and antibhelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a manufacture of a medicament for treating a syndrome associated with a carport, testis and uterus, neurological disorders (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, discase), disorders of vesicular transport (e.g. cystic fibrosis, disorders en litus, Grave's disease, Alzheimer's disperse or pick's disorders (e.g. ulcerative colltis, or gastric and duodenal disorders), cancemia, or rheumatoid artritis), viral, bacterial, fungal, helminthic and protozoal infections. The NOVX proteins can be used as immunogens to conduce antibodies and as vaccines. The NOVX nucleotide sequences may be biological samples (tissue typing), and in forense entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering entering
     3896 CCCAAAGGAATGGCAGTTGATAAGAATGGATTAATCTACTTGTTGATGGAACCATGATT 3955
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101 ProArgGlyIleThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMetIle 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgarglleAspGlnAsnGlylleIleSerThrLeuLeuGlySerAsnAspLeuThrSer 140
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                                                                                                                                                                                                                                                                                                    61 ValvaliysAspLeuValiysAspSerGluValValAlaGlyThrGlyAspGlnCySLeu
                                                                                          AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer
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New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune

Claim 8; Page 114-117; 444pp; English.

diseases.

Wolenc AR, Vernet CAM, Eisen A, Liu X; kets RA, Tchernev VT, Spaderna SK, Gorman L; jan M, Gusev V, Gangolli EA, Guo X, Shenoy S; n SJ, Boldog F, Burgess CE, Edinger S, Ellerman K; on G, Millet I, Macdougall JR;

Shimkets RA,

Li L,

Spytek KA,

Malyankar U, Shimkets RA Kekuda R, Patturajan M, Rastelli L, Casman SJ, Gunther B, Smithson G,

WPI; 2002-732706/79.

P-PSDB; ABP53587

29-MAY-2001; 2001US-0294080P. 16-AUG-2001; 2001US-0312915P. 17-AUG-2001; 2001US-0313325P. 17-SEP-2001; 2001US-0322699P.

26-NOV-2001; 2001US-0333350P

(CURA-) CURAGEN CORP.

2001US-0284447P. 2001US-0286683P. 2001US-0283889P

25-APR-2001; 29-MAY-2001; 13-APR-2001;

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40
                                                                                                                                                            1 TyrlleArgArgllePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLyS 20
                                                                                                                                                                                                                                                                   GlyAlaValPheLeuSerAspSerAspSerArgArgValPheLysIleLysSerThrVal 60
                                                                                                                                                                                                                 AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer
                                                                                                                                                                                                                               3832 GATTTTAGACATAGCAGCACCCAGCTCATAGATACTACCTTGCAACGGATCCAGTCAG
Sequence 8645 BP; 2343 A; 2060 C; 2200 G; 2038 T; 0 U; 4 Other;
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Conservative:
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Best Local Similarity:
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biological samples (tissue typing), and in forensic identification of a biological sample. The present sequence encodes human NOV15b, which is

located on chromosome 4

Location/Qualifiers /\*tag= a /product= "NOV15b"

Homo sapiens

151. .8316

2000US-0258928P. 2001US-0259415P. 2001US-0259785P. 2001US-0279863P. 2001US-0279863P.

09-MAR-2001; 29-MAR-2001; 29-MAR-2001; 04-JAN-2001; 20-FEB-2001; 29-DEC-2000; 02-JAN-2001;

31-DEC-2001; 2001WO-US049976

WO200262999-A2

15-AUG-2002

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4011
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                                                                                                           3892 GGAGAICTGTACGITTCTGACACAAACACCCGCAGAATTTATCGCCCAAAGTCACTTACG 3951
                                                                                        ProPheAspAspIhrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100
                                                                                                                                                         120
                                                                                                                                                                                                                 ArgArglleAspGlnAsnGlyIleIleSerThrLeuLeuGlySerAsnAspLeuThrSer 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; notropic; antidiabetic; antinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antialergic; virucide; antianaemic; antibacterial; procozoacide; antihalminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemia; lymphoma; melanoma; neurological disorder; epilepsy; pick's disease; vesicular transport disease; Alzheimer's disease; allergy; pick's disease; vesicular transport disease; cystic fibrosis; goitre; ulcerative; collits; gastric disorder; duodenal disorder; vaccine; ulcerative collits; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.
                                80
                                             GGGGCAAAAAACACTTGACTAAAAATGCAGAAGTCGTCGCAGGGAGCAGGGAGCAATGCCTT
                                                                                                                                                    ProArgGly11eThrvalAsplysPheGlyLeulleTyrPheValAspGlyThrMet11e
                           61 ValValLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu
                                                                                                                                                                                  4072 CCCAAAGGAATGGCAGTTGATAAGAATGGATTAATCTACTTTGTTGATGGAACCATGATT
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/transl_except= (pos:1249. .1251, aa:Ser)
                                                                                                                                                                                                                                                                                                141 AlaArgProLeuSerCysAspSerValMet 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NOV15a encoding cDNA SEQ ID NO:35.
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2001US-0259485P.
2001US-0269814P.
2001US-0279863P.
2001US-0279832P.
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2001US-0283889P.
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2001US-0286683P.
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2001US-0322699P.
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29-MAR-2001;
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13-APR-2001;
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26-NOV-2001;
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3784 TACGTGCGGCGGATATTCCCCTTCTGGAAATGTAACAAGTGTCTTAGAACTAAGAAATAAA 3843

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TyrlleArgArg1lePheProSerG1yAsnValThrAsnIleLeuGluLeuArgAsnLys

US-10-029-020-14\_COPY\_1250\_1400 (1-151) x ABQ82343 (1-8675)

8675 1111 255 14

Length:
Matches:
Conservative:
Mismatches:

1.31e-72 619.00 90.67% 74.00%

Similarity:

Query Match: Best Local

Percent Similarity:

Alignment Scores:

Indels:

21 AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer 40

41 GlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThrVal

61 ValValLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu 3964 GGGGCAAAAGACTTGACTAAAATGCAGAAGTCGTCGCAGGGACAGGGGGGAGCAATGCCTT

80

81 ProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrCluAlaThrLeuThrAsn 100

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The present invention describes novel human proteins designated NoVX, where X is 1 to 20 e.g. NoV1. NoVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, antidiabetic, antidonilamatory, antidonetic, antiarthritic, vivicide, immunosuppressive, antiallergic, antianemmic, antiarthritic, vivicide, immunosuppressive, antiallergic, antianemmic, indicaterial, fungicide, protozoacide and antihalminithe activities, and can be used in gene to therapy. The NOVX proteins, nucleotides or antibodies can be used in the numan disease selected from NOVX associated disorder, such as cancers convary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or pick's cischaemic cerebrovascular disease, Alzheimer's disease or pick's disease, disease, alzheimer's disease or pick's disease, alzheimer's disease or pick's disease, or goitre), gastrointestinal correctors of vesicular transport (e.g. cystic fibrosis, disorders (e.g. ulcerative callergic reactions, autoimmune haemolytic autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be biological samples (tissue typing), and in forensic identification of a which is
                                                                                                                                                                                                                                                                  New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
                                                                                    Tchernev VI, Spaderna SK, Gorman L;

sev V, Gangolli EA, Guo K, Shenoy S;

Goog F, Burgess CE, Edinger S, Ellerman K;

llet I, Macdougall JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sample. The present sequence encodes human NOV15a, which is
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                                                                    Liu X;
                                                                    Vernet CAM,
                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 110-112; 444pp; English.
                                                          U, Shimkets RA, Tcherne,
Patturajan M, Gusev V, G
L, Casman SJ, Boldog F, F
                                                                                           Malyan.
Kekuda R, Pattur.,
Rastelli L, Casman SJ,
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                     (CURA-) CURAGEN CORP.
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                                                                                      Malyankar U,
                                                            Spytek KA,
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3506 CGGAAGGTTGACCAGAATGGAATCATCTCCACCTGCTGGGCTCCAATGACCTCACGCC 3565
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                                                                                                                                                                                                                                                                                                                                                                      3386 CCCTTTGATGAAGCCCGCTGCGGGGATGGAGGGAAGGCCATAGATGCAACCTTGATGAGG
                                                                                                                                    3146 TACATCCGACGCATCTTTCCCTCTCGAATGTGACCAGCATCTTCGAGTTACGAAATAAA
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                                                                                                1 TyrileArgArgilePheProSerGlyAsnValThrAsnileLeuGluLeuArgAsnLys
                                                                                                                                                                                 21 AsppheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer
                                                                                                                                                                                                                                                                41 GlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThrVal
                                                                                                                                                                                                                                                                                                                                               61 ValValLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu
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14-MAY-2002; 2002US-00144194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polymuclectides which are differentially-regulated in breast cancer. The methods and compositions of the present invention are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and/or treating diseases and conditions relating to breast cancer, and may be used in gene therapy or antisense therapy. They can also be used in research, drug discovery, clinical medicine and forensic medicine. Sequences given in records ACC72012-ACC72074 represent polynucleotides of the invention that are this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at Itp.wipo.int/pub/published_pct_sequences
                                              ProArgGlyIleThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMetIle 120
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                                                                          BP; 2387 A; 2430 C; 2263 G; 1978 T; 0 U; 0 Other;
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chromosome 5q33.3; ds.
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Conservative:
Mismatches:
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14-MAY-2002; 2002US-00144194.
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74.17%
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P-PSDB; ABR58317.
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10-APR-2003

cancer.

Sun Z,

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conditions relating to breast cancer, and may be used in gene therapy or antisense therapy. They can also be used in research, drug discovery, clinical medicine and forensic medicine. Sequences given in records ACC72012-ACC72074 represent polynucleotides of the invention that are differentially-regulated in breast cancer. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differentially-regulated in breast cancer. The methods and compositions of the present invention are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and/or treating diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to isolated polynucleotides which are
                                                                                                                                                                                                               NO 81; 127pp + Sequence Listing; English.
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Length: Matches: Conservative: Mismatches: Indels: 1.01e-71 613.00 89.40% 74.17% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB: Score:

Sequence 9695 BP; 2567 A; 2582 C; 2434 G; 2112 T; 0 U; 0 Other;

AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer 40 TyrlleArgArgllePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLys 3843 GAGITTIAAACATAGCAACAACCAGCACACAAGTACTACTIGGCAGTGGACCCCGTGTCC GlyAlaValPheLeuSerAspSerAspSerArgArgValPheLysIleLysSerThrVal 61 ValValLysAspLeuValLysAspSerGluValValAlAgGlyThrGlyAspGlnCysLeu (1-9695)US-10-029-020-14\_COPY\_1250\_1400 (1-151) x ACC72052 Gaps: 21 à qq à ð 셤 8

3963 GGAACCAAAGACCTGGCTGGGAATTCGGAAGTTGTGGCAGGGACGGGAGGAGCCAGTGTCTA 4022 ProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100 ProArgGlyIleThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMetIle 81 101 4023 g  $\delta$ dd à g

g

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AAS14089 standard; DNA; 9729 RESULT 10 g

(first entry) 18-DEC-2001 AAS14089

DNA sequence. Human FCTR3f

Human; FCTRX; myelogenous leukaemia; carcinoma; melanoma; glioma; ds; astrocytoma; congenital neonatal alloimmune thrombocytopaenia; infection; neurological disorder; neurodegenerative disorders; nerve trauma; AAS14089
ID AAS1
AC AAS1
XX AS1
DT 18-D
DT 18-D
XX BHUMA
XX HUMA
XX ASI
XX HUMA

demyelinating Gardner syndrone, familial myelodysplastic syndrone, mental health condition; immunological disorder; allergy; infertility; bronchial asthma; Avellino type eosinophilia; lung disease; deafness; reproductive disorder; glycoprotein Ia deficiency; desmoid disease; turcot syndrome; liver cirrhosis; hepatitis C; virucide; gastric disorders; pancreatic disease; Schistosoma mansoni infection; Spinocerebellar ataxia; Plasmodium falciparum parasitaemia; diabetes; Corneal dystrophy. Greenouw type I; Corneal dystrophy.lattice type I; Reis-Bucklers corneal dystrophy; cytostatic; immunosuppressive; antialtergic; antiactermatic; antiinfertility; antiinflammatory; antidabetic; protozoacide; hepatotropic; virucide; ophthalmological; gene therapy; FCTR3a; neurestin-like protein; FCTR3I. neuropathy; Eamilial myelodysplastic

Homo sapiens

/\*tag= a /product= "Human FCTR3f" Location/Qualifiers 1. .209 8385. .9729 .8384 Ω /\*tag= \*tag= Key 5'UTR 3'UTR CDS

WO200166747-A2

13-SEP-2001

2000US-0186718P. 2000US-0187293P. 2000US-0187294P. 2000US-0190400P. 2000US-0196018P. 05-MAR-2001; 2001WO-US007160 2000US-0186592P 03-MAR-2000; 06-MAR-2000; 06-MAR-2000; 17-MAR-2000; 03-MAR-2000; 07-APR-2000; 03-JAN-2001; 

3902

09

(CURA-) CURAGEN CORP.

80

Majumder Herrmann JL, Shimkets RA, Herrm Mezes PS, Rastelli щ Mishra V, Fernandes Macdougall J, Vernet CAM,

P-PSDB; AAU08681

WPI; 2001-596837/67.

detection, Novel polypeptides designated as FCTRX polypeptides, useful in de prevention and treatment of a broad range of pathological states.

Claim 9; Page 37-39; 215pp; English.

The invention relaters to numear Clara purperplaces, colling inventions relaters to numear the sequences are useful for the treatment or puedencing them. These sequences are useful for the treatment or prevention of numerous disorders including myelogenous leukaemia, acarcinomas, melanomas, astrocytomas, congenital neonatal alloimmune thrombocytopaenia, neurological disorders, neurodegenerative disorders, neuropathy, demyelinaling myelodysplastic syndrome, charcot-Marie Tooth neuropathy, demyelinaling dardner syndrome, immunological disorders, allergy and infection, bronchial asthma, Avellino type cosinophila, lung diseases, reproductive disorders, infertility, male and female reproductive disorders, plasmodic diseases, turcot syndrome, liver cirrhosis, hepaticis C, gastric desmoid disease, turcot syndrome, liver cirrhosis, hepaticis C, gastric disorders, pancreatic diseases such as diabetes, Schistosoma mansoni infection Spinocerebellar ataxia, Plasmodium falciparum parasitaemia, corneal dystrophy-Greonouw type I, Corneal dystrophy-lattice type I and the promose, he mental mystrophy. This sequence represents DNA encoding The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the FCTR3a homologue FCTR3f

Sequence 9729 BP; 2548 A; 2629 C; 2438 G; 2114 T; 0 U; 0 Other;

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The invention relates to FCTRX polypeptides and the polynucleotides encoding them. The sequences of the invention are useful for the manufacture of a medicament for diagnosing and treating disorders associated with the FCTRX polypeptide, such as colorectal cancer.

Cadenomatous polyposis coli, myelogenous leukaemia, congenital neonatal autoimmune thrombocytopenia, malignant ovarian tumours, malignant brain tumours, mammary tumours, human gliomas, astrocytomas, renal cell carcinoma, breast adenocarcinoma, ovarian carcinoma, melanomas, cell and granular cell carcinoma, neurological disorders, cell and granular cell carcinomas, neurological disorders, conditions, immunological disorders, allergy and infection, asthma, lung diseases, male and femmale reproductive disorders, despetis, despatitis cell disorders, pancreatic disorders, syndrome, liver cirrhosis, hepatitis cell disorders, pancreatic diseases, diabetes, schistosoma mansoni diffection, spinocerebellar ataxia, plasmodium falciparum infection, milection, spinocerebellar ataxia, plasmodium falciparum infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New FCTRX polypeptide and encoding polynucleotide, useful for preventing or treating FCTRX-related disorders, such as cancer, autoimmune, neurodegenerative, gastrointestinal, reproductive and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Groenouw's corneal dystrophy and lattice corneal dystrophy. Thi represents cDNA encoding an FCTRX polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                Majumder K;
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05-MAR-2001; 2001US-00800198.
                                                03-MAR-2000; 2000US-0186592P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4071 CCCTTTGATGAAGCCCGCTGCGGGGATGGAGGGAAGGCCATAGATGCAACCCTGATGAGGC
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                                                                                                                                                                                              (1-151) x AAS14089 (1-9729)
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            Alignment Scores:
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                                  Pred. No.:
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              ProPheAspAspIhrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100
                                                                                     ProArgGly1leThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMetIle
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                                                                                                            Novel polypeptides designated as FCTRX polypeptides, useful in detection, prevention and treatment of a broad range of pathological states.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders, pancreatic diseases such as diabetes, Schistosoma mansoni infection Spinocerebellar ataxia, Plasmodium falciparum parasitaemia, Corneal dystrophy-Greonouw type I, Corneal dystrophy-lattice type I and Reis-Bucklers corneal dystrophy. This sequence represents DNA encoding FCTR3b, a neurestin-like protein
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Groenouw's corneal dystrophy and lattice corneal dystrophy. This sequence represents cDNA encoding an FCTRX polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New FCTRX polypeptide and encoding polynucleotide, useful for preventing or treating FCTRX-related disorders, such as cancer, autoimmune, neurodegenerative, gastrointestinal, reproductive and inflammatory
                                                                                                                                                                                                                        myelogenous leukaemia; congenital neonatal autoimmune thrombocytopenia; ovarian cancer; brain tumour; breast cancer; glioma; astrocytoma; renal cell carcinoma; melanoma; clear cell carcinoma; granular cell carcinoma; neurological disorder; nerve trauma; femilial myelokysplastic syndrome; charcot marie-Tooth neuropathy; gardners syndrome; charcot marie-Tooth neuropathy; allergy; asthma; lung disease; reproductive disorder; deafness; allergy; asthma; lung disease; reproductive disorder; deafness; alvoprotein deficiency; desmoid tumour; turcot syndrome; liver cirrhosis; hepatitis C; gastric disorder; pancreatic disease; diabetes; schistosoma mansoni infection; spinocerebellar ataxia; plasmodium falciparum infection; Groenouw's corneal dystrophy;
                                                                                                                                                                                                          gene; ss; FCTR3b; colorectal cancer; adenomatous polyposis coli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herrmann J, Majumder K;
Rastelli L;
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Mezes PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 29-32; 155pp; English.
                                ADB32023 standard; cDNA; 9826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-2001; 2001US-00800198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAR-2000; 2000US-0186592P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lattice corneal dystrophy
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J, Mishra V,
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FERNANDES E.
SHIMKETS R.
HERRMANN J.
MAJUMDER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-625633/59.
P-PSDB; ADB32024.
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MEZES P S.
                                                                                                                                                                 CDNA
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                                                                                                                                                                 Human FCTR3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                     04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vermet C,
                                                                       ADB32023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FERN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHIM/)
                                                                                                                                                                                                          Human;
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3928 TACATCCGACGATCTTTCCCTCTCGAAATGTGACCAGCATCTTGGAGTTACGAAATAAA 3987
                                                                                                                                                                                                                                                                                                                                                        4168 cccriricargaagccccccrcccccccardcaacccaracarccaacccrcarance 4227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ArgargileAspGlnAsnGlyIleIleSerThrLeuLeuGlySerAsnAspLeuThrSer 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProArgGly11eThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMetIle 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100
                                                                                                                                                                                                                                                                                                                             40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, differentially regulated protein; prevention; therapy; vaccine; prostate cancer; gene therapy; Pc099; teneurin-2; chromosome 5q34; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4228 CCGAGAGGIAITIGCAGIAGACAAGAATGGGCTCAIGIACTTIGITGCATGGCCACCAIGAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TyrlleArgArgllePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLys
                                                                                                                                                                                                                                                                                                                             21 AspPheArgHisSerHisSerProAlaHisLysTyrLeuAlaThrAspProMetSer
                                                                                                                                                                                                                                                                                                                                                                                                           41 GlyAlaValPheLeuSerAspSerAspSerArgArgValPheLysIleLysSerThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ValValLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu
Sequence 9826 BP; 2567 A; 2645 C; 2476 G; 2138 T; 0 U; 0 Other;
                                                             9826
1112
23
23
16
0
                                                                                                                                                                                                      US-10-029-020-14_COPY_1250_1400 (1-151) x ADB32023 (1-9826)
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/product= "Human Pc099 protein"
/note= "No start codon"
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
                                                                                                                          Mismatches:
Indels:
                                                             Length:
Matches:
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1. .4056
/*tag= a
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                                                             1.03e-71
613.00
89.40%
74.17%
78.39%
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The present invention relates to novel differentially regulated genes and polypeptides encoded by them. Sequences of the invention are useful in diagnosing, staging, monitoring, prognosticating, preventing treating or determining the predisposition to diseases or conditions such as prostate cancer. They may be used as molecular markers, drug targets, vaccines, in gene therapy, research, clinical medicine or forensic science. The present sequence is a differentially regulated prostate cDNA, Pc099 which codes for teneurin-2. Pc099 gene is located on chromsome 5q34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1524 GGAACCAAAGACCTGGCTGGGAATTCGGAAGTTGTGGGCAGGACGGGAGAGCAGTGTCTA 2583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 ProPheAspAspIhrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgArglleAspGlnAsnGlyIleIleSerThrLeuLeuGlySerAsnAspLeuThrSer 140
                                                                                                                                                                                                                                                                       New polynucleotide for diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to, diseases or conditions such as prostate cancer, and for research or forensic science.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrileArgArgIlePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2464 GGCTCGCTCTACGTGTCCGACACCAGCAGGAGAATCTACCGCGTCAAGTCTCTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2365 TACATCCGACGCATCTTTCCCTCTCGAAATGTGACCAGCATCTTGGAGTTACGCAAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -------AACCCAGCACACAAGTACTTGGCAGTGACCCCGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ValValLysAspLeuValLysAsnSerGluValValAlaGlyThrGlyAspGlnCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2584 CCCTTTGATGAAGCCCGCTGCGGGGAATGGAGGGAAGGCCATAGATGCAACCCTGATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProArgGlylleThrValAspLysPheGlyLeuIleTyrPheValAspGlyThrMetIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 GlyAlaValPheLeuSerAspSerAsnSerArgArgValPheLysIleLysSerThrVal
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108
20
16
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                  Claim 29; Page 158-163; 100pp; English.
                                                                                                                                                                                 Kovacs KF,
                                                                                                                                          (ORIG-) ORIGENE TECHNOLOGIES INC
                                                2001US-0331041P.
2001US-0331042P.
2001US-0340251P.
2002US-0344791P.
               07-NOV-2002; 2002WO-US035563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.36e-66
571.50
84.77$
71.52$
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                                                                                                                                                                                                                   WPI; 2003-449451/42.
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                                                                                                                                                                                                                                      P-PSDB; AA029571.
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                                                  07-NOV-2001;
                                                                     07-NOV-2001;
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                                                                                                       07-JAN-2002;
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The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancerassociated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancerassociated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer associated genes are useful for diagnosing or treating prostate cancer is sociated genes are useful for diagnosing or treating prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

MARY2115_ABK92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                                          cancer; prostate tumour tissue; human; mammal; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; 2768 G; 3585 T; 0 U; 0 Other;
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Conservative:
                                                                                                             Prostate cancer-associated DNA sequence #116.
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                ABK92230 standard; DNA; 12879 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gish KC, Mack DH, Wilson KE,
                                                                                                                                                                                                                                                                                                                 13-OCT-2000; 2000US-00687576.

08-DEC-2000; 2000US-00732288.

08-DEC-2000; 2000US-00733742.

24-DAN-2001; 2001US-026357P.

16-MAR-2001; 2001US-0276988P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0286214P.
2001US-00847046.
2001US-0288589P.
                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-0281922P
                                                                                                                                                                                                                                                                                     12-OCT-2001; 2001WO-US032045
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534.50
82.78%
66.23%
                                                                                                                                                           gene therapy; gene; ds
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24-APR-2001;
30-APR-2001;
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                                                                             15-AUG-2002
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                                              ABK92230;
                                                                                                                                                                                          Mammalia.
                                                                                                                                            Prostate
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DB:
ABK92230
                             2421
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3758 ------AGCACAAGTCCTGCTCAAAAACTATCTGGCTATGGACCTGTGTCT 3805
                                                                                                                                          4045
                                                 3707 TITGTAAGGAGAATATITCCCTCGGGAAACTCCGTIAGTATTTTGGAATTA----- 3757
                                                                                                                                                                                                                                                                           81 ProPheAspAspThrArgCysGlyAspGlyGlyLysAlaThrGluAlaThrLeuThrAsn 100
                                                                                                                                                                                                                                                                                                                101 ProArgGlyIleThrValAspLysPheGlyLeulleTyrPheValAspGlyThrMetIle 120
                                                                                                                                                                                                                                                                                                                                                                       121 ArgArgileAspGlnAsnGlylleIleSerThrLeuLeuGlySerAsnAspLeuThrSer 140
                             1 TyrlleArgArgllePheProSerGlyAsnValThrAsnIleLeuGluLeuArgAsnLys 20
                                                                                      21 AspPheArgHisSerHisSerProAlaHisLysTyrTyrLeuAlaThrAspProMetSer 40
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US-10-029-020-14_COPY_1250_1400 (1-151) x ABK92230 (1-12879)
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OM protein

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Title: Perfect sc Sequence:

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APPLICANT: Alsobrook II, John et al.
TILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE
FILE REPERENCE: 21402-568A
CURRENT APPLICATION NUMBER: 10/10/383,201
CURRENT PAPLICATION NUMBER: 10/02902
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2002-03-20
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
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PRIOR FILING DATE: 2002-06-14
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PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-13
PRIOR FILING DATE: 2002-06-13
PRIOR FILING DATE: 2002-06-13
PRIOR FILING DATE: 2002-09-13
                                                                                                                                                                                                                                                                                               Sequence 81, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 66, Appl
Sequence 61, Appl
Sequence 49758, A
Sequence 49758, A
Sequence 49758, A
Sequence 49758, A
                                                                                                         Sequence 37, Appl
Sequence 35, Appl
Sequence 67, Appl
Sequence 74, Appl
Sequence 77, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 67, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 64, Appl
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Sequence 2577, Ap
Sequence 1867, Ap
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Sequence 9600, Ap
Sequence 9600, Ap
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Sequence 4, Appli
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Sequence 1424, Ap
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                                                           Sequence 1, Appli
Sequence 39, Appl
Sequence 41, Appl
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                                             Sequence
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154 13 US-10-383-201-43

155 13 US-10-029-020-13

156 13 US-10-029-020-13

157 13 US-10-038-854-39

17 US-10-038-854-31

17 US-10-038-854-37

17 US-10-038-854-37

17 US-10-038-854-37

18 US-09-808-602-79

19 US-09-808-602-74

17 US-09-808-602-74

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19 US-09-808-602-74

10 US-09-808-602-74

10 US-09-808-602-76

10 US-09-808-602-76

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10 US-09-808-138-12

10 US-09-808-138-12

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11 US-10-125-968-11

12 US-10-125-968-11

13 US-10-027-632-49758

15 US-10-027-632-49758

15 US-10-027-632-49758

15 US-10-029-386-1277

15 US-10-029-386-1277
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US-10-057-475B-9600
US-10-154-884B-9600
US-09-795-651-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
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US-10-383-201-43
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221
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-MODEL=frame+ p2n.model -DEV=xlh
-Gegra 1/USPTO spool/US10029020/runat_06082004_112218_29331/app_query.fasta_1.3519
-Ge-cgnz 1/USPTO spool/US10029020/runat_06082004_112218_29331/app_query.fasta_1.3519
-DB=Published Applications NA -OFRM=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNIT$=bits -START=1 -END=-1 -MATRIX=blosum62
-LOOPCL=0 -LOOPEXT=0 -UNIT$=bits -START=1 -END=-1 -MATRIX=blosum62
-TRR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pc0 -NORM=ext -HEAPSTEE=500 -MINLEN=0
-MAXTEN=200000000 -USER=US10029020 @CGN 1 1 2156 @runat 06082004_112218_29331
-NCPU-6 -ICPD=3 -NO MMAP -LASGEQUERY* NEG $CORES=0 - WAIT -DSERLOCK=100
-LONGLOG -DEV TIMBOUT=120 -WARN TIMBOUT=30 -THREADS=1 -XGAPPOF=10 -XGAPPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7
                                                                                                                              (without alignments)
2448.158 Million cell updates/sec
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                                                                                                                                                                         US-10-029-020-14_COPY_1100_1200
549
1 RLFRKWFAAAPDLSYYFIMD......IQSGILHKGNGENQFVSQQP 101
                                                                                                            August 14, 2004, 01:33:47; Search time 202.425 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                             nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                   hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 3225727 seqs, 2453303834 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                       BLOSUM62
Xgapop 10.0 , Xgapext C
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext -
Pelop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Match Length DB
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Database

Result

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TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 13, Application US/10029020

Publication No. US20040033971A1

GENERAL INFORMATION:

APPLICANT: Gangolli et al.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-225

CURRENT APPLICATION NUMBER: US/10/029,020

CURRENT PLING DATE: 2001-12-19

PRIOR PILING DATE: 2000-12-19

PRIOR FILING DATE: 2000-12-19

PRIOR FILING DATE: 2000-12-20

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-29

PRIOR PLILING DATE: 2001-08-29

PRIOR FILING DATE: 2001-08-29

PRIOR FILING DATE: 2001-08-29

PRIOR APPLICATION NUMBER: 60/315,617

PRIOR APPLICATION NUMBER: 60/315,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-029-020-14_COPY_1100_1200 (1-101) x US-10-383-201-43 (1-8354)
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Mismatches:
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Matches:
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            PRIOR APPLICATION NUMBER: 100051,874
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-03-22
PRIOR PLING DATE: 2002-03-22
PRIOR PLLING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                               1.53e-70
549.00
100.00%
100.00%
FILING DATE: 2002-09-23
                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                       ; LOCATION: (35)..(8341)
US-10-383-201-43
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
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NAME/KEY: CDS
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                                                                                                                                                                                          LENGTH: 8354
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JUNEARL INFORMATION:

JUNEARLI LINFORMATION:

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-568A

CURRENT PELICATION NUMBER: US/10/383,201

CURRENT FILING DATE: 2003-03-06

PRIOR APPLICATION NUMBER: 10/029020

PRIOR PELING DATE: 2001-12-19

PRIOR PELING DATE: 2002-03-06

PRIOR APPLICATION NUMBER: 60/365,984

PRIOR PELING DATE: 2002-04-12

PRIOR PELING DATE: 2002-04-12

PRIOR PELING DATE: 2002-04-12

PRIOR PELING DATE: 2002-06-14

PRIOR PELING DATE: 2002-06-26

PRIOR PELING DATE: 2002-09-14

PRIOR FILING DATE: 2002-09-14

PRIOR FILING DATE: 2002-09-23

PRIOR FILING DATE: 2002-09-23

PRIOR FILING DATE: 2002-09-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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PRIOR FILING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: 60/322,358

PRIOR FILING DATE: 2001-09-14

PRIOR FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: 60/294,075

PRIOR PILING DATE: 2001-05-29

PRIOR FILING DATE: 2001-05-02

NUMBER OF SEQ ID NOS: 190

SEGFWARE: PATENTIN VET: 2.1

SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 55, Application US/10383201
Publication No. US20040029226A1
GENERAL INFORMATION:
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3311 CGCCTCTTCAGGAAGTGGTTCGCTGCAGCCCCAGACCTGTCCTTTTATTTTCATTTGGGAC 3370
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                                                                                                                                                                                                                             AFPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Meth
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
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Mismatches:
Indels:
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Matches:
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                                                                                                  MacDougall, John
Malyankar, Uriel M
Millet, Isabelle
Peyman, John
Smithson, Glennda
Gunther, Erik
                        Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
    Alsobrook II, John
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LENGTH: 8438
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: 10/051,874
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SEG ID NO 55
LENGTH: 8355
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Publication No. US20040029216A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
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Zerhusen, Bryan D
Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
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Tchernev, Velizar T
Miller, Charles E
Guo, Xiaojia
Boldog, Ference L
Grosse, William M
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US-10-383-201-55
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                                                          21 LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly 40
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION WUMBER: US/10/038,854
CURRENT APPLICATION NUMBER: 60/28,928
FRIOR PAPLICATION NUMBER: 60/28,928
FRIOR FILING DATE: 2000-12-29
FRIOR FILING DATE: 2001-01-02
FRIOR APPLICATION NUMBER: 60/259,415
FRIOR APPLICATION NUMBER: 60/259,835
FRIOR FILING DATE: 2001-01-04
FRIOR FILING DATE: 2001-02-20
FRIOR FILING DATE: 2001-03-29
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Publication No. US20040022781A1
GENERAL INFORMATION:
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Shimkets, Richard P
Tchernev, Velizar
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Edinger, Shlomit R
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Gorman, Linda
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Patturajan, Meera
Gusev, Vladimir Y
Gangolli, Esha A
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Boldog, Ferenc
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Liu, Xiaohong
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Gunther, Erik
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Rastelli,
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PRIOR APPLICATION NUMBER: 60/258,228

PRIOR FILING DATE: 2000-12-29

PRIOR FILING DATE: 2000-12-29

PRIOR FILING DATE: 2000-10-29

PRIOR FILING DATE: 2001-01-04

PRIOR FILING DATE: 2001-01-04

PRIOR FILING DATE: 2001-03-29

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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
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Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
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Rastelli, Luca
Casman, Stacie J
Boldog, Ferranc
Burgess, Catherine E
Edinger, Shlomit R
                        Spytek, Kimberly A
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Susev, Vladimir Y
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Millet, Isabelle
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Gangolli, Esha A
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Gunther, Erik
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Liu, Xiaohong
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Vernet, Corine
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CORGANISM: Homo sapiens
US-10-038-854-39
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Catherine
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     Burgess,
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PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR PILING DATE: 00.201-04-25
PRIOR FILING DATE: 2001-04-25
REMAINING PATE: 2001-04-25
REMAINING PATE: 2001-04-25
REMAINING TO SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                    US-10-029-020-14_COPY_1100_1200 (1-101) x US-10-038-854-41 (1-8487)
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Mismatches:
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Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytck, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Wolenc, Corine
APPLICANT: Wenet, Corine
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Shimkets, Nichard A
APPLICANT: Shimkets, Richard A
APPLICANT: Tchernev, Velizar
APPLICANT: Spaderna, Steven K
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Shenoy, Suresh G
Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
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91.09%
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Gusev, Vladimir Y
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Gangolli, Esha A
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Kekuda, Ramesh
                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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US-10-038-854-37
                                                                                                                                    SEQ ID NO 41
LENGTH: 8487
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                                                                                            APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT PAPLICATION NUMBER: US/10/038,854
CURRENT PILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/259,928
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-02
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PLING DATE: 2001-03-29
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PRIOR PLING DATE: 2001-04-13
PRIOR PLING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR PLING DATE: 2001-04-18
PRIOR PLING DATE: 2001-04-18
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PRIOR APPLICATION NUMBER: 60/286,683
PRIOR PLING DATE: 2001-04-18
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PRIOR PLING DATE: 2001-04-18
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Mismatches:
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Edinger, Shlomit
Ellerman, Karen
Gunther, Erik
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APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Herman, John L
APPLICANT: Mishra, Vishnu
APPLICANT: Mishra, Vishnu
APPLICANT: MacLougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
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                                                                                             3334 AGACTCTTCCAAAAGTGGTTTCCTGCCTCACCAAACTTGGCCTATACTTTCATATGGGAT
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                                                1 ArgleuPheArglysTrpPheAlaAlaAlaProAspLeuSerTyrTyrPheIleTrpAsp
                                                                                                                                           21 LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly
US-10-029-020-14_COPY_1100_1200 (1-101) x US-10-038-854-35 (1-8675)
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Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
FRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 9409
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Gaps:
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Patent No. US20020155115A1
GENERAL INFORMATION:
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426.00
89.00%
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APPLICANT: Fernandee
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US-09-808-602-79
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PRIOR APPLICATION NUMBER: 60/258,928
PRIOR PILING DATE: 2000-12-29
PRIOR PILING DATE: 2000-12-29
PRIOR PILING DATE: 2001-01-29
PRIOR PAPLICATION NUMBER: 60/259,415
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR PILING DATE: 2001-01-02
PRIOR PILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-03-29
PRIOR PAPLICATION NUMBER: 60/279,832
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR PAPLICATION NUMBER: 60/279,833
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-04-3
PRIOR PILING DATE: 2001-04-3
PRIOR PILING DATE: 2001-04-13
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APPLICANT: Gunther, Brik
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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Matches:
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                                 Sequence 35, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Vernet, Corine
APPLICANT: Will Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Shimkets, Nichard M
APPLICANT: Shimkets, Nichard A
APPLICANT: Shakets, Nichard A
APPLICANT: Spaderna, Steven K
APPLICANT: Gyadenna, Steven K
APPLICANT: Rekuda, Ramesh
APPLICANT: Rekuda, Ramesh
APPLICANT: Gorwan, Linda
APPLICANT: Gargolli, Baha A
APPLICANT: Gargolli, Esha A
APPLICANT: Gargolli, Esha A
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Edinger, Shlomit R
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Rastelli, Luca
Casman, Stacie J
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; ORGANISM: Homo sapiens
US-10-038-854-35
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LENGTH: 8675
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                                                                     3589 TITGAGCTACATCTTCCAATCTAGGAGGATGGTCTTTGGATAAACATCATGTACTGAAT 3648
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                                 42 GluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGlnGly
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Mismatches:
Indels:
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Matches:
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US-09-800-198-67
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Best Local Similarity:
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US-09-800-198-67
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US-09-808-602-74 ; Sequence 74, Application US/09808602

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GENERAL INFORMATION:
APPLICANT: Vernet, Corine A
APPLICANT: Pernandes, Elma
APPLICANT: Shimkers, Richard A
APPLICANT: Shimkers, Richard A
APPLICANT: Majunder, Kamund
APPLICANT: Majunder, Kamund
APPLICANT: Majunder, Kamund
APPLICANT: Mazes, Peter S
APPLICANT: Mazes, Peter S
APPLICANT: Mazes, Peter S
APPLICANT: Mazes, Peter S
APPLICANT: Mazes, Peter S
APPLICANT: MacDougall, John
TITLE OF INVENTION: NO. US20020155115Alel Proteins and Nuclec Acids Encoding Same;
FILE REPERENCE: 15866-697 CIP
CURRENT APPLICATION NUMBER: US/09/800,198
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Herrann, John L
APPLICANT: Majunder, Kumud
APPLICANT: Mishra, Vishnu
APPLICANT: Mishra, Vishnu
APPLICANT: Macao, Peter S
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REPRENCE: 15966-697 CIP
CURRENT APPLICATION NUBBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-808-602-74
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APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Herrman, John L
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishnu
APPLICANT: Mezes, Peter S
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Best Local Similarity:
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3527 GAATATGAGACCTGCCCCAGTCTCATCCTGTGGAGAAAAAGGACAGCCCTGCTTCAGGGA 3586
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                                                                                                                              2 LeuPheArglysTrpPheAlaAlaAlaProAspLeuSerTyrTyrPheIleTrpAspLys
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is Sequence 65, Application US/09800198

publication No. US20030087816A1

igeneral INFORMATION:

hypelication No. US20030087816A1

igeneral INFORMATION:

hypelicant: Snimkets, Richard

hypelicant: Snimkets, Richard

hypelicant: Majumder, Kumud

hypelicant: Majumder, Kumud

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hypelicant: Majumder, Sumud

hypelicant: Nover Peter S

hypelicant: 1596-697

CURRENT PELING DATE: 2001-03-05

hypelication NUMBER: 60/186,596

hypelication NUMBER: 60/186,596

hypelication NUMBER: 2000-03-03

hypelication Ver: 2.1

hypelication Ver: 2.1
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      Best Local Similarity:
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Best Local Similarity:
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                            Query Match:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vernet, Cornie AM
APPLICANT: Fernandes, Elma
APPLICANT: Majumder, Richard A
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Mastelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 1596-697
CURRENT APPLICATION NUMBER: US/09/800,198
CURRENT APPLICATION NUMBER: G0/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 62
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Matches:
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PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR PILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 77
LENGTH: 8797
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; ORGANISM: Mus musculus
US-09-808-602-77
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Query Match:
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US-09-800-198-62
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APPLICANT: MacDougall, John
TITLE OF INVENTION No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REPERBNCE: 15966-697 CIP
CURRENT FILING DATE: 2001-03-14
CURRENT FILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 76
LENGTH: 6560
                                                                                                             3527 GAATATGAGACCTGCCCCAGTCTCATCCTGTGGGAGAAAAGGACAGCCCTGCTTCAGGGA 3586
                                                              3587 TTCGAGCTGGACCTTCCAACCTTGGAGGCTGGTCCCTGGACAAAACACCACCACCCTCAAT 3646
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. US20020155115A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine A
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Vishnud
APPLICANT: Mashra, Vishnud
APPLICANT: Mashra, Vishnud
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Best Local Similarity:
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APPLICANT:
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                                                   Sequence 2495, Ap
Patent No. 5273901
Patent No. 5482709
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PCT-US96-12158-8

US-08-508-786-7

PCT-US96-12158-7

US-08-508-786-6

US-08-508-786-6

US-08-508-786-6

US-08-508-786-4

PCT-US96-12158-5

PCT-US96-12158-4

PCT-US96-12158-4

US-08-508-786-3

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US-08-508-786-1

US-08-99-1386-2

US-09-976-594-345-1

US-09-976-594-345-1

US-09-976-594-345-1

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US-09-976-594-345-1

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US-09-976-594-345-1

US-09-976-594-345-1
US-08-726-883-1
US-09-023-655-55
US-09-976-594-1044
US-08-030-096-1
US-09-134-000C-2495
5273901-2
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Mismatches:
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US-09-894-844-89

US-08-160-524A-3

US-08-160-524A-1

US-08-46.773-15

US-09-103-840A-1

US-09-103-840A-1

US-09-103-840A-1
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Best Local Similarity:
    Alignment Scores:
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-Q=/cgn2_1/USPTO_spool/US10029020/runat_06082004_112217_29301/app_query.fasta_1.3519
-Q=/cgn2_1/USPTO_spool/US10029020/runat_06082004_112217_29301/app_query.fasta_1.3519
-Q=/cgn2_1/USPTO_spool/US10029020/runat_06082004_112217_29301/app_query.fasta_1.3519
-USB=15sued_Patents_NA -QFMT=fastap_sUSFIX=p2n.rni -MINÄATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits_START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits_START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits_START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-USPE-LOCALIGN=200 -TRANS=human40.cdi
-USPE-LOCALIGN=200 -GRANT=1 -SPB-GRANT=0 -MAXLEN=2000000000
-NO MMAP -LARGEQUERY -NGG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 3, Appli
Sequence 3, Appli
Sequence 799, App
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Sequence 2, Appli
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1875.793 Million cell updates/sec
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                                                                                                                                                                        1 RLFRKWFAAAPDLSYYFIWD......IQSGILHKGNGENQFVSQQP 101
                                                                                             August 14, 2004, 01:16:21 ; Search time 29.8807 Seconds
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                    nucleic search, using frame_plus_p2n model
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US-09-900-236-4
US-08-683-743-3
US-09-489-039A-5660
US-09-221-017B-799
US-08-306-546C-1
US-08-30-524A-1
US-08-103-840A-2
US-09-113-840A-2
US-09-113-840A-2
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Match Length DB
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Database :

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                                                       ----SerGlyIleLeuHisLysGlyAsnGlyGluAsn
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                                                                                                                                                                                                                                    Sequence 3, Application US/08683743
Patent No. 5843697
GENERAL INFORMATION:
APPLICANT: Pearka, Sidney
APPLICANT: Kotenko, Serguei
TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TITLE OF INVENTION: CHAIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
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31
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,743
FILING DATE: 1.7-JUL-1996
CLASSIFICATION: 435
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Mismatches:
Indels:
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Matches:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1
TELECOMINICATION INFORMATION:
TELEPHONE: 201-497-5800
TELEFRAX: 201-437-580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: doub
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STATE: New Jersey
COUNTRY: USA
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US-08-683-743-3
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                                                                           167 CAGCCTCTTTGCCCAGATCTTCCT----GAACTTGATCTTTCTGAACTAGATGTGAAC 220
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107 AACCAGGACTCTGAATCTGTATGGACTGACTGCTGCTGCTTGGTTGAAGAC 166
                                            23 AspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGlyTyrGlu 42
                                                                                                                     43 TyrGluSerCysProAspLeulleLeuTrpGluLysArgThrThrValLeuGlnGlyTyr 62
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                                                                                                                                                                                              GlulleAspAla---SerLysLeuGlyGly-----TrpSerLeuAspLysHisHisAla 79
                                                                                                                                                                                                                                                                         -----SerGlyIleLeuHisLysGlyAsnGlyGluAsn 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TGGGACATGTGC 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Adelmant, Guilaure Title OF INVENTION: Guilaure TITLE OF INVENTION: COACTIVATOR
TITLE OF INVENTION: COACTIVATOR
TITLE OF INVENTION: COACTIVATOR
FILE REFERENCE: DEN-023CP
CURRENT FILING DATE: 2001-10-09
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-01
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-01
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-01
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-01
NUMBER: OF SEQ ID NOS: 6
SOFTWARE: PATENTING DATE: EARLIER FILING DATE: 1997-05-30
NUMBER: OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6525178
GENBRAL INPORMATION:
GENBRAL INPORMATION:
APPLICANT: Spiegelman, Bruce M.; Puigserver, Pere; Wu, Zhidan and APPLICANT: Adelmant, Gullaume
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Matches:
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Indels:
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Patent No. 6525178
           TTCAGGAGCTGGATGGCG
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-900-236-4
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US-09-900-236-4
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2585 GCTTACGAITATTGGTGCCTTAGCCGATTGGCACAGTTCTCCGGCCACGAGCACGAAGCG 2526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GluTyrGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 SerCysProAspLeuIleLeuTrpGluLysArgThrThrVal---
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23
13
32
27
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                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27340-20021.00
                                                                                                                                                                                                         FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
FILING DATE: 31-DEC-1997
FILING DATE: 30-JAN-1998
FILING DATE: 30-JAN-1998
FILING DATE: 00-AR-1998
PRIOR APPLICATION NUMBER: PP2911
APPLICATION NUMBER: PP2911
PILING DATE: 00-AR-1998
FILING DATE: 10-DEC-1998
ATTORNEY, AGENT INFORMATION:
NAME: MOMEON, GLAGYS H
REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 LeuSerGluAlaPheValSerValGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                     UMBER: US/09/221,017B
23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 706141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 3532 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.89%
24.21%
12.66%
                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO ANTI-SENSE: UNKNOWN
                                    RY: USA
94304-1018
Palo Alto
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLE TYPE: DN
MOLECULE TYPE: NO
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STRANDEDNESS:
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                                                                                                                                                                                                                                                          APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                958 TTTAACTGGAACTACGACAAGGTGCCGCAGCCCAAAGTGATGAGCCAGTCGTTTCAC 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LeulleLeuTrpGluLysArgThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
TyrGluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-221-017B-799/C
Sequence 799, Application US/09221017B
Sequence 799, Application US/09221017B
Settle No. 6444799
TITLE OF INVENTION:
TITLE OF INVENTION:
DUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORESTER
CTREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TrpSerLeuAspLysHisAlaLeuAsnIleGlnSerGlyIleLeuHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-029-020-14_COPY_1100_1200 (1-101) x US-09-489-039A-5660 (1-2367)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 AspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheVal--
                                                                                                                   620 GGGTTTCTTCCTGATCGGAACAAGCTGGGGAATGGAGT 658
                                                                               73
                                                                               GlyTyrGluIleAspAlaSerLysLeuGlyGlyTrpSer
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5660
LENGTH: 2367
                                                                                                                                                                            US-09-489-039A-5660
; Sequence 5660, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CRCANISM: Klebsiella pneumoniae
US-09-489-039A-5660
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69.50
36.97%
21.85%
12.66%
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Best Local Similarity:
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Pred. No.:
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1788 ---GAAGAGACTGGTCTTACAGAAGCAGCTTTGCACTTCATCGGCAACATTTGATTAAC 1844
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                                          62 TyrGlulleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeuAsn
      1740 GGATATCAGTCCTGGCCTTCCTTCAGTACATTAGAAAAGGTTTCCTCT-----
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Friderici, Karen
APPLICANT: Ornes, Margaret
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Cavanagh, Kevin
TITLE OF INVENTION: Bovine Beta-Mannogidase Gene and Methods
TITLE OF INVENTION: Of Use
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-029-020-14_COPY_1100_1200 (1-101) x US-08-530-524A-1 (1-3852)
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26
17
34
11
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Conservative:
Mismatches:
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                                                                                                                                                845 GGTAACAATGAAATGCTTCACCAG 1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,524A
FILING DATE: September 19, 1995
CLASSIFICATION: 536
                                                                                                                        82 IleGlnSerGlyIleLeuHisLys 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        Sequence 1, Application US/08530524A Patent No. 5837836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 653
REFERENCE/DOCKET NUMBER: 655
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3852 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: Michigan
COUNTRY: USA
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68.50
48.86%
29.55%
12.48%
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harness,
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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2525 CGTGAATTTCTGCGTAGGAGCTACGACTACCGACATCTTTACAATTCGGAGACGGGATTC 2466
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                                                                                                                                                                                                         APPLICANT: Priderici, Karen
APPLICANT: Jones, Margaret
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Cavanagh, Kevin
TITLE OF INVENTION: Beta-Mannosidase Gene and Methods
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS: ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STRIE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-029-020-14_COPY_1100_1200 (1-101) x US-08-306-546C-1 (1-3852)
                                    87 LeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGlnPro 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 48303
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,546C
FILING DATE: September 15, 1994
CLASSIFICATION: 435
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Mismatches:
Indels:
                                                                         2465 TTTCATCCCAAGGATGAGAAGGGACGCTTCATA~
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36,683
REFERENCE/DOCKET NUMBER: 6550-00003
TELEPHONE: (810) 641-1600
TELEPHONE: (810) 641-1600
                                                                                                                                                  Sequence 1, Application US/08306546C Patent No. 5605797 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3852 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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29.55%
12.48%
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75..2711
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Best Local Similarity:
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LOCATION:
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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT
APPLICANT: WHITE, OWEN R.
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36.27%
21.57%
12.11%
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                            1686 AGTGACTGCTGGAATTGGAGAACTTTCCCCAAAGCTCGA---TTTGTATCT---GAGTAT 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                   81
                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValSerValGlyTyrGluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThr
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                                       42 GluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGlnGly
                                                                                                                       62 TyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-029-020-14_COPY_1100_1200 (1-101) x US-09-103-840A-2 (1-4403765)
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                                                                             1740 ggarárcagiccrgccrrcagracatragaaaaggrrrccrcr
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                            82 ileGlnSerGlyIleLeuHisLys 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.2e+05
66.50
36.27%
21.57%
12.11%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPhe 36
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                                                                                                                                    APPLICANT: FRASER, CLAIRE M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-029-020-14_COPY_1100_1200 (1-101) x US-09-103-840A-2 (1-4403765)
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Sequence 3, Application US/08419078

Patent No. 5587306

GENERAL INFORMATION:
APPLICANT: BELIHAMER, JEFFREY J.
APPLICANT: SELIHAMER, JEFFREY J.
TILLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3330 HILLVIEW AVENUE
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Matches:
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Sequence 2, Application US/09103840A Patent No. 6294328
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04-OCT-1996
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COUNTRY: US.
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                US-08-726-883-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
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                                                            COMPUTER FRANABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,078
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
RESERRENCE/POCKET NUMBER: 33954
TELEFRONAINICATION INFORMATION:
TELEFRONAINICATION INFORMATION:
TELEFRONAINICATION INFORMATION:
TELEFRONE: 415-855-0555
TELEFRONE: ATS-855-0552
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BAPE PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/726,883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08726883
Patent No. 5676946
GENERAL INFORMATION:
APPLICANT: SEILHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC,
STREET: 3330 HILLVIEW AVENUE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.48
66.00
54.29%
40.00%
12.02%
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PALO ALTO
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Query Match:
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                                   USA
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LIBRARY: Hume
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                                                    94304
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Pred. No.:
                                 COUNTRY:
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52 TrpGluLysArgThrThrValLeuGlnGlyTyrGluIleAspAlaSerLysLeuGlyGly 71
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SEILHAMER, JEFFRRY J.
ITILE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/419,078
FILING DATE: 10-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-855-0572
INFORMATION FOR EGG ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 régaagaaagcagcaacrgcarraaaa-
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NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: Human Mast Cell
CLONE: 9118
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 898 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.00
54.29%
40.00%
12.02%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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; LIBRARY: No. 5676946e
; CLONE: 9118
US-08-726-883-1
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APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PALO ALTO
: CALIFORNIA
RY: USA
                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: Cocks,
                    IMMEDIATE SOURCE:
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Pred. No.:
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                                                                                                                                        Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GTTGATGCAGATAAGCATCATTCCCTAGAAGGTCAGTATGGTGTT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 TrpSerLeuAspLysHisHisAlaLeuAsnIleGlnSerGlyIle 86
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Matches:
Conservative:
Mismatches:
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APPLICATION NUMBER: US/08/726,883 FILING DATE: 04-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HANKINS, PHILLIP R.
APPLICANT: SEILHAMER, JEFFREY J.
ITILE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
TORRESPONDENCE: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                          Indels:
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3330 HILLVIEW AVENUE
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/419,078
FILING DATE: 10-APR-1995
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5676946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 3954
REFERENCE/DOCKET NUMBER: PFOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TELEFAX: 415-855-0572
INPORMATION FOR SEQ ID NO: 1:
SEGUENCE CHARACTERISTICS:
LENGTH: 1322 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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66.00
54.29$
40.00$
12.02$
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CLONE: 9118
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Query Match:
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CITY: PALO ALTO
STATE: CA
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LIBERRY: 118 0. 5676946e

15-08-76-483-118

Alignment Goores: 7,84

Percent Similarity: 66.00 Meants: 114

Percent Similarity: 54.239 Minatches: 14

Description: 12.024 Minatches: 14

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RESULT 15
US-09-976-594-1044

I Sequence 1044, Application US/09976594

| Sequence 1044, Application US/09976594

| Sequence 1044, Application US/09976594

| Patent No. 6673549

| GENERAL INFORMATION:
| APPLICANT: Furness, Michael
| APPLICANT: Buchbinder, Jenny
| TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
| FILE REPRENCE: PA-0041 US
| CURRENT APPLICATION NUMBER: US/09/976,594
| CURRENT RILING DATE: 2001-10-12
| PRIOR APPLICATION NUMBER: 60/240,409
| PRIOR PRILING DATE: 2000-10-12
| PRIOR PILING DATE: 2000-10-12
| NUMBER OF SEQ ID NOS: 1143
| SOFTWARE: PERL PROGram
| SEQ ID NO 1044
| LENGTH: 2936
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; OTHER INFORMATION: Incyte ID No. 6673549 1383263.14
US-09-976-594-1044
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Matches:
Conservative:
Mismatches:
Indels:
Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                    Gaps:
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299 TGGAAGAAAGCAGCAACTGCATTAAAA-
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54.29%
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    7.85
66.00
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Best Local Similarity:
                                                Percent Similarity:
Best Local Similarity:
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Pred. No.:
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DB:
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AY405420 Homo sapi
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AL710250 DKFZp686F
AL519858 AL519858
CA75216 UI-M-FOO-
CD803315 UI-M-GV0-
CD803315 UI-M-GV0-
CD8704746 AMGNNUC:S
BB538418 BB538418
BB501284 BB501284
BJ016612 BJ016612
CF536185 UI-M-GIO-
AL148051 Anopheles
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AY413476 Pan trogl
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AL699161 DKFZp686F
AC098731 Pan trogl
AL221061 Tetraodon
AL192136 Tetraodon
AC0970978 RPCI-23-3
BU705631 UI-M-GV0-
CP182768 UI-M-GV0-
CC238800 CH261-50M
BZ165653 CH230-463
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AJ387033 GH17448.5
CF745263 UT.M-CV0-
AL066865 Drosophil
CC574461 CH240 451
AL331828 Tetraodon
AL318958 Tetraodon
AL098692 Drosophil
AL296909 Tetraodon
AL673129 RFCI-24-2
CC611675 OGUACUSTRO
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6246)
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Homo sapiens HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence,
                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                      Description
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AL271172
AL350962
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                                                                  SUMMARIES
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CD578516
AL710250
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BB501284
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CNS03J5I
CNS0428B
CNS05RSP
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CE611069
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CNS02D8V
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BU705631
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CF745263
CNS00765
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KEYWORDS
SOURCE
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-Q=/cgn2_1/USPTO_spool/US10029020/runat_06082004_112216_29287/app_query.fasta_1.3519
-Q=/cgn2_1/USPTO_spool/US10029020/runat_06082004_112216_29287/app_query.fasta_1.3519
-DB=EST_0FWH=fastap_s-SUFFIX=P2n.rst - WINMATCH=0.1 - LOOPEL=0 - LOOPEXT=0
-UNITS=bits - STRART=1 - FND=1. -MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGN=15 - MODE=LOCAL
-OUTPWT=pto - NORNE=ext - HEASPIXE=500 - MINLEN=0 - MAXLEN=200000000
-USR=STS-US10029020_@CGN_1 1_13135_@TUNATC - 0082D004_112216_29287 - NCPU=6 - ICPU=3
-NO MMAP_LARGEQUERY - NGG SCORES=0 - WAIT - DSPBLOCK=100 - LONGLOG
-DEV_TIMEOUT=120 - WARN_TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
                                                                      August 14, 2004, 01:13:26; Search time 1184.51 Seconds (without alignments) 2546.273 Million cell updates/sec
                                                                                                                                           1 RLFRKWFAAAPDLSYYFIWD......IQSGILHKGNGENQFVSQQP 101
                                                                                                                                                                                                                                                           55026578
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                               nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                          Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB
                                                                                                                                            Sequence:
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Tetraodon Tetraodon Tetraodon

UI-M-GHO

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Pan troglodytes HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence, AY413476

AY413476.1 GI:39769438
GSS.
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1 (bases 1 to 3190)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Pan troglodytes
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA.
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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                                                                                                                                                                                             Thomas, P., Kejariwal, A.
                                                                                                                                                                       Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                     Science 302 (5652), 1960-1963 (2003)
14671302
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="HCM4903"
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544.00
99.01%
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Best Local Similarity:
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KEYWORDS
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AY413476
    REFERENCE
                        AUTHORS
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                Inferring nonneutral evolution from human-chimp-mouse orthologous
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Mus musculus HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                         Clark, A.G. Glamowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glamowski, S., Nielson, R., Tuu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wanny, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ArgleuPheArglysTrpPheAlaAlaAlaProAspLeuSerTyrTyrPheIleTrpAsp
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    Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Mismatches:
Indels:
Gaps:
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Science 302 (5652), 1960-1963 (2003)
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Matches:
                                                                                                                                                                                                                                                                                                                                                                           1. .6246
/organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="HCM4903"
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Query Match:
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Pan troglodytes HCM2218 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. AY405421. GI:39761395
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 5087)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                                                                          Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) USA Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Direct Submission
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Conservative:
Mismatches:
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Science 302 (5652), 1960-1963 (2003)
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1. .>5087
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454.00
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78.22%
82.70%
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Best Local Similarity:
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AUTHORS
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SOURCE
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AY405421
                                           REFERENCE
                                                             AUTHORS
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                                                                                                                 Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                Clark, A.G., Glancwski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glancwski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M. A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers

1. 5970
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     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 5970)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                       gene trios
Science 302 (5652), 1960-1963 (2003)
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Gaps:
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Query Match:
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1 (bases 1 to 5094)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbam, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Mang, G., Sheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                  Submitted (16-NOV-2003) Celexa Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tod, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Direct Submission
                                                                                                                                                                                     Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
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/locus_tag="HCM2218"
      sapiens (human)
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                        Homo sapiens
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CD578516
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                                                                                    AUTHORS
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AY405420
AY405420
GSS.
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             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Primates, Catarrhini, Hominidae, Pan.

(Dases 1 to 5069)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                             Inferring nonneutral evolution from human-chimp-mouse orthologous
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542 TATGAGTATGAGTCGTGTTTGGACCTCTGTGGGAAAAGAGGACTGCCATTCTGCAG
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Matches:
Conservative:
Mismatches:
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Science 302 (5652), 1960-1963 (2003)
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
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Length: Matches:

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CD578516
UI-M-GI0-cgg-e-23-0-UI.rl NIH BMAP_GI0 Mus musculus cDNA clone IMAGE:6852960 5', mRNA sequence.
CD578516
CD578516
G1:31742907
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                                                                                                         US-10-029-020-14_COPY_1100_1200 (1-101) x AY405420 (1-5094)
5094
78
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                               Conservative:
Mismatches:
                                                             Indels:
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750 bp mRNA linear EST 04-SEP-2003 lonym: hlcc3) Homo sapiens cDNA clone
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                           81 AsnIleGlnSerGlyIleLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGln 100
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGlyTyr 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 GluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGlnGly 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                    LeuPheArgLysTrpPheAlaAlaAlaProAspLeuSerTyrTyrPheIleTrpAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone (DKFZp686F1868) is available at the RZPD in Berlin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ottenwaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Weil, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wiemann,S.
EST (Ottenwaelder,B., Obermaier,B., Mewes,H.W., Weil,B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        750
72
16
12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="mrnh" | /mol type="mrnh" | /mol xref="taxon:9606" | /clone="DKFZp686F1869" | /dev stage="adult" | /lab_nost="DH10B"
                                                                                                                                                                                                                                                                                          DKFZp686F1868_rl 686 (synonym: h.
DKFZp686F1868_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                   AL710250.1 GI:19693605
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403.00
87.13%
71.29%
73.41%
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .750
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wiemann, S.)
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                                                                                                                                                                       763 CCT 765
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COMMENT
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AL710250
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /docume="INMAGE:682960"
/tissue_type="whole brain"
/dev_stage="whole brain"
/dev_stage="whole brain"
/dev_stage="mbryo 13.5,14.5,16.5,17.5dpc"
/lab host="DH10B (TT phage resistant)"
/clone_lib="NIH BMAP GIO"
/clone_lib="NIH BMAP GIO"
/clone_lib="organ: Brain; Vector: pYx- Asc; Site_l: EcoR I;
/site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcse
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and then polyA tail
is AGGGAGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nib.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 796)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GlyTyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 AGACTCTTCCAGAAGTGGTTTCCTGCCTCGCCAAACTTGGCCTACACGTTCATCTGGGAT
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                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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78
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: pYX-5.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'mol_type="mRNA"
'strain="C57BL/6"
                         Mus musculus (house mouse)
Mus musculus
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89.11%
77.23%
76.87%
                                                                                                                                                                                           Unpublished (1999)
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DB:
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ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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TyrGlulleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeuAsn 81
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1. .725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                      CA752216.1 GI:25582370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.44e-43
390.00
89.89%
76.40%
71.04%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: pYX-5.
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
 62
                                                                                                                                                                                 DEFINITION
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TITLE
JOURNAL
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KEYWORDS
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                               임
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                                                                  8
                                                                                                                                                                                                                          539 bp mRNA linear EST 18-SEP-2002
AL919858 PUR-Z1+Z2 Danio rerio cDNA clone 069-H12-2, mRNA sequence.
AL919858
                     82 IleGlnSerGlyIleLeuHisLysGlyAsn-GlyGluAsnGlnPheValSerGlnGlnPr 101
                                                                                      644 GTTABAAGTGGAATCCTACACAAAGGCACTGGGGGAAAACCAGTTCCTGACCCAGCGCGC 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTGATGCCTACAGGCAGAGGGTCCACGGCTTGACCGAAGCATTGGTTTCTGTGGGGTAC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (Bases i to 539)

Lo.J., Lee,S., Xu,M., Liu,F., Ruan,H., Bun,A., He,Y., Ma,W., Wang,W., Wen,Z. and Peng,J.

15000 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCTCCAGAAATGGTTCCATGCCTCTCCTAACCTGGCATATACCTATATCTGGGACAAG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluTyrGluSerCysProAspLeu1leLeuTrpGluLysArgThrThrValLeuGlnGly 61
 81
 62 TyrGlulleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuPheArgLysTrpPheAlaAlaAlaAraProAspLeuSerTyrTyrPheIleTrpAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThraspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Peng J
Lab of Functional Genomics
Institute of Molecular and Cell Biology
30 Medical Drive, Singapore, 117609, Singapore
Email: pengyr@imcb.a-star.edu.sg
Clone requests: pengjr@imcb.a-star.edu.sg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strālis="local wildtype"
/db xref="taxon: 9955"
/clone="069-H12-2"
/tissue type="whole embryo or fish"
/dev stage="mixed stages"
/clone_llb="PUR-Z1+Z2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-029-020-14_COPY_1100_1200 (1-101) x AL919858 (1-539)
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115
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Matches:
Conservative:
Mismatches:
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/organism="Danio rerio"
                                                                                                                                                                                                                                                                                     AL919858.1 GI:23185156
                                                                                                                                                                                                                                                                                                                       Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.58e-43
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83.84%
68.69%
71.22%
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Best Local Similarity:
Query Match:
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ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
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PUBMED
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/ db xref="taxon:10090"
/ db xref="taxon:10090"
/ clone="IMAGE:6830720"
/ tissue_type="whole brain"
/ dev stage="whole brain"
/ dev stage="mbryole.5dpc"
/ lab_host="DH10B (TI phage resistant)"
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/ note="Organ: Brain, Vector: pvx- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-4806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pvx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the University
Iowa Brain Anatcmy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIWH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                       UI-M-FOO-cdn-g-07-0-UI.rl NIH BMAP_FOO Mus musculus cDNA clone IMAGE:6830720 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.mih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Prarayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (Dases 1 to 725)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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215 TATGAGCTCAACCCCTCAAACTTGGGCAGCTGGTCTCTGGACAAACACCCACATGCGGAAC 274
                                                                                        82 IleGlnSerGlyIleLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGln 100
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Conservative:
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Indels:
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CB704746 348 bp mRNA linear EST 10-APR-2003 AMGNNUC:SRPB2-00285-D10-A srpb2 (10220) Rattus norvegicus CDNA clone srpb2-00285-d10 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/db xref="teaxon:10116"
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/tissue_type="prostate tissue"
/clone=lib="srpb2 (10220)"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; rat
prostate normalized double selected poly(A+) mRNA size
fraction > 1 kb"
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Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Contact: Dan Fitzpatrick
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Amgen EST Program.
Amgen Rat EST Program
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WING WAGO-Chu-m-02-0-UI.rl NIH_BMAP_GVO Mus musculus CDNA clone
IMAGE:30545857 5', mRNA sequence.
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Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                               518
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                  61 GlyTyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
           US-10-029-020-14_COPY_1100_1200 (1-101) x CA752216 (1-725)
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/mol_type="mRNA"
/strain="C57BL/6"
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Mus musculus (house mouse)

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 262)

Konno,H. Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Hara, A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,J., Kadi,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kogawa,J., Kaji,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,Y., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Sugemoto,Y., Shinagawa,A., Shiraki,T., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P. Nishiyama,Y. Westover,A., Itoh,M., Nagaoka,S.,
Carninci,P., Okazaki,Y. Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length ODNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Automated filtration-based high-throughput plasmid preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB538418 RIKEN full-length enriched, 0 day neonate eyeball Mus musculus cDNA clone E13001M11 3' similar to AF195418 Mus musculus cODZ3 (Qdz3) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                232
                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(SCS), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                             62 TyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeuAsn
                                                                                                                                 LeuPheArgiysTrpPheAlaAlaAlaProAspLeuSerTyrTyrPheIleTrpAspLys
                                                                                                                                                                                                                       ThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGlyTyr
                                                                                                                                                                                                                                                                                                              GluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGlnGly
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                                                                                     US-10-029-020-14_COPY_1100_1200 (1-101) x CB704746 (1-348)
    Mismatches:
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Unpublished (2000)
Contact: Yoshihide Hayashizaki
                         Indels:
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Fax: 81-45-503-9216
Email: genome-res@qs
71.88%
68.49%
Best Local Similarity:
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BB538418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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Incremisite 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCAACTCGAGTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
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BBS01284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
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system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                 /tissue_tree="eyeball"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate
eyeball"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer adapter of sequence [5' GAGAGAGATTTCCCCCCCCCCC 3'].
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Matches:
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/db_xref="taxon:10090"
/clone="E130011M11"
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57.14%
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BJ016612/c
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
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Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y. Shibata,Y. (1999)
Carninci,P. and Hayashizaki,Y. (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length CDNA cloning. Methods Enzymol. 303,
19-44 (1999)
                                                                                                                      L. (Dates J. C.) 210).

Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hiozane, T., Hori, F., Ishi, Y., Ishikawa, T., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, K., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shibata, Y., Shibata, Y., Suzuki, H., Suzuki, H., Tagawa, A., Shibata, Y., Suzuki, H., Suzuki, H., Tagawa, A., Katahashi, F., Tominaga, M., Toya, T., Tsunoda, Y., Watahaki, A., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Watamatsu, M. and
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Unpublished (2000)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Site 1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Biken Genomic Sciences Center and Genome Science Laboratory in
                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 318)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.rtc.riken.go.jp) for
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/dev_stage="0 day_neonate"
/lab_host="DH10B"
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l. .318
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musculus (house mouse)
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                            Mus musculus
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                            ORGANISM
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JOURNAL
COMMENT
                                                                                                           REFERENCE
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FEATURES

Alignment Scores:

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BJ016612 BF01SSA CDNA Oryzias latipes CDNA clone MF01SSA030F08 3',
                                                                                                                                                                                                                            46 CGTCGTTGGGAGACTCTTCCACAACTCTTTCCTGCCTCCCTAACTTGCCCTACACTTT 105
                                                                                                                                                                                                                                                                                                            226 TITITCCAAGGCTATGAGITGGAIGCTICGAACATGGGCGCCTGGACGTIGGACAAGCAC 285
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Mohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Modaka EST Project in Takeda's lab
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                          -----PheAlaAlaProAspLeuSerTyrPhe 17
                                                                                                                                                                                                                                                                                     18 IleTrpAspLysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheVal 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 ValLeuGinGlyTyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHis 77
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Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="segmentation stage 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MF01SSA030F08"
/sex="mixture of female and male"
                                           Conservative:
Mismatches:
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Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 CATTTACTGGACGTTCAGAACGGTATACTATAC 318
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Oryzias latipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db xref="taxon:8090"
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/strain="Hd-rR"
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Gaps:

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DB:

Ads14085 Human FCT
Adb23023 Human FCT
Abc1688 Breast ca
Abl29075 Drosophil
Abl29074 Drosophil
Abl04855 Drosophil
Abl04854 Drosophil
Abs90574 Human PGC
Ada20977 Human PGC
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Human mdd Human pol

Ade37148 F Aac47819 A Abx34555 H Aai85693 H Aat67351 H Aat67351 H

Human Pol Human FCT Human FCT Human FCT

Human Pc0 BCU0205A BCU0205B

Prostate

Title:

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Human, NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cell signal processing; metabolic pathway modulation; metabolic disorder; corders, obesity; diabetes; infectious disease; neurodegenerative disorder; acne; Alzheimer's disease; parkinson's disease; immune disorder; cancer; hacematopoietic disorder; cirrhosis; pancreatitis; learning defect; kW memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health; gastro-intestinal disease; reproductive; neurological disease; health; we prome arrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disease; allergy; inflammation; we neuropsychiatric disorder; bGF-related protein; SCUBEI; TEN-M; we adipocyte complement-related Clq tumour necrosis factor; out at first; we adipocyte complement-related Clq tumour necrosis factor; out at first; we beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; kW type la membrane sushi-containing domain; butyrophilin; kW type la membrane sushi-containing domain; butyrophilin;
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-MODEL=frame+ p21.model -DEV=xlh
-De-cgnz_1/USFTO-spool/VISI0029020/runat_06082004_112215_29265/app_guery.fasta_1.3519
-DB=N Geneseq_29Gan04 -QFMT=fastap -SUFFIX=p2n.rng -MINWATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MARTAX=blosum62 -TRANS=human40.cdi
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-USER=USI0029020 @CGN 1 1 1868 @runat_06082004 112215_29265 -NCPU=6 -ICFU=3
-NO_WARA -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPBICCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRENDES=1 -KGAPEXT=0.5 -FGAPEOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Abs78652 Human CDN
Abn85378 Human NOV
Aac74626 Human ORF
Abq82345 Human NOV
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                                                                                                                                                                                      August 13, 2004, 17:03:51; Search time 171.323 Seconds
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                    - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
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geneseqn1980s:*
geneseqn1990s:*
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                       OM protein
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Result No. 3452 TATGAATATGAATCCTGCCCAGATCTAATCCTGTGGGAAAAAAGAACAACAGTGCTGCGGG 3511

TyrGluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGln

41

g à d à 셤 ò 셤 à 셤

3392 AAGACAGACGTCTACAACCAGAAGGTGTTTGGGCTTTTCAGAAGCCTTTGTTTCCGTGGGT

21 LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly

09

80

3572 AACATTCAAAGTGGTATCCTGCACAAAGGGAATGGGAGAACCAGTTTGTGTCTCAGCAG 3631

ABS78652 standard; cDNA; 8645 BP,

3632 CCT 3634 Pro 101

> RESULT 2 ABS78652

101

16-DEC-2002 (first entry)

ABS78652;

61 GlyTyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu

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The present invention relates to new NOVX polypeptides. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, preferably human. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders, haematopoietic disorders, preventing or preventing of the invention are also useful for treating or preventing distributions and useful for treating or preventing distributions. Constituted the invention are also useful for treating or preventing distributions, cancers, acre, hair growth, pigmentation disorders, endocrine disorders, respiratory disease, gastro-intestinal diseases, reproductive, health, caurological diseases, bone marrow transplantation, endocrine diseases, allergy and inflammation, nephrological disorders, urinary system disorders neuropsychiatric disorders and age-related disorders. The present nuclear acid sequence represents a NOVX gene. This sequence encodes a NOVX protein of the invention
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 "Single nucleotide polymorphism (SNP)"
                                                     "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n M, Vernet CAM, Malyankar UM, Kekuda R;
Shimkets RA, Burgess CE, Zerhusen BD, Liu ;
Boldog FL, Smithson G, Li L, Ji W;
                                                                                                                 "Single nucleotide polymorphism (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease
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standard name=
                                                                                               /*tag= c
/standard_name=
                                                       /standard name=
                                                                                                                                                                                                                                                                                20-DEC-2000; 2000US-0257314P.
02-MAY-2001; 2001US-0298153P.
29-MAY-2001; 2001US-0294075P.
24-JUL-2001; 2001US-0307506P.
10-AUG-2001; 2001US-0311590P.
10-AUG-2001; 2001US-0311613P.
29-AUG-2001; 2001US-0315617P.
                 replace (2<u>2</u>5,C)
                                                                         replace (260, A)
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                                                                                                                                                                                                                                                                    2000US-0256704P
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                                                                                             /*tag=
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                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-590744/63.
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                                                                                                                                                     WO200257453-A2
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                   variation
                                                                           variation
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Human; ss; gene; cell growth; differentiation; death; CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal nocturnal haemoglobiunta; psoriasis; polycythaemia vera; primary thromobocytopaenia; developmental disorder; renal tubular acidosis; anaemia; mental retardation; epilepsy; ALDS; neurological disorder; hlzheimer disease; parkinson's disease; asthma; reproductive disorder; infertility; autoimmune disorder; gout; allergy; inflammatory disorder; acquired immunodeficiency syndrome; uveitis; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; multiple sclerosis; osteoarthritis; irritable bowel syndrome; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baughn MR;
Burford N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Lu Y, Warren BA, Elliott VS,
KJ, Tang TY, Lal PG, Duggan BM,
Tran UK, Khare R, Walia NK;
                                                                                                                                                                                                                                 Human cDNA encoding CGDD10, INCYTE 7488573CB1.
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23-FEB-2001; 2001US-0271175P.
08-MAR-2001; 2001US-0274503P.
09-MAR-2001; 2001US-0274552P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2002; 2002WO-US003715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yao MG, Ison CH, Xu Y, Gietzen KJ,
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Ding L,
Lu DAM,
THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S
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Claim 5; Page 175-178; 181pp; English.

US-10-029-020-14\_COPY\_1100\_1200 (1-101) x ABS52100 (1-8354)

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8354 101 0 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

549.00 100.00% 100.00% 5.1e-66

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

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The invention featers to an isolated polypeptic comprising vocurring amino acid sequence at least 90% identical to GGDD, a biologically active comprising an immunoperic fragment. Also included are the fragment or an immunopenic fragment. Also included are the cragment or an immunopenic fragment a recombinant polymuclectide comprising a promoter sequence operably linked to the GGDD pull promoter sequence operably linked to the GGDD pull promoter sequence operably linked to the GGDD pull promoter sequence operably linked to the GGDD pull promoter sequence operably linked to the GGDD pull promoter sequence operably linked to the GGDD pull promoter or alter the expression of GGDD pull promoter are useful for diagnosing, treating or antiquorables are useful for diagnosing, treating or greventing disorders associated with aberrant expression of GGDD, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, particularly cell proliferative (e.g. arteriosclerosis, atherosclerosis, or infertilis, parcoxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thromobocytopaenia or cancer), developmental disorders (e.g. than acidosis, anaemia or mental retardation), cell sorders (e.g. Alzheimer disease, Parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the measure and cycle), or autoimmune/inflammatory disease, diabetes mellitus, contact dermatitis, crohn's disease, diabetes mellitus, contendericiency syndrome, allergies, athematoid arthritis, or viral, bacterial, fungal, parasitic, protozoal or helminthic contact dermatitis, fundal, parasitic, protozoal or helminthic contact dermatitis, or stepoporosis, panceratitis, and acid attribute of infections. They are also useful in the assessment of the effects of infections of the effects of the mental and acid of the effects of the mental and acid of the effects of the mental and acid of the effects of the mental acid of the effects of the mental acid of the effects of the mental acid of the effects of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exogenous compounds on the expression of nucleic acid and amino acid sequences of proteins associated with CGDD. The present sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        assessment of the effects of
f nucleic acid and amino acid
invention relates to an isolated polypeptide comprising CGDD1-12
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Sequence 8645 BP; 2060 A; 2494 C; 2319 G; 1771 T; 0 U; 1 Other;

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3461
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                                                                                                                                                                                                                                                                                                                                            3522 TATGAATATGAATCCTGCCCAGATCTAATCCTGTGGGAAAAAAGAACAACAGTGCTGCAG 3581
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                                                                                                                                                                      1 ArgleuPheArglysTrpPheAlaAlaAlaProAspLeuSerTyrPheIleTrpAsp
                                                                                                                                                                                                                                     LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly
                                                                                                                                                                                                                                                                         3462 AAGACAGACGTCTACAACCAGAAGGTGTTTGGGCTTTTCAGAAGCCTTTGTTTCCGTGGGT
                                                                                                                                                                                                                                                                                                          TyrGluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGln
                                                                                                                                                                                                                                                                                                                                                                              GlyTyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu
                                                                                                                                     US-10-029-020-14_COPY_1100_1200 (1-101) x ABS78652 (1-8645)
            Length:
Matches:
Conservative:
Mismatches:
Indels:
              5.35e-66
549.00
                                             100.00%
100.00%
100.00%
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Alignment Scores:
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DB:
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Sequence 8438 BP; 2001 A; 2434 C; 2268 G; 1735 T; 0 U; 0 Other;

US-10-029-020-14\_COPY\_1100\_1200 (1-101) x ABN85378 (1-8438)

Conservative: Mismatches:

1.57e-64 538.50 99.02% 99.02%

Similarity:

Query Match: Best Local

BP.

DNA; 8438

ABN85378 standard;

RESULT 3 ABN85378 (first entry)

21-OCT-2002

ABN85378;

axaxa

Percent Similarity:

Alignment Scores:

Indels:

Matches:

Length:

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The present sequence is a coding sequence for a NOV protein. The NOV proteins and coding sequences are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma, 1gA nephropathy, cirthosis, arthritis, Albahamer's disease, inflections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. NOVI is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOVX polypeptides and encoding polynucleotides, useful for preventing or treating NOVX-associated disorders e.g. cancer, inflammation, or Alzheimer's disease, and in chromosome mapping, tissue typing or
                                                   Human, NOV1; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive;
Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic;
Antiasthmatic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic;
Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant;
                                                                                                                                                   obesity;
                                                                                                                             Gene Therapy; NOV; cancer; heart disease; inflammation; autoimune disorder; allergy; blood disorder; Allos; diabetes; obesit asthma; IgA nephropathy; cirrhosis; arthritis; Allheimer's disease; infection; stroke; muscular dystrophy; epilepsy; wasting disorder;
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Zhong M, Gangolli EA, Burgess CE, Patturajan M, Vernet CAM;
Taylor S, Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse V
Alsobrook JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman I
Macdougall J, Malyankar U, Millet I, Peyman J, Smithson G;
                                                                                                                                                                                                                                                                                                                                          (pos: 1138. .1147, aa:Met)
                 TEN-M4 like protein, coding sequence.
                                                                                                                                                                                                      TEN-M4 like protein; chromosome 11; gene; ds
                                                                                                                                                                                                                                                                                                                                                             /product= "NOV1 protein"
                                                                                                                                                                                                                                                                                  Socation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-2001; 2001US-0260417P.
10-JAN-2001; 2001US-0260831P.
1-FEB-2001; 2001US-0272338P.
09-MAR-2001; 2001US-0277338P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JAN-2002; 2002WO-US000554
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3430
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                                          3311 CGCCTCTTCAGGAAGTGGTTCGCTGCAGCCCCAGACCTGTCCTATTATTTCATTTGGGAC 3370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vulnerary, antipsoriatic, antiparkinsonian, nootropic, neuroprotective, anticonvulsant, osteopathic, antiarthritic, immunosuppessant, cardiant, immunostimulant, thrombolytic, coagulant, vasotropic, antidabetic, hypotensive, dermatological, immunosuppressive, antiinflammatory;
                                                                                                                                                                                                3371 AAGACAGACGICIACAACCAGAAGGIGITIGGGCITICAGAAGCCITIGIIICCGIGGGI
                                                                                                                                                                                                                                                                                                                                        GlyTyrGlulleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu
ArgleuPheArgLysTrpPheAlaAlaAlaProAspLeuSerTyrTyrPheIleTrpAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnileGlnSer---GlyIleLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGln
                                                                                                                                    LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX ORF181 polynucleotide sequence SEQ ID NO:361.
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99US-0127636P.
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02-APR-1999;
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anticonvulsant; antiarthitic; immunosuppressant; immunostimulant; dermathological; immunosuppressant; antidiabetic; hypotensive; dermathological; immunosuppressive; antidiametory; antibacterial; antiviral; antifungal; antintemmatic; antithyroid; and antibacterial; sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders osteoarthritis, graff ve host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SCID), AlDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                   AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCCTCTTCAGGAAGTGGTTCGCTGCAGCCCCAGACCTGTCCTATTATTTCATTTGGGAC 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 453 BP; 115 A; 117 C; 116 G; 104 T; 0 U; 1 Other;
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Matches:
Conservative:
Mismatches:
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                         5; Page 617; 5507pp; English.
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100.00%
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autoinmune diseases (e.g. allergic reactions, autoimmune haemolytic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be used in chromosome mapping, identifying individuals from minute biological samples (tissue typing), and in forensic identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease), disorders of vesicular transport (e.g. cystic fibrosis, diabetes mellitus, Grave's disease, or goitre), gastrointestinal disorders (e.g. ulcerative colitis, or gastric and duodenal disorders),
                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-732706/79
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29-MAR-2001;
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                                                                                                                                                                                                                                                                                        26-NOV-2001;
                                            Homo sapiens
                                                                                                                                                            29-DEC-2000;
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                                                                                                                         15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases
                                                             Key
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biological sample. The present sequence encodes human NOV15c, which is located on chromosome 4 М В RESULT 6 ABQ82346 Score: SSX8 d g g à 셤 ਨੇ g à 셤 8 à ਨੇ The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, antidiabetic, antiinflammatory, antiheumatic, antiarthritic, virucide, immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), meurological disorders (e.g. epilepsy, stroke, ischemic cerebrovascular disease, Alizheiner's disease or pick's Spytek KA, Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X; Malyankar U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L; Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S; Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K; Gunther E, Smithson G, Millet I, Macdougall JR; associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune diabetes mellitus, Grave's disease, gastrointestinal disorder, vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss. New NOVX polypeptides and polynucleotides useful for treating NOVX-Claim 8; Page 119-121; 444pp; English Location/Qualifiers 258. .8144 /product= "NOV15c" 2001US-0259415P. 2001US-0259785P. 2001US-0259785P. 2001US-0279832P. 2001US-0279833P. 2001US-0298484P. 2001US-0286683P. 2001US-0296683P. 2001US-0294080P. 2001US-0312915P. 2001WO-US049976 2001US-0322699P 2001US-0333350P /\*tag=

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3390 GATGTACAGAACGGTATACTGTACAAGGGAAACGGGAAAACCAGTTCATCTCCCCAGCAG 3449
                                                                                                                                                                                                                                                                                                                    3210 AAAACAGATGCATATAATCAGAAAGTCTATGTGTCTATCTGAAGCTGTTGTGTCTCGGTTGGA 3269
                                                                                                                                                                                                                                                                                                                                                                                           3330 GGCTATGAATTGGATGCGTCCAACATGGGTGGCTGGACATTAGATAAACATCACGTGCTG 3389
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                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GlyTyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu
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                                                                                                                                                                                                                                                                                                 LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly
Sequence 8473 BP; 2301 A; 2017 C; 2145 G; 2006 T; 0 U; 4 Other;
                                                    8473
78
14
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Mismatches:
Indels:
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91.09%
77.23%
82.51%
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                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3450 ¢cr 3452
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                                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                      Alignment Scores:
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                                                                                                                                                                                                                                                                                               21
                                                                                                                           Query Match
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31-DEC-2001; 2001WO-US049976

3146 AGACTCTTCCAAAAGTGGTTTCCTGCCTCAAACTTGGCCTATACTTTCATATGGGAT 3205

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% 29-DEC-2000; 2000US-0228928P.

PR 27-AN-201; 2001US-0228938P.

PR 27-AN-201; 2001US-0228938P.

PR 27-AN-201; 2001US-0228938P.

PR 29-ANR-2010; 2001US-0228938P.

PR 29-ANR-2010; 2001US-0228938P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-022893P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-023898P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

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PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

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PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

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PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

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PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

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PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010; 2001US-02389P.

PR 29-ANR-2010US-02389P.

PR 29-ANR-2010US-02389P.

PR 29-ANR-2010US-02389P.

PR 29-ANR-2010US-02389P.

PR 29-ANR-2010US-02389P.

PR 29-ANR-2010US-02389P.

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PR 29-ANR-2010US-02389P.

PR 29-ANR-2010US-02389P.

PR 29-ANR-2010US-02389P.

PR 29-ANR-2010US-02389P.

PR 29-ANR-2
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Pred. No.: 1.83e-52 Length: 6487

Score: 453.00 Matches: 78

Percent Similarity: 91.03% Conservative: 14

Best Local Similarity: 77.23% Mismatches: 9

Query Match: 82.51% Indels: 0

DB: 6 Gaps: 0

US-10-029-020-14_COPY_1100_1200 (1-101) x ABQ82346 (1-8487)
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Alignment Scores:

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3206 AAAACAGATGCATATAATCAGAAAGTCTATGGTCTATCTGAAGCTGTTGTGTCTCAGTTGGA 3265
                                                                             3386 GATGTACAGAACGGTATACTGTACAAGGGAAACGGGGAAAACCAGTTCATCTCCCAGCAG 3445
                                                                                                                                                                       81 AsnIleGlnSerGlyIleLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; notropic; antidiabetic; antiinflammatory; fungicide; antirheumatic; antiarile; immunosupressive; antiallergic; virucide; antianaemic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Altehemer's disease; allergy; pick's disease; vesicular transport disease; cystic fibrosis; goitre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative collitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.
  21 LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly 40
                                                                                                                  80
                                                           41 TyrgluTyrgluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGln
                                                                                                                 GlyTyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                      Human NOV15b encoding cDNA SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/product= "NOV15b"
                                                                                                                                                                                                                                                                                                                      ABQ82344 standard; cDNA; 8645 BP
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2001US-0259785P.
2001US-0269814P.
2001US-0279863P.
2001US-0279832P.
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2001US-0284447P.
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2001US-0312915P.
2001US-0313325P.
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2001US-0333350P.
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/*tag= a
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09-MAR-2001;
29-MAR-2001;
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13-APR-2001;
18-APR-2001;
25-APR-2001;
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16-AUG-2001;
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04-JAN-2001;
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26-NOV-2001;
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(CURA-) CURAGEN CORP Spytek KA, 

Sequence 8645 BP; 2343 A; 2060 C; 2200 G; 2038 T; 0 U; 4 Other;

Length: Matches: Conservative: Mismatches: Indels: 1.88e-52 453.00 91.09% 77.23% 82.51\$ Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: Pred. No.:

3561 3322 AGACTCTTCCAAAAAGTGGTTTCCTGCCTCACCAAACTTGGCCTATACTTTCATATGGGAT 3381 3382 AAAACAGAIGCAITATAAICAGAAAGICTAIGGICTAICTIGAGGITGGG 3441 3562 GATGTACAGAACGGTATACTGTACAAGGGAAACGGGGAAAACCAGTTCATCTCTCCCAGCAG 3621 AsnIleGlnSerGlyIleLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGln 100 40 80 TyrGluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGln 60 ArgleuPheArglysTrpPheAlaAlaAlaProAspleuSerTyrTyrPheIleTrpAsp 21 LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly GlyTyrGlulleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHlsAlaLeu US-10-029-020-14\_COPY\_1100\_1200 (1-101) x ABQ82344 (1-8645) 41 61 81 à g ò g à g 8 à

Human; NOVX, cytostatic, neuroprotective, anticonvulsant, cardiovascular, cerebroprotective, nootropic, antidiabetic, antinflammatory, fungicide, antirheumatic, antiarthritic, immunosuppressive, antiallergic, virucide, antianaemic, antibacterial, protozoacide, antihelminthic, gene therapy, cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzehener's disease; allergy; Pick's disease; vesicular transport disease; cystic fibrosis; goitre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; uccrative collitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss. /\*tag= a /product= "NOV15a" /transl\_except= (pos:1249. .1251,aa:Ser) Human NOV15a encoding cDNA SEQ ID NO:35. Location/Qualifiers ABQ82343 standard; cDNA; 8675 .8328 (first entry) 101 Pro 101 Homo sapiens. 17-DEC-2002 3622 ABQ82343; ABQ82343 

31-DEC-2001; 2001WO-US049976 WO200262999-A2 02-JAN-2001; 04-JAN-2001; 20-FEB-2001;

09-MAR-2001, 20010S-029863P-29-MAR-2001, 2001US-0279832P-29-MAR-2001, 2001US-0279833P-13-APR-2001, 2001US-028889P-18-APR-2001, 2001US-0284447P-29-APR-2001, 2001US-0286683P-29-MAY-2001, 2001US-0296683P-2001US-0259415P. 2001US-0259785P. 2001US-0269814P. 2001US-0313325P. 2001US-0322699P. 2001US-0333350P. 2001US-0312915P 17-AUG-2001; 17-SEP-2001; 16-AUG-2001; 26-NOV-2001;

(CURA-) CURAGEN CORP.

Wolenc AR, Vernet CAM, blben n, --ikets RA, Tchernev VT, Spaderna SK, Gorman L;
ljan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
an SJ, Boldog F, Burgess CE, Edinger S, Ellerman K; Spytek KA, li L, WOLLLL.
Malyankar U, Shimkets RA, Tchell.
Kekuda R, Patturajan M, Gusev V,
Kekuda R, Patturajan SJ, Boldog F,

WPI; 2002-732706/79. P-PSDB; ABP53586.

New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders disorders of vesicular transport, gastrointestinal disorders, and autoimmune diseases

The present invention describes novel human proteins designated NoVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, antidiabetic, antidiahetic, antidiahetic, antidiahetic, antidiahetic, antidiahetic, antidiahetic, antidiahetic, antidiahetic, intucide, immunosuppressive, antidiahetic, antidiahetic, virucide, immunosuppressive, antidiahetic, antidiahetic, virucide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the campacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or Pick's disease), disorders disease, or goitte), gastrointestinal disorders), autoimmune diseases (e.g. allergic reactions, autoimmune hamolytic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic used in chromosome mapping, identifying individuals from minute

Diological samples (tissue typing), and in forensic identification of a biological sample, The present sequence encodes human NOV15b, which is Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X;
, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;
Patturajan M, Gusev V, Gangolli RA, Guo X, Shenoy S;
Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
Smithson G, Millet I, Macdougall JR; New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune Claim 8; Page 114-117; 444pp; English Spyten ...,
Malyankar U, Shimker.
Kekuda R, Patturajan M,
Casman SJ, Malyum. Kekuda R, Patlumu, Rastelli L, Casman SJ, WPI; 2002-732706/79. P-PSDB; ABP53587. ocated on

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1918 CTCTTCCAGAAGTCATTCCAGGCTTCTCCCAACCTGGCCTACATCTGGGACAAG 1977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel differentially regulated genes and polypeptides encoded by them. Sequences of the invention are useful in diagnosing, staging, monitoring, prognosticating, preventing, treating or determining the predisposition to diseases or conditions such as prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer. They may be used as molecular markers, drug targets, vaccines, in gene therapy, research, clinical medicine or forensic science. The present sequence is a differentially regulated prostate cDNA, Pc099 which codes for teneurin-2. Pc099 gene is located on chromosome 5q34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide for diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to, diseases or conditions such as prostate cancer, and for research or forensic science.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrGlulleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeuAsn 81
prostate cancer; gene therapy; Pc099; teneurin-2; chromosome 5q34; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 GluTyrGluSerCysProAspLeulleLeuTrpGluLysArgThrThrValLeuGlnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuPheArgLysTrpPheAlaAlaAlaProAspLeuSerTyrTyrPheIleTrpAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4245 BP; 1035 A; 1132 C; 1115 G; 963 T; 0 U; 0 Other;
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72
16
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Mismatches:
                                                                                                                   י אינטמטנב= "Human Pc099 protein"
/note= "No start codon"
/partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 29; Page 158-163; 100pp; English.
                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kovacs KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                 (ORIG-) ORIGENE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                   07-NOV-2001; 2001US-0331041P.
07-NOV-2001; 2001US-0331042P.
18-DEC-2001; 2001US-0340251P.
                                                                                                                                                                                                                                                                                                  07-NOV-2002; 2002WO-US035563
                                                                                                                                                                                                                                                                                                                                                                                            07-JAN-2002; 2002US-0344791P.
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416.00
88.00%
72.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-449451/42.
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                                                                                                                                                                                                                            WO2003040331-A2
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                                                      sapiens
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                                            the present threathous unescribes movel numen profeshis designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, contidibateic, anticinflammatory, anticinflammator, antichacterial, funciode, immunosuppressive, anticillergic, anticinflammator, antichacterial, funciode, proteozoacide and antihelminthic activities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a convert. It is a manufacture of a medicament for treating a syndroder, such as cancers of unamial lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or pick's disease, disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. ulcerative colitis, or gastric and duodenal disorders), antendimmune diseases (e.g. ulcerative colitis, or gastric and protozal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be consed in chromosome mapping, identifying individuals from minute consequence and proteozal samples (tissue typing), and in forensic identification of a biological sample. The present sequence encodes human NOV15a, which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3394 AAAACAGATGCATATAATCAGAAAGTCTATGTGTCTATCTGAAGCTGTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrGluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGln
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                                     present invention describes novel human proteins designated NOVX
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 8; Page 110-112; 444pp; English
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2819 GAATATGAGACCTGTCCCCAGTCTAATTCTCTGGGAGAAAAGGACAGCCCTCCTTCAGGGA

GluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGlnGly

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human differentially-regulated breast cancer polynucleotide and polypeptide, useful for diagnosing, staging, prognosticating, preventing and/or treating diseases and conditions relating to breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug discovery; cytostatic; gene therapy; antisense therapy; regulated;
drug discovery; clinical medicine; forensic medicine; gene;
chromosome 5q33.3; ds.
82 IleGlnSerGlyIleLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGlnPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 79; 127pp + Sequence Listing; English.
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                                                                                                                                                                                                                   standard; DNA; 9058
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GITAAAAGIGGAATCCTACACAAAGGCACTGGGGAAAACCAGTTCCTGACCCAGCAGCCT 2998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human differentially-regulated breast cancer polynucleotide and polypeptide, useful for diagnosing, staging, prognosticating, preventing and/or treating diseases and conditions relating to breast
                                                                                                                                                                                                                 gene therapy; antisense therapy; regulated;
82 IleGlnSerGlyIleLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 2567 A; 2582 C; 2434 G; 2112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 clinical medicine; forensic medicine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 81; 127pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jay
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (ORIG-) ORIGENE TECHNOLOGIES INC
                                                                                          BP
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14-MAY-2002; 2002US-00144194.
                                                                                                                                                                                                                                                                                                                                                                     32-OCT-2002; 2002WO-US031287.
                                                                                          DNA; 9695
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416.00
88.00%
                                                                                                                                                                                                             Breast cancer; cytostatic;
                                                                                                                                                                                  BCU0205B gene #SEQ ID 81.
                                                                                                                                                                                                                               drug discovery; clinic chromosome 5q33.3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fan W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-381623/36.
P-PSDB; ABR58318.
                                                                                       ACC72052 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li X,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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                                                                                                                       ACC72052;
                              2939
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CTCTTCCAGAAGTCATTCCAGGCTTCTCCCAACCTGGCCTACACCTTCATCTGGGGACAAG 2758

LeuPheArgLysTrpPheAlaAlaAlaProAspLeuSerTyrTyrPheIleTrpAspLys

US-10-029-020-14\_COPY\_1100\_1200 (1-101) x ACC72051 (1-9058)

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Length:
Matches:
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3.34e-47 416.00 88.00% 72.00% 75.77%

Similarity:

Best Local

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Indels:

Gaps:

ThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGlyTyr 41

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3497 AATCCTCAAAGTGGAATCATACATAAAGGGAATGGAGAAAATATGTTCATTTCCCAGCAG 3556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3377 TATGAATATGAAACGTGCCCTGACTTTATTCTCTGGGAGCAAAGGACAGTCGTTTTACAA 3436
associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-sociated polymucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polymucleotide sequences are differentially expressed in prostate tumour fissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 AsnileGinSerGlyIleLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrGluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGln
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                                                                                                                                                                                    useful in gene therapy, as a vaccine or in antisense applications. ABK92115-ABK92163 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                                                Sequence 12879 BP; 3852 A; 2674 C; 2768 G; 3585 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                    US-10-029-020-14_COPY_1100_1200 (1-101) x ABK92230 (1-12879)
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                                                                                                                3336 CTCTTCCAGAAGTCATTCCAGGCTTCTCCCAACCTGGCCTACACCTTCATCTGGGAAAG
                                                                                                                                                                                                                                       3456 GAATATGAGACCTGTCCCAGTCTAATTCTCTGGGAGAAAAGGACAGCCCTCCTTCAGGA
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                                                                                                                                                                                                                                                                                                3516 TTCGAGCTGGACCCCTCCAACCTGGTGGCTGGTCCCTAGACAAACACACCCATCCTCAAT
                                                                                                                                                                                                                                                                                                                                           82 IleGlnSerGlyIleLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGlnPro
                                                                                                LeuPheArgLysTrpPheAlaAlaAlaProAspLeuSerTyrTyrPheIleTrpAspLys
                                                                                                                                                           ThraspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGlyTyr
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16-MAR-2001;
16-MAR-2001;
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production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis requlating activity, tissue growth factor activity, immunomodulatory activity and activity, infinibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
(AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
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, Chen R, Wang ZW;
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                                                                                                                                                                                                                                  Ren F,
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Wang D, Wang J, Zhang J,
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1414-1426; 6221pp; English
                                              2000US-00560B75.
2000US-0059B075.
2000US-0054935.
2000US-0063561.
2000US-0063352.
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 2001WO-US004098
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                                              27-APR-2000;
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19-JUL-2000;
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Ma Y, Zh
Xue AJ,
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TyrGluTyrGluSerCysProAspLeuIleLeuTrpGluLysArgThrThrValLeuGln 1 ArgleuPheArglysTrpPheAlaAlaAlaProAspleuSerTyrTyrPheIleTrpAsp LysThrAspValTyrAsnGlnLysValPheGlyLeuSerGluAlaPheValSerValGly 3703 TATGAATATGAAACGTGCCCTGACTTTATTCTCTGGGAGCAAAGGACAGTCGTTTTACAA GlyTyrGluIleAspAlaSerLysLeuGlyGlyTrpSerLeuAspLysHisHisAlaLeu US-10-029-020-14\_COPY\_1100\_1200 (1-101) x AAK51828 (1-13202) 21 41 61 g Db ò g à ð

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AsnileGlnSerGlyileLeuHisLysGlyAsnGlyGluAsnGlnPheValSerGlnGln 100

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Human, FCTRX, myelogenous leukaemia; carcinoma; melanoma; glioma; ds;

M sstrocytoma; congenital neonatal alloimmune thrombocytopaenia; infection;

neurological disorder; neurodegenerative disorders; nerve trauma;

familial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy;

M demyelinating Gardner syndrome; familial myelodysplastic syndrome;

M mental health condition; immunological disorder; allergy; infertility;

M conchial asthma; Avellino type eosinophilia; lung disease; deafness;

M reproductive disorder; reproductive disorder; glycoprotein Ia deficiency;

M desmoid disease; turcot syndrome; liver cirrhosis; hepatisis C; virucide;

M spinocerebellar ataxia; Plasmodium falciparum parasitaemia; diabetes;

M corneal dystrophy-Greonouw type I; Corneal dystrophy-lattice type I;

R eis-Bucklers corneal dystrophy; antiinflammatory;

M antidalergic; antiasthmatic; antiinfertility; antiinflammatory;

M antidabetic; protozoacide; hepatotropic; virucide; ophthalmological;

M gene therapy; FCTR3a; neurestin-like protein; FCTR3f. The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the nucleic acids encoding them. These sequences are useful for the treatment or prevention of numerous disorders including myelogenous leukeemia, carcinomas, melanomas, gliomas, astrocytomas, congenital neonatal alloimmune thrombocytopaenia, neurological disorders, neurodegenerative Novel polypeptides designated as FCTRX polypeptides, useful in detection, prevention and treatment of a broad range of pathological states. Majumder K; Herrmann JL, Mezes PS, Rastelli L; "Human FCTR3f" Shimkets RA, Location/Qualifiers Claim 9; Page 37-39; 215pp; English. BP. AAS14089 standard; DNA; 9729 03-MAR-2000; 2000US-0186592P.
03-MAR-2000; 2000US-0186718P.
06-MAR-2000; 2000US-0187294P.
17-MAR-2000; 2000US-0187294P. 07-APR-2000; 2000US-0196018P 03-JAN-2001; 2001US-0259548P 05-MAR-2001; 2001WO-US007160 /product= "F 8385. .9729 g= b .8384 (first entry) Human FCTR3f DNA sequence U /\*tag= a Fernandes E, Mishra V, .209 '\*tag≕ /\*tag= CURA-) CURAGEN CORP. WPI; 2001-596837/67. P-PSDB; AAU08681. WO200166747-A2 Macdougall J, Homo sapiens 18-DEC-2001 13-SEP-2001 Vernet CAM, AAS14089; Key 5'UTR 3'UTR CDS 

05-MAR-2001; 2001US-00800198 03-MAR-2000; 2000US-0186592P.

08-MAY-2003

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The invention relates to FCTRX polypeptides and the polynucleotides encoding them. The sequences of the invention are useful for the manufacture of a medicament for diagnosing and treating disorders associated with the FCTRX polypeptide, such as colorectal cancer, adenomatous polyposis coli, myelogenous leukaemia, congenital neonatal cumune thrombocytopenia, malignant ovarian tumours, malignant brain tumours, manumat ovarian tumours, malignant brain carcinoma, breast adenocarcinoma, ovarian carcinoma, melanomas, clear carcinoma, breast adenocarcinomas, neurological disorders, cell and granular cell carcinomas, neurological disorders, mental health conditions, immunological disorder trauma, familial myelodysplastic syndrome, Charcot-Marie-Tooth neuropathy, Gardner syndrome, mental health conditions, immunological disorders, allergy and infection, asthma, lung diseases, male and female reproductive disorders, deafness, glycoprotein deficiency, desmoid tumour, turcot syndrome, liver dirrhosis, hepatitis c, gastric disorders, pancreatic diseases, diabetes, schistosoma mansoni infection, spinocerebellar ataxia, plasmodium falciparum infection, groenouw's corneal dystrophy and lattice corneal dystrophy. This sequence represents cDNA encoding an FCTRX polypeptide of the invention.
                   3563
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disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Mari-Tooth neuropathy, demyelinating Gardner syndrome, familial myelodysplastic syndrome, mental health conditions, immunological disorders, allergy and infection, bronchial asthma, Avellino type eosinophilia, lung diseases, reproductive disorders, infertility, male and female reproductive disorders, deafness, glycoprotein Ia deficiency desmoid disease, turcot syndrome, liver cirrhosis, hepaticis C, gastric disorders, panoreatic diseases such as diabetes, Schistosoma mansoni infection Spinocerebellar ataxia, Plasmodium falciparum parasitaemia, Corneal dystrophy-Greonouw type I, Corneal dystrophy-lattice type I and Reis-Bucklers corneal dystrophy. This sequence represents DNA encoding the PCTR3a homologue PCTR3f
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New FCTRX polypeptide and encoding polynucleotide, useful for preventing or treating FCTRX-related disorders, such as cancer, autoimmune, neurodegenerative, gastrointestinal, reproductive and inflammatory

9; Page 34-37; 155pp; English

Claim

diseases.

Majumder K;

Herrmann J, Rastelli L;

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Shimkets R, Mezes PS,

, C, Mishra

Fernandes

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Vermet

RASTELLI L

(MACD/) N (MISH/) N (MEZE/) N (RAST/) I

2003-625633/59

WPI; 2003-625633 P-PSDB; ADB32029 Macdougail J,

SHIMKETS R.
HERRMANN J.
MAJUMDER K.
MACDOUGALL J.
MISHRA V.
MEZES P S.

(HERR/)
(MAJU/) FERN/) SHIM/)

VERMET C. FERNANDES E.

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3384 CICTICCAGAAGTCAITCCAGGCITCTCCCAACCTGGCCTCCACCTTCATCTGGGACAAG
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Sequence 9729 BP; 2548 A; 2629 C; 2438 G; 2114 T; 0 U; 0 Other;
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                                                                                                                                                        Human; gene; ss; FCTR3f; colorectal cancer; adenomatous polyposis coli; myelogenous leukaemia; congenital neonatal autoimmune thrombocytopenia; ovarian cancer; brain tumour; breast cancer; glioma; astrocytoma; renal cell carcinoma; melanoma; clear cell carcinoma; granular cell carcinoma; neurological disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                familial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy; dardner syndrome; mental health condition; immunological dasorder; allersy; asthma; lung disease; reproductive disorder; dasfness; glycoprotein deficiency; desmoid tumour; turcot syndrome; liver cirrhosis; hepatitis C; gastric disorder; panoreatic disease; diabetes; schistosoma mansoni infection; spinocerebellar ataxia; plasmodium falciparum infection; Groenouw's corneal dystrophy;
                                                            (first entry)
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                                                                                                                Human FCTR3f cDNA.
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Homo sapiens.

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Sequence 49, Application US/10383201

Publication No. US2004002926A1

Publication No. US2004002926A1

Publication No. US2004002926A1

APPLICANT: Alsobrook II, John et al.

ITILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE

PURENT FILING DATE: 2003-03-06

PRICR FILING DATE: 2001-12-19

PRICR FILING DATE: 2002-03-20

PRICR PLICATION NUMBER: 60/385,984

PRICR FILING DATE: 2002-04-12

PRICR FILING DATE: 2002-06-14

PRICR FILING DATE: 2002-06-14

PRICR FILING DATE: 2002-06-26

PRICR FILING DATE: 2002-06-36

PRICR FILING DATE: 2002-06-36

PRICR FILING DATE: 2002-06-36

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PRICR FILING DATE: 2002-06-13

PRICR FILING DATE: 2002-09-13

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2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/prodata/2/pubpna/USO6_NEW_PUB.seq:*
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5: /cgn2_6/prodata/2/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/prodata/2/pubpna/USO7_NEW_PUB.seq:*
7: /cgn2_6/prodata/2/pubpna/USO8_PUBCOMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-383-201-43

i Sequence 43, Application US/10383201

j Sequence 43, Application NS/10383201

j Sequence 43, Application NS/10383201

j Publication NS-10-204

j GENERAL INFORMATION: HERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD TITLE REFERENCE: 21402-5684

j TITLE REFERENCE: 21402-5684

j CURRENT APPLICATION NUMBER: 06/365,984

j PRIOR FILING DATE: 2002-03-20

j PRIOR FILING DATE: 2002-04-12

j PRIOR FILING DATE: 2002-04-12

j PRIOR FILING DATE: 2002-04-12

j PRIOR FILING DATE: 2002-06-14

j PRIOR FILING DATE: 2002-06-14

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PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 60/412,957
PRIOR FILING DATE: 2002-09-23
PRIOR FILING DATE: 2002-09-23
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-03-22
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Publication No. US20040029226A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-568A
CURRENT APPLICATION NUMBER: US/10/383,201
CURRENT FILING DATE: 2003-03-06
PRIOR PAPLICATION NUMBER: 60/30-03
PRIOR PILING DATE: 2002-03-20
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 10/051,874
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-01-16
PRIOR PILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SEQ ID NO 49
LENGTH: 1399
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617.00
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                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
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; LOCATION: (2)
US-10-383-201-49
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Pred. No.:
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US-10-383-201-59
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Alignment Scores:
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; Sequence 13, Application US/10029020
; Sequence 13, Application US/10029020
; Publication NO. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same;
; TITLE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR PRILING DATE: 2000-12-19
; PRIOR PLING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-10
; PRIOR PLING DATE: 2001-08-10
; PRIOR PLING DATE: 2001-12-20
; PRIOR PLING DATE: 2001-08-10
; PRIOR PLING DATE: 2001-08-10
; PRIOR PLING DATE: 2001-08-10
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Mismatches:
Indels:
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Matches:
            PRIOR APPLICATION NUMBER: 60/410,755
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-23
PRIOR FILING DATE: 2002-09-23
PRIOR PILING DATE: 2002-09-23
PRIOR PLICATION NUMBER: 10/051,874
PRIOR APPLICATION NUMBER: 00/366,928
PRIOR PILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 10/055,877
PRIOR PILING DATE: 2002-03-22
PRIOR PILING DATE: 2002-03-22
PRIOR PILING DATE: 2002-03-22
PRIOR PILING DATE: 2002-03-22
PRIOR PILING DATE: 2002-03-22
PRIOR PILING DATE: 2002-03-22
PRIOR PILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SOFTWARE: CuraseqList version 0.1
| SEQ ID NO 43
FILING DATE: 2002-06-26
APPLICATION NUMBER: 60/410,755
FILING DATE: 2002-09-13
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617.00
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ORGANISM: Homo sapiens
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US-10-383-201-43
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Query Match:
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NAME/KEY: CDS
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RESULT 5
US-10-383-201-55
US-10-383-201-55
Sequence 55, Application US/10383201
Publication No. US20040029226A1
GENERAL INFORMATION:
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE;
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE;
CURRENT APPLICATION NUMBER: US/10/383,201
PRIOR FILING DATE: 2003-03-06
PRIOR PLICATION NUMBER: 10/029020
PRIOR PLICATION NUMBER: 60/365,984
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR PLICATION NUMBER: 60/389,143
PRIOR PLICATION NUMBER: 60/389,143
PRIOR FILING DATE: 2002-06-14
PRIOR PLICATION NUMBER: 60/391,779
PRIOR FILING DATE: 2002-06-26
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Mismatches:
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Matches:
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR FILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/302,358
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR APPLICATION NUMBER: 60/298,153
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 13
LENGTH: 8354
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CRGANISM: Homo sapiens
US-10-029-020-13
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Best Local Similarity:
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APPLICANT: ROLEBORGE, MAIK E
APPLICANT: ROLEBORGE, MAIK E
APPLICANT: Blerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Malbarker, Uriel M
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Stone, John
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, David
TITLE OF INVENTION: Uring the Same
APPLICANT: Later Called
FILE REFERENCE: 21402-537
CURRENT PLING DATE: 2002-05-17
PRIOR PELING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR PELING DATE: 2001-01-01
PRIOR PELING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
NUMBER OF SEQ ID NOS: 264
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Matches:
Conservative:
Mismatches:
Indels:
                                Boldog, Ference L
Grosse, William M
Alsobrook II, John F
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2549 GGAGATGGCCTGGTG 2563
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94.29%
93.33%
93.84%
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ORGANISM: Homo sapiens
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2479 AGAGGAGCTGGCTGTGACCTTCCATGGAGACTGCCTGCGGTGACAGCAAAGACAATGAT 2538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 GlyAsnGlyArgCysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrp
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 60/412,957
PRIOR APPLICATION NUMBER: 60/412,957
PRIOR PILING DATE: 2002-09-23
PRIOR FILING DATE: 2002-01-16
PRIOR PRILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 60/366,928
PRIOR PILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 10/055,877
PRIOR FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 55
LIBNOTH 18355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/10042865; Publication No. US20040029216A1; GENERAL INFORMATION: APPLICANT: Padigaru, Muralidhara
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Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
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Zerhusen, Bryan D
Casman, Stacie J
Shency, Suresh G
Spytek, Kimberly
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96.19%
96.43%
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ORGANISM: Homo sapiens
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; LOCATION: (1)..(8325)
US-10-383-201-55
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Best Local Similarity:
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US-10-042-865-1
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APPLICANT:
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CURRENT FILING DATE: 2003-01-22

PRIOR FILING DATE: 2000-12-29

PRIOR FILING DATE: 2000-12-29

PRIOR FILING DATE: 2000-12-29

PRIOR FILING DATE: 2000-10-2-29

PRIOR PRILOR PRICATION NUMBER: 60/259,785

PRIOR PRILOR APPLICATION NUMBER: 60/259,814

PRIOR PRILOR DATE: 2001-01-02-20

PRIOR PRILOR DATE: 2001-03-29

PRIOR PLILNG DATE: 2001-03-29

PRIOR PRILOR DATE: 2001-03-29

PRIOR PRILOR DATE: 2001-03-29

PRIOR PRILOR DATE: 2001-03-29

PRIOR PRILOR DATE: 2001-03-29

PRIOR PRILOR DATE: 2001-03-29

PRIOR PRILOR OWNER: 60/279,863

PRIOR PRILOR DATE: 2001-03-19

PRIOR PRILOR DATE: 2001-04-13

PRIOR PRILOR DATE: 2001-04-13

PRIOR PRILOR DATE: 2001-04-13

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APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 2003-01-22
                                                                                                                           ; Sequence 39, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                   APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Wolenc, Corine
APPLICANT: Eisen, Andrew J
APPLICANT: Lisen, Andrew J
APPLICANT: Lisen, Andrew J
APPLICANT: Malyankar, Uriel M
APPLICANT: Tchernev, Velizar
APPLICANT: Tchernev, Velizar
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
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Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
Burgess, Catherine E
Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
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Gusev, Vladimir Y
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515.00
85.05%
78.50%
83.47%
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Gangolli, Esha A
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Best Local Similarity:
Query Match:
851 GTG 853
                                                                                            US-10-038-854-39
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LENGTH: 8473
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                                     Sequence 51, Application US/10383201

| Publication No. US20040029226A1
| Sequence 51, Application US/10383201
| Publication No. US20040029226A1
| GENERAL INFORMATION: THERREDIT COLVERED FOR ENCODING SAME, AND METHOD FILE REFERENCE: 21402-568A
| CURRENT APPLICATION NUMBER: US/10/383,201
| CURRENT APPLICATION NUMBER: US/10/383,201
| CURRENT APPLICATION NUMBER: G0/365,984
| PRIOR FILING DATE: 2002-03-20
| PRIOR FILING DATE: 2002-03-20
| PRIOR FILING DATE: 2002-04-12
| PRIOR PILING DATE: 2002-04-12
| PRIOR PILING DATE: 2002-06-65
| PRIOR PILING DATE: 2002-06-65
| PRIOR PILING DATE: 2002-06-13
| PRIOR PILING DATE: 2002-06-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          731 TGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGGAGGAGCTGGC
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Matches:
Conservative:
Mismatches:
Indels:
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SEQ ID NO 51
LENGTH: 1371
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555.50
91.09%
91.09%
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ORGANISM: Homo sapiens
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NAME/KEY: CDS

LOCATION: (2)..(1369)

US-10-383-201-51
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Best Local Similarity:
Query Match:
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2494 GGATGGAGGGAGGCTGTGACGTAGCCATGGAGACTCTTTGCACACGATAGCAAGGAC 2553
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PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 6/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR PELICATION NUMBER: 60/279,863
PRIOR FILING DATE: 2001-03-29
PRIOR PELICATION NUMBER: 60/284,447
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR APPLICATION NUMBER: 60/284,683
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-28
NUMBER FO SEQ ID NOS: 411
SOFTWARE: PARENTIN Ver: 2.1
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84
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
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515.00
85.05%
78.50%
83.47%
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APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Vernet, Corine
APPLICANT: Eisen, Andrew J
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Gusev, Vladimir Y
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Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                               LENGTH: 8645
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                                                                                        TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr
                                                                                                                                                                      CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThr11eAla
                                                  US-10-029-020-14_COPY_750_850 (1-101) x US-10-038-854-39 (1-8473)
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IIILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
              Gaps:
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PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR PILING DATE: 2001-02-20
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Publication No. US20040022781A1
GENERAL INPORMATION:
APPLICANT: Spytek Kimberly A
APPLICANT: Li, Li
APPLICANT: Vernet, Corine
APPLICANT: Vernet, Corine
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Shimkets, Uriel M
APPLICANT: Shimkets, Richard A
APPLICANT: Spaderney, Vellzar
APPLICANT: Spaderney, Vellzar
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Edinger, Shlomit R
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Millet, Isabelle
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Gusev, Vladimir Y
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Gangolli, Esha A
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Rastelli, Luca
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unther, Erik
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Kekuda, Ramesh
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              17
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APPLICANT:
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APPLICANT: Alsobrook II, John et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE PILE REPERENCE: 21402-568A
CURRENT APPLICATION NUMBER: US/10/383,201
CURRENT FILING DATE: 2003-03-06
  2506 GGATGGAGGAGGCTGTGACGTAGCGAGGACTCTTTGCACAGATAGCAAGGAC 2565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638 TGCCGCGACGGCAAGTGCGAGTGCAGCCCTGGCTGGAATGGCGAACACTGCACCATCGCT 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr
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Matches:
Conservative:
Mismatches:
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PRIOR FILING DATE: 2001-12-19
PRIOR PELING DATE: 2001-12-19
PRIOR PELING DATE: 2001-12-19
PRIOR PELING DATE: 2002-03-20
PRIOR PLING DATE: 2002-03-20
PRIOR PELING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 60/312,022
PRIOR PELING DATE: 2002-06-14
PRIOR PELING DATE: 2002-06-14
PRIOR PELING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/410,755
PRIOR PELING DATE: 2002-09-13
PRIOR PELING DATE: 2002-09-13
PRIOR PELING DATE: 2002-09-14
PRIOR PELING DATE: 2002-01-16
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                                                                                                                           2566 AATGAAGGGATGGACTCATT 2586
                                                                              95 AsnAspGlyAspGlyLeuVal 101
                                                                                                                                                                                             US-10-383-201-47; Sequence 47, Application US/10383201; Publication No. US20040029226A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-383-201-47
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NUMBER OF SEQ ID NOS: 411
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                                                                                                                                                                                                                                     APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
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PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-03-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR PRILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR APPLICATION NUMBER: 60/279
PRIOR APPLICATION NUMBER: 60/289,89
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-18
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Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
Gangolli, Esha A
Guo, Xiaojia S
Shenoy, Suresh G
Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
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ORGANISM: Homo sapiens
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LENGTH: 8675
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publication No. USZUG40022226A1

GENERAL INFORMATION:
APPLICANT: Alsobrook II, John et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-56BA
CURRENT APPLICATION NUMBER: US/10/383,201
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: 00/372,022
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
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ORGANISM: Homo sapiens
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US-10-383-201-45
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PRIOR FILING DATE: 2003-03-06

PRIOR PALICATION NUMBER: 60/365, 984

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PRIOR PALLICATION NUMBER: 60/372, 022

PRIOR PALLICATION NUMBER: 60/372, 022

PRIOR PALLICATION NUMBER: 60/372, 022

PRIOR PALLING DATE: 2002-04-12

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PRIOR PALLING DATE: 2002-06-14

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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 61
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ORGANISM: Homo sapiens
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Query Match:
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US-10-383-201-61
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APPLICANT: Alsobrook II, John et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE
FILE REFERENCE: 21402-568A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1282 TGCCGCGACGCCAAGTGCGAGTGCAGCCCTGGCTGGAATGGCGAACACTGCACCATCGCT 1341
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Mismatches:
Indels:
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CURRENT FILING DATE: 2003-03-06

PRIOR APPLICATION NUMBER: 10/029020

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2002-03-20

PRIOR FILING DATE: 2002-03-20

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14

PRIOR PILING DATE: 2002-06-26

PRIOR PLING DATE: 2002-06-26

PRIOR PLING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: 60/410,755

PRIOR FILING DATE: 2002-09-13

PRIOR FILING DATE: 2002-09-13

PRIOR PELING DATE: 2002-09-13

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Job time : 216.425 secs
Sequence 41, Application US/10383201
Publication No. US20040029226A1
GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                               GRERRAL INCRINATION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILLS REFERENCE: 21402-5684

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILLS REPRENCE: 21402-5684

CURRENT APPLICATION NUMBER: 105/02902

PRIOR APPLICATION NUMBER: 107/02902

PRIOR FILLING DATE: 2003-03-06

PRIOR FILLING DATE: 2002-04-12

PRIOR FILLING DATE: 2002-04-13

PRIOR FILLING DATE: 2002-04-13

PRIOR FILLING DATE: 2002-04-13

PRIOR FILLING DATE: 2002-04-13

PRIOR FILLING DATE: 2002-09-13

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Matches:
Conservative:
Mismatches:
Indels:
                                                    Sequence 53, Application US/10383201
Publication No. US20040029226Al
GENERAL INFORMATION:
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; LOCATION: (7)
US-10-383-201-53
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Fatent No. 6672186

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT PLICATION NUMBER: US/09/833,381
CURRENT PLICATION NUMBER: 09/516,448
FRICK FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
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Mismatches:
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US-08-611-729A-5
US-08-400-155-9
US-08-400-155-9
US-08-101-729A-9
US-08-701-725-1
US-08-157-135-3
US-08-157-135-3
US-08-157-135-3
US-08-157-135-3
US-09-230-652-1
US-09-230-652-1
US-09-423-753-8
US-09-423-753-8
US-08-981-392-3
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US-08-635-872A-18
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US-09-919-172-23
US-09-919-172-23
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; OTHER INFORMATION: n = A,T,C (US-09-833-381-1072
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ORGANISM: Homo sapiens
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      Percent Similarity:
Best Local Similarity:
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      -MODEL-frame+ p20...model -DEV=x1h
-Q=(cgn2_1/USPTO_spool/US10029020/runat_06082004_112217_29301/app_query.fasta_1.3519
-Q=(cgn2_1/USPTO_spool/US10029020/runat_06082004_112217_29301/app_query.fasta_1.3519
-DB=Lssued_Patrentes_NA -QEMT=fastap_SUFFIX=p20..rni, -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-USFR=CAL_COAL_OUTFWT=ptc -NORM=ext -HEASIZE=500 -MINLEN=0 -MAXLEN=200000000
-USFR=US10029020_@CGN_1 1.258 @cunat_6082004_112217_29301 -NOFUS=6 -ICPU=3
-NO_MMAP_LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE6 -DELEXT=7
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5, Appli
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                                                                                                                                                                                                         August 14, 2004, 01:16:21 ; Search time 29.8807 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                          OM protein - nucleic search, using frame_plus_p2n model
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US-09-620-312D-75
US-08-793-273C-3
PCT-US95-11684-3
US-09-214-278-6
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US-08-400-159-1
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US-09-199-865-2
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Xgapop 10.0, Xgapext
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Fgapop 6.0, Fgapext
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Maximum DB seq length: 200000000
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                                                                                                                                  1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCys---AlaGluHisGly 19
                                                                                                                                                                                                                 20 ThrCys --- ArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThr 38
                                                                                                                                                                                                                                                                                                  57
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APPLICANT: 18th-Horowicz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Myat, Anna M.
APPLICANT: Rleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace B.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON NUMBER OF SEQUENCES: 20
                                                                                                 US-10-029-020-14_COPY_750_850 (1-101) x US-08-400-159-1 (1-5561)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1462 GGCATATTGTGCGATCAAGATTTA---AATTTCTGCGGC 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 GlyAlaGlyCysAspThrSerMetGluThrAlaCysGly 90
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APPLICATION NUMBER: US/08/611,729A
TILING DATE: 06-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
    Conservative:
                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08611729A Patent No. 6004924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
45.168
37.638
27.478
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: U.S.A.
  Percent Similarity:
Best Local Similarity:
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TOPOLOGY: ur
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STREET: 11
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US-08-611-729A-1
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                                                                                     ----gagggrigcccrgggrigrgcaarggcaacggcaga 115
                                                                                                                          61 CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGlyAlaGly 80
                                               9
      23 TGCCGCGACGGCAAGTGCGAGTGCAGCCCTGGCAATGGCGAACACTGCACCATC---
                                             41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gray, Grace E. TITLE OF INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF THE TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5561
35
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FILING DATE: 07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ish-Horowicz, David
Henrique, Domingos M.P.
Lewis, Julian H.
Myat, Anna M.
Fleming, Robert J.
Artavania-Tsakonas, Spyridon
Mann, Robert S.
Gray, Grace E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7326-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08400159
Patent No. 5869282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5561 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.48e-08
169.50
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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                                                                                           80 -----
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US-08-400-159-1
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Pred. No.:
Score:
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APPLICANT: M
APPLICANT: F
APPLICANT: A
APPLICANT: M
APPLICANT: M
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APPLICANT:
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; NAME/KEY: CDS
; LOCATION: (309)..(5741)
US-08-793-273C-3
                                      .. (13857)
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                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                   ; NAME/KEY: CDS
; LOCATION: (1)
US-09-620-312D-75
                                                                                         Alignment Scores:
Pred. No.:
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US-08-793-273C-3
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        FEATURE:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AsnGlyArgCysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArg 77
                                                                                                                                                                                                                                                                                                                                                                                                    39 IleAlaHisTyrLeuAspArgValValLysGluGlyCysPro---GlyLeuCysAsnGly
                                                                                                                                                                                                                                 US-10-029-020-14_COPY_750_850 (1-101) x US-08-611-729A-1 (1-5561)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1462 GGCATATTGTGCGATCAAGATTTA---AATTTCTGCGGC 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE OF INVENTION: Polypeptides
                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                     Length:
Matches:
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CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR PILING DATE: 2000-04-25
PRIOR PPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
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8-09-620-312D-75
; Sequence 75, Application US/09620312D
; Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: pt_FL_genes Version 1.0 SEQ ID NO 75 LENGTH: 13857
                                                                                                               6.48e-08
169.50
45.16%
37.63%
27.47%
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunqing
                               CDS
442..4653
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ORGANISM: Homo sapiens
                                                                                                                                               Percent Similarity:
Best Local Similarity:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1426 ----
                                                                                                Alignment Scores:
Pred. No.:
                             ; NAME/KEY:
; LOCATION:
US-08-611-729A-1
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APPLICANT:
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JOSEPHONE 3. Application US/08793273C

SEQUENCE 3. Application US/08793273C

Patent No. 648240

GENERAL INFORMATION:

APPLICANT: Crossin, Kathryn L.

APPLICANT: Prieto, Anne L.

TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE ATTACHMENT AND TITLE OF INVENTION: NUMBER: US/08/793,273C

CURRENT APPLICATION NUMBER: DS/08/793,273C

CURRENT FILING DATE: 1995-09-14

PRIOR APPLICATION NUMBER: PCT/US95/11684

PRIOR APPLICATION NUMBER: 08/308,359

PRIOR FILING DATE: 1994-09-16

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH. 6049
                                                                                                                                                                                                                                                     1555 ĠĠĪGAGGACTĠĨĠGGAGCĊĠĪCGCTĠĪCCCGGGGACĪĠĊCGTGGGĊĀĊĠĠĊCTTĪĠĊGAG 1614
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                                                                                                                                                                                                                                                                                                                                                                                               43 LeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArgCysThr 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1663 ------ACGCGCAGCTGCCCGGGGCCTGCCGAGGCCGCGGGC
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                                                                                                                                                                                                                                                                                                                                                   1615 GAIGGCGTGTGTGTGTGACGCAGGCTACTCAGGGGAAGACTGCAGC-----
                                                                                                                                                          US-10-029-020-14_COPY_750_850 (1-101) x US-09-620-312D-75 (1-13857)
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                                            Conservative:
Mismatches:
Indels:
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Conservative:
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160.00
48.86%
37.50%
25.93%
.38e-07
                 169.00
43.75%
36.46%
27.39%
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---GATAAGTGCATCCCACACCCGGGATGCGTCCACGCATCTGTAAT 1239
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                                                                                                                    20 Thrcygarg---AspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThr 38
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                                                                                                                                                                                                                                                                                                                                   61 CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGlyAlaGly 80
                                                                                           1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr 20
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                                                                                                                                                                           21 CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrIleAla
                                                                                                                                                                                                                                                          41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg
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Sequence 6, Application US/09214278

Sequence 7, Application US/09214278

Patent No. 6291210

SEGNERAL INFORMATION:
APPLICANT: Sakano, Seiji

APPLICANT: Itoh, Akira

TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

CURRENT APPLICATION NUMBER: US/09/214,278

CURRENT FILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6
                                                      US-10-029-020-14_COPY_750_850 (1-101) x PCT-US95-11684-3 (1-6049)
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
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LOCATION: (409)..(501)
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Best Local Similarity:
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Query Match:
Query Match:
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ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
AND USING SAME
                                                                                                                                                                                                                                                                    2028 IGT------GTCGAGGGA---CGGTGTCTGTGTGAGGAAGGTTACATGGGGATCGAC 2075
                           ----gaacegreciéceceaargaciecaacaaceregedecee 2027
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                                                                                   40
    TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr 20
                                                                                   21 CysargaspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrlleAla
                                                                                                                                                                  41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 North Torrey Pines Road, TPC 8 CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OFFRAING SYSIEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11684
FILING DATE: 14-SEP-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,359
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOGAN, April C.
REGISTRATION NUMBER: BECO019P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Conservative:
Mismatches:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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37.50%
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309..5740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A NUMBER OF SEQUENCES:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA
USA
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PCT-US95-11684-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CENGTH:
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1078 IGGAIGGGCCCCGAAIGTAAACAGAGCTATTTGCCGAACAAGGCTGCAGTCCTAAGCATGGG 1137
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1138 TCTTGCAAACTCCCAGGTGACTGCCAGTACGGCTGGGAAGGCCTGTACTGT--- 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GAGCCCTGGCAGTGCCTCTGTGAGACCAACTGG 1272
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APPLICANT: Zimrin, Ann B.
APPLICANT: Maciag, Thomas
APPLICANT: Mondael K.K.
APPLICANT: Pepper, Michael K.K.
APPLICANT: Pepper, Michael S.
APPLICANT: Montesano, Roberto
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS
TITLE OF INVENTION: BASED ON JAGGED/NOTCH PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: 0036-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAla---GluHisGly
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       TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1273 GGCGGCCAGCTCTGTGACAAGATCTC---AATTACTGTGGG 1311
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Mismatches:
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Matches:
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CURRENT FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: 60/018,841
EARLIER FILING DATE: 1996-05-31
EARLIER FILING DATE: 1996-05-31
EARLIER FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                         PILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/09/855,722
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/214,278
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09199865 Patent No. 6433138
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46.81%
32.98%
25.12%
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LOCATION: (502)..(4062)
                                                                                                                                                                                                                                                                                                                                                   (409)..(4062)
                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   LOCATION: (409)..(4062
NAME/KEY: sig_peptide
LOCATION: (409)..(501)
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Best Local Similarity:
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                                                                                                                                                                                                   SEQ ID NO 6
LENGTH: 4208
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                                                                                                                                                                                                                                                       TYPE: DNA
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DB:
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                                 GAGCCCTGGCAGTGCCTCTGTGAGACCAACTGG 1272
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57 GlyAsnGlyArgCysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrp
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                                                                                                                                                                                                                                                                                                          APPLICANT: ARCAND. SELUI
APPLICANT: ITOH, AKIRA
TITLE OF INVENTION: DIPERENTIATION-SUPPRESSIVE POLYPEPTIDE
TITLE OF INVENTION: DIPERENTIATION-SUPPRESSIVE POLYPEPTIDE
TITLE REFERENCE: KP-8447
CURRENT APPLICATION NUMBER: US/09/068,740A
CURRENT APPLICATION NUMBER: UP 7-299611
PRIOR FILING DATE: 1995-11-17
PRIOR APPLICATION NUMBER: UP 7-311811
PRIOR APPLICATION NUMBER: PCT/JP96/03356
PRIOR APPLICATION NUMBER: PCT/JP96/03356
PRIOR APPLICATION NUMBER: PCT/JP96/03356
PRIOR APPLICATION NUMBER: PCT/JP96/03356
PRIOR APPLICATION NUMBER: PCT/JP96/03056
PRIOR APPLICATION NUMBER: PCT/JP96/03056
PRIOR APPLICATION NUMBER: DCT/JP96/03056
PRIOR APPLICATION NUMBER: DCT/JP96/03056
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PRIOR APPLICATION NUMBER: DCT/JP96/03056
PRIOR APPLICATION NUMBER: DCT/JP96/03056
PRIOR APPLICATION NUMBER: DCT/JP96/03056
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                                                                                               77 ArgGlyAlaGlyCysAspThrSerMetGluThrAlaCysGly
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-855-722-6
; Sequence 6, Application US/09855722
; Patent No. 6638741
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155.00
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32.98%
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APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local Similarity:
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Length:
Matches:
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1155 Avenue of the Americas
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-400-159-5; Sequence 5, Application US/08400159; Patent No. 5869282
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155.00
46.81%
32.98%
25.12%
              STRANDEDNESS: single
                                                                                                      414..4068
nucleic acid
                                  TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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STATE: New York
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                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                    NAME/KEY:
                                                                                                      LOCATION:
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DB:
                                                                                                                                                                              Pred. No.:
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757 ------GATAAGTGCATCCCACACCCGGATGCGTCCACGGCATCTGTAAT 801
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                                                                                                                                                                                                                                                                                                                                       20 ThrCysArg---AspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThr 38
                                                                                                                                                                                                                                                                 1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAla---GluHisGly
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                                                                                                                                                                                                                                US-10-029-020-14_COPY_750_850 (1-101) x US-09-199-865-2 (1-5458)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Li, Linheng
APPLICANT: Hood, Leroy
APPLICANT: Hood, Leroy
APPLICANT: Spinner, Nancy B.

TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Human Jagged Polypeptide, CockersPowners: 110
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      835 GGCGCCCAGCTCTGTGACAAGATCTC---AATTACTGTGGG 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 ArgGlyAlaGlyCysAspThrSerMetGluThrAlaCysGly 90
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                           Matches:
Conservative:
Mismatches:
                                                                                                                                                                                Indels:
                                                                                                            Length:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08882046
Patent No. 6136952
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SEQUENCE CHARACTERISTICS:
LENGTH: 5590 hard
                                                                                                            07e-06
                                                                                                                         155.00
46.81%
32.98%
25.12%
                      TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                          Alignment Scores:
Pred. No.:
     LENGTH: 5458
                                                       US-09-199-865-2
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APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Lewis, Julian H.
APPLICANT: Fleming, Robert J.
APPLICANT: Atleavanis-Tsakonas, Spyridon
APPLICANT: Atleavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Mann, Robert S.
APPLICANT: Mann, Robert S.
APPLICANT: Grav, Grace E.
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                    US-10-029-020-14_COPY_750_850 (1-101) x US-08-882-046-1 (1-5590)
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CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/400,159
FILING DATE: 07-WAR-1995
CLASSIFCATION: 435
ATTORY AGENT INFORMATION:
NAMB: Misrock, S. Leslie
Conservative:
Mismatches:
Indels:
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IBM PC compatible YSTEM: PC-DOS/MS-DOS
                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-08-400-159-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
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1100 TCTTGCAAACTCCCAGTGACTGCCAGTACGGCTGGCAAGGCCTGTACTGT--- 1156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 ThrCysArg---AspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThr 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-029-020-14_COPY_750_850 (1-101) x US-08-400-159-5 (1-6464)
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Pennie & Edmonds
1155 Avenue of the Americas
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08611729A Patent No. 6004924
                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6464 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECTHE
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155.00
46.81%
32.98%
25.12%
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Gray, Grace E.
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MEDIUM TYPE: Floppy disk
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371..4027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : New York
'RY: U.S.A.
10036-2711
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Query Match:
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; LOCATION:
US-08-400-159-5
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APPLICANT:
APPLICANT:
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----GATAAGTGCATCCCACACCCGGGATGCGTCCACGGCATCTGTAAT 1201

    ---GAGCCCTGGCAGTGCCTCTGTGAGACCAACTGG 1234

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APPLICANT: Gray, Grace E.
TITLE OF INVENTION: UNCLEOTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-029-020-14_COPY_750_850 (1-101) x US-08-611-729A-5 (1-6464)
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/611,729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5869200.

GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Lewis, Julian H.
APPLICANT: Anna M.
                                                                                                                    ACTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-0
TELEPAN: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPEN: 66-141 PENNIE
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERICTICS:
LENGTH: 64-64 base pairs
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
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Patent No. 5869282
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155.00
46.81%
32.98%
25.12%
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; LOCATION: 371..4024
US-08-611-729A-5
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[ndels:
                                                                                                                                                 APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                             APPLICANT: ISh-Horowicz, David
APPLICANT: Henrique, Doningos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
                                          ; Sequence 9, Application US/08611729A; Patent No. 6004924; GENERAL INFORMATION:
APPLICANT: ISh-Horowicz, David;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET NUMBER: 7326-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9030
TELEPHONE: (212) 869-9741/8864
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3582 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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41.80%
27.05%
25.04%
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CORRESPONDENCE ADDRESS:
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Best Local Similarity:
Query Match:
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CLASSIFICATION:
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STRANDEDNESS:
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                          US-08-611-729A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 CysAsnGlyAsnGlyArgCysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeu 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 GlyThrCysArgAsp-----GlyLysCysGluCysSerProGlyTrpAsnGly 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AspIhrSerMetGluThrAlaCysGlyAspSerLysAspAsn 95
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                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                        CURRENT AFFLICATION NUMBER: US/08/400,159
PILING DATE: 07-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET NUMBER: 7326-029
TELECHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 GlyTrpArgGlyAlaGlyCys-----
                                                                                                ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3582 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.35e-06
154.50
41.80%
27.05%
25.04%
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nucleic acid
3DNESS: double
CORRESPONDENCE ADDRESS:
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1366 GATCACTGT----
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                                                                   New York
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Query Match:
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                                                                   STATE: NA
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TITLE OF INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF THE TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
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APPLICATION NUMBER: US/08/611,729A FILING DATE: 06-MAR-1996
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Matches:
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1366 GATCACTGTGAGAAAGACATCAATGAATGTGCAAGTAACCCT 1407	55 CysAsnGlyAsnGlyArgCysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeu 74	1408 16CATGAATGGGGGTCACTGCCAGGATGAAATCGATGGATTCCAATGTCTGTGTCCTGCT 1467	75 GlyTrpArgGlyAlaGlyCys81	::-      1468 GGTTTCTCAGGAAACCTCTGTCAGCTGGATATAGACTACTGTGAGCCAAACCCTTGCCAG 1527	82AspThrSerMetGluThrAlacysGlyAspSerlysAspAsn 95		96 AspGly 97	1588 GAAGGC 1593
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Search completed: August 14, 2004, 19:40:00 Job time: 44.8807 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

August 14, 2004, 01:13:26; Search time 1184.51 Seconds (without alignments) 2546.273 Million cell updates/sec 1 WMGAACDQRACHPRCAEHGT......DTSMETACGDSKDNDGDGLV 101 US-10-029-020-14\_COPY\_750\_850 617 Title: Perfect score Sequence: Run on:

0.5 7.0 7.0 BLOSUM62 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext Scoring table:

27513289 segs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/CQm201/USB1029020/TURDED202014 112216 29287/app query.fasta\_1.3519
-Q=/CQm2\_1/USBTO spool\_1/USB1029020/runat\_06082004\_112216\_29287/app query.fasta\_1.3519
-DB=EST -QFWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
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-USER=US10029020 @CGN 1 1.1313 @runat\_06082004 112216\_29287 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7

EST:\* Database :

gb\_htc:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

bb633431 RIKEN full-length enriched, adult male spinal cord Mus musculus cDNA clone A330048C04 5', mRNA sequence. BB633431.1 GI:16469876 VERSION KEYWORDS SOURCE ORGANISM DEFINITION RESULT 1 BB633431 LOCUS ACCESSION

Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 610) REFERENCE

AUTHORS

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Email: genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
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Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Kono,H., Kouda,M., Koya,S., Mateuyama,T., Miyazaki,A., Nomura,K.
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Tanaka,T., Muramatsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                      RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
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/db_xref="taxon:10090"
/clone="A330048C04"
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FEATURES

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AK039472 1284 bp mRNA linear HTC 19-SEP-2003 Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330048C04 product:neuregulin 1, full
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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MEDLINE PUBMED

TITLE JOURNAL AUTHORS

AUTHORS REFERENCE

JOURNAL

TITLE

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL, send email to:

Seq primer: -40UP_from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE671538 464 bp mRNA linear EST 08-SEP-2000 7e53£01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3286201 3' similar to TR:070465 070465 DOC4. ;, mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                  41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg
                                                                 227 TGCCGGGACGGCAAGTGCGAATGCAGCCCCGGCTGGAATGGAGAGCACTGCACCATC
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="spinal cord"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                      The FANTOM Consortium and the RIKEN Genome Exploration Research decoup Phases I & 11 Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
                                                                            RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="neuregulin 1 (MGD|MGI:96083, MGD|MGI:1345182,
GB|NM_011858, evidence: BLASTN, 99%, match=186)"
                                                                                                                          Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site for further details. URL.http://genome.gsc.riken.go.jp/.URL.http://fantom.gsc.riken.go.jp/.location/Qualifiers
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clone="A330048C04"
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                                                                                                                                                        Nature 409, 685-690 (2001)
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Conservative: Length: Matches:

5.67e-37 537.50 89.80%

Percent Similarity:

1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr 20

Pred. No.:

Alignment Scores:

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/ Organism=This marks mascatus.
/ Organism=This marks mascatus.
/ Observation=1000"
/ Clone="UT-W-BH1-akr-d-12-0-UI"
/ dev stage="27-32 days"
/ lab host="MH18 Map M s2"
/ lab host="WH18 Map M s2"
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/ clone lib="NH18 Map M s2"
/ clone lib="NH18 Map M s2"
/ library is a subtracted library derived from NH18 Map M s2 library is a subtracted library derived from a mixture of normalized library derived from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NH18 Map M s1 library and a pool of 5,000 clones obtained from non-normalized and normalized mouse brain
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number of
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Fax: 301 443 1980
Email: mEST@mail.nih.gov
Email: mEST@mail.nih.gov
Email: mEST@mail.nih.gov
Email: mEST@mail.nih.gov
Researchers may obtain EMAP CDNA clones from RESEARCH GENETICS.
should be noted that Bento Soares is generating a small number o additional specialized non-redundant arrays of BNAP CDNAs whose availability will be considered under appropriate and limited collaborative arrangements
Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                BE646762
UI-M-BH1-akr-d-12-0-UI.rl NIH BMAP_M_S2 Mus musculus CDNA clone
UI-M-BH1-akr-d-12-0-UI 5', mRNA sequence.
          CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrIleAla
                                                                                                                 CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGlyAlaGly
                                                                                                41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB793108 435 bp mRNA linear EST 16-MAY-2003 AMGNNUC:NRHYS-00339-E12-A W Rat hypothalamus (10471) Rattus norvegicus cDNA clone nrhy5-00339-e12 5', mRNA sequence.
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/db xref="taxon:10116"
/clone="nrby5-00339-e12"
/clone=lib="W Rat hypothalamus (10471)"
/clone=lib="W Rat hypothalamus (10471)"
/clone=lib="W Rat hypothalamus AppRRI; Site 2: Not1; W Rat hypothalamus adult female Wistar rat avg. insert size 2:3 kb fraction 6 and 7"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                       TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr
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Plate: 00339 row: e column: 12.
Location/Qualifiers
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464
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
                                                                               US-10-029-020-14_COPY_750_850 (1-101)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 718)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BU341069 718 bp mRNA linear EST 28-NOV-2002 603406859F1 CSEQCHN67 Gallus gallus cDNA clone ChEST315e16 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                         141 AGGCAAACGGCAGCACCGAAACAGATGGCTGCCCTGATTTGTGCAACGGTAACGGGAGA 200
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Mismatches:
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/dev stage="16 day embryo"
/lab_host="DH10B"
/clone_lib="CSEQCHN67"
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University of Manchester Institute of
                    Length:
Matches:
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/organism="Gallus gallus"
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Gallus gallus (chicken)
Gallus gallus
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Tel: 01612008930
Fax: 01612360409
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/note="Organ: brain; Vector: pBluescript II KS(+); Site_1: BCORI; Site_2: Not1; This normalized library was constructed_from 1 million independent clones. CDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand reaction, double-stranded cDNA was blunted, ligated to Not1 adapters, digested with ECORI, size-selected, and cloned into the Not1 and ECORI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
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E (Pariniformes: Cyprinidae; Danio.

S NIH-MGC http://mgc.nci.nih.gov/.

I (Dases 1 to 847)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Rml0A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Len Zon, Harvard
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Schistosoma mansoni
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                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
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                                                                                                                                                                    /organism="Danio rerio"
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/db_type="mRNA"
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/note="Vector: pExpress."
/note="Vector: pExpress."
/note="Vector: person of this library is also available (NHH ZGC 7). Library was constructed by Open Blosystems (Huntsville, AL)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CysaspThrSerMetGluThrAlaCysGlyAspSerLysAspAsnAspGlyAspGlyLeu 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGlyAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov. l column: 17
Plate: LLANI4806 row: l column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg
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64
8
20
9
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Conservative:
Mismatches:
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                                                                                                                        High quality sequence stop: 585.
Location/Qualifiers
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AL710634.1 GI:19693989
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410.50
71.29%
63.37%
66.53%
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Best Local Similarity:
Query Match:
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ATG 484
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Pred. No.:
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VERSION
KEYWORDS
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LOCUS
                                                                                                                                            FEATURES
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Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosoma.

1 (bases 1 to 492)

1 (bases 1 to 492)

2 (bases 1 to 492)

3 (bases 1 to 492)

4 (construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the 
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                                                                                                                                                                                                                                                                                                                                                                                             Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
1 (bases 1 to 314)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.
EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No all sequence available.

This clone (DKFZp686G1170) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr
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Mismatches:
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/dev stage="adult"
/lab_host="DH10B"
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Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosoma.

1 (bases 1 to 501)
Strigeidida; S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M., Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A., Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A., Sak, Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T., Rodriques, V., Madeira, A.M.B.M., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
Transcriptome analysis of the acoelomate human parasite Schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Bmail: verjo@iq.usp.br.
This sequence was derived from the FAPESP Schistcosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schistc/
Plate: MS1-0131U-A342 row: 4 column: A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrlleAla 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-029-020-14_COPY_750_850 (1-101) x CD202234 (1-501)
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Schistosoma mansoni"
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/sex="mixed pool"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="schistosomulum"
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/clone lib="MS1-0131"
/note="Vector: pGBM T-easy"
              MS1-0131U-A342-A04.B, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
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                                                           CD202234.1 GI:34731943
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Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A., Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A., Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T., Sedriques, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
Transcriptome analysis of the accelomate human parasite Schistosoma
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                                                                                                                                                                                                                                                                                                                                                                                           Email: verjo@ig.usp.br

This sequence was derived from the FAPESP Schistosoma mansoni EST decome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: Mil.0081F-M291 row: 11 column: B. Location/Qualifiers
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                                                                                                                                                                                                                                Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo -
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/organism="Schistosoma mansoni"
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/db_xref="taxon:6183"
/clone="ML1-0081T-M291-B11.G"
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 633)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tarakeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. Unpublished (2001)
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Email: genome-results.

URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

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and Hayashizaki,Y.
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
79 AlaGlyCysAspThrSerMetGluThrAlaCysGlyAspSerLysAspAsnAspGlyAsp
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/tissue_type="eyeball"
/dev_stage="0 day neonate"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 683)
S. Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Metsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Saito,F., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB665259 RIKEN full-length enriched, 0 day neonate eyeball Mus musculus CDNA clone El30115C05 5', mRNA sequence.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 TGGATGGGGGCGGATGCGACCAACGGGCCTGCCACCCACGCTGTGCAGAACACGGGACC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 TGCCGGGACGGCAAGTGCGAATGCAGCCCCGGCTGGAATGGAGAGCACTGCACCATCGGT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 ATG-----GCAGGCGCACGTCCTGGGCCATTTGGGTTGCTCTCAAGACATTTCCAG 353
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/clone lib="RIKEN full-length enriched, 0 day neonate eyeball"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGly 78
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Indels:
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69.23%
61.54%
40.92%
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--TGGATTGGC 382

78

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AK053790 1376 bp mRNA linear HTC 20-SEP-2003 Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130308/18 product:neuregulin 1, full insert
236 TGCCGGGACGCCAAGTGCGAATGCAGCCCCGGCTGGAATGGAGGAGCACTGCACCATCGGT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                         41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg
                                                                            61 CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGly
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                                                            347 GGCAGCCTGGTTCTC----CTCCATTGCATG
                                                                                                                                                                                                                                                                                                                                                                                                     HTC; CAP trapper.
Mus musculus (house mouse)
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AK053790.1 GI:26095991
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                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Arzawa, K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shinagawa,A., Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001
Flease visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-reseges.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Ltch,M., Komno,H., Okazahi,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
penes. Genome Res. .10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Antanini,M., Noreda,Y., Ishikawa,T., Muramatsu,M., Inoue,Y., Kira,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="RIKEN full-length enriched, 0 day neonate eyeball"
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/dev stage="0 day neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="E130115C05"
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                                                                                                                                                                                                                                                           and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e mouse tissues.
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                             Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, Y., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yonake, S., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Chazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FANTOM Consortium.
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1 TrpWetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr 20

US-10-029-020-14\_COPY\_750\_850 (1-101) x BB665259 (1-683)

ð g

683 48 6 15 9

Conservative: Mismatches: Indels:

Matches: Length:

4.62e-12

Pred. No.:

Score:

252.50 69.23% 61.54% 40.92%

> Best Local Similarity: Percent Similarity:

Query Match:

21 CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThr11eAla 40

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A1415475
Homo sapiens HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6246)

1 (lases 1 to 6246)

1 clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 TGCCGGGACGGCAAGTGCGAATGCAGCCCCGGCTGGAATGGAGAGCACTGCACCATC 342
clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submitsion
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Direct Submission
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Indels:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/locus_tag="HCM4903"
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                             Direct Submission

1. Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN). Laboratory for Genome Physical and Chemical Research (RIKEN) (RIEN) Genomic Sciences Center (GSC), RIKEN Vokohama Institute; 1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Uapan (E-mail:genome-res@gesc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9227, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="eyeball"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr 20
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Mus musculus HCM4903 gene, VIRTUAL TRANSCRIPT, partial sequence,
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/63"
             Muramatsu, M. and Hayashizaki, Y.
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gene <1	_	OKIGIN	Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

US-10-029-020-14\_COPY\_750\_850 (1-101) x AY413475 (1-6246)

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Search completed: August 14, 2004, 18:02:56 Job time: 1193.51 secs

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Aas14089

Adb32028 Human FCT
Ad16066 Human PCO
Acc72051 BCU0205A
Acc72052 BCU0205B
Ab129074 Drosophil
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Ab277285 Nucleotid
Ab277285 Nucleotid
Adb37427 Human can

Scoring table:

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Human, NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; May be a signal processing; metabolic pathway modulation; metabolic disorder; May cell signal processing; metabolic pathway modulation; metabolic disorder; May beenty; diabetes; infectious disease; neurodegenerative disorder; acne; Maltheimer's disease; Parkinson's disease; immune disorder; cancer; May memory defect; infertility; congenital heart defect; hair growth; May pigmentation disorder; endocrine disorder; respiratory disease; health; May gastro-intestinal disease; reproductive; neurological disease; May bone marrow transplantation; endocrine disease; allergy; inflammation; May meluropsychiatric disorder; EGF-related protein; SCUBEI; TEN-M4; Mairopsychiatric disorder; EGF-related protein; SCUBEI; TEN-M4; May eadipocyte complement-related of quimour necrosis factor; out at first; May beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; May type la membrane sushi-containing domain; butyrophilin; Mairopsychiatric disorder; domain, butyrophilin; Mairopsychiatric disorder; domain, containing; SNP; gene; ds;
                                               AAS14089
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Abs78652 Human CDN
Abn85378 Human NOV
Abq82345 Human NOV
Abq82344 Human NOV
Abq82346 Human NOV
Abq82346 Human NOV
Abq8230 Prostate
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                                                                                                                                                                                Description
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                              OM protein - nucleic search, using frame_plus_p2n model
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Database :

Score

H 2 K 4 S 9 C 8

Result No.

Aav03674 Human Jag Aav63753 Human JAG Acd06196 Human cDN Abz34802 Coding se

Gene JAG1

Abk35564

Novel hum Human cDN Prolifera Human ser Human cDN

Abs51834 DACA04023 Abx63790 Aat70175 Aav15201 Acd06197

Breast ca

Acf79935

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100

2522 TGTGACACTTCCATGGAGACTGCCTGCGGTGACAGAGACAATGATGGAGATGGCCTG 2581

81 CysAspThrSerMetGluThrAlaCysGlyAspSerLysAspAsnAspGlyAspGlyLeu

2461

41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg

61 CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGlyAlaGly 2462 TGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGGAGCTGGC

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CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrIleAla 40

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useful for treating interacts to new NOVA polypeptines. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, or signal processing and metabolic pathway modulation in a subject, or signal processing and metabolic pathway modulation in a subject, or signal processing and metabolic pathway infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), immune clasorders, haematopoical for treating or preventing cirrhosis, the invention are also useful for treating or preventing cirrhosis, pancreatitis, learning and memory defects, infertility, congenital heart of defects, acne, hair growth, pigmentation disorders, endocrine diseases, respiratory disease, bone marrow transplantation, endocrine diseases, allergy and infilammaticion, nephrological disorders includes infilammaticion, nephrological disorders and age-related disorders. The present nucleic acid sequence represents a NOVX gene. This sequence corresponds a NOVX protein of the invention
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Liu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to new NOVX polypeptides. The invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease or
                                                        "Single nucleotide polymorphism (SNP)"
                                                                                                                  /standard_name= "Single nucleotide polymorphism (SNP)"
name= "Single nucleotide polymorphism (SNP)
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Shimkets RA, Burgess CE, Zerhusen BD,
Boldog FL, Smithson G, Li L, Ji W;
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                                                          /standard name=
                                                                                                                                                                                                                                                                  19-DEC-2000; 2000US-0255704P.
20-DEC-2000; 2000US-0257314P.
29-MAY-2001; 2001US-0298153P.
24-UJL-2001; 2001US-0307506P.
10-AUG-2001; 2001US-031159PP.
29-AUG-2001; 2001US-031159PP.
                      replace(225,C)
/*tag= b
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Casman SJ, Bol
    /standard
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                        variation
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Human cDNA encoding CGDD10, INCYTE 7488573CB1

16-DEC-2002 (first entry)

ABS78652;

ABS78652 standard; cDNA; 8645

RESULT 2 ABS78652

2582 GTG 2584

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Human; ss; gene; cell growth, differentiation; death, CGDD; cancer; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis; polycythaemia vera; primary thromobocytopaenia, developmental disorder; renal tubular acidosis; anaemia, mental retardation; epilepsy; ALDS; neurological disorder; Alzheimer disease; Parkinson's disease; asthma; reproductive disorder; infertility; autoimmune disorder; gout; allergy; inflammatory disorder; acquired immunodeficiency syndrome; uveitis; autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection; multiple sclerosis; osteoarthritis; irritable bowel syndrome; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baughn MR;
Burford N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human proteins associated with cell growth, differentiation and death, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atherosclerosis or hepatitis.
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TY, Lal PG, Duggan BM,
Khare R, Walia NK;
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Richardson TW, Tran UK,
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23-FEB-2001; 2001US-0271175P.
08-MAR-2001; 2001US-0274503P.
09-MAR-2001; 2001US-0274552P.
                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-2002; 2002WO-US003715.
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Ding L,
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Claim 5; Page 175-178; 181pp; English.

2282 TGGATGGGGCAGCTGCGACCAGCGGGCCTGCCACCCGGGCTGTGGGGACC 2341

TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr

US-10-029-020-14\_COPY\_750\_850 (1-101) x ABS52100 (1-8354)

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Length:
Matches:
Conservative:
Mismatches:
Indels:

1.57e-40 617.00 100.00% 100.00%

Alignment Scores:

Percent Similarity: Best Local Similarity:

Query Match:

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The polyphore of the microarray. The polypeptides, polymucleotides, agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of GODD, particularly cell proliferative (e.g. arteriosolescion de GODD, particularly cell proliferative (e.g. arteriosolescions), atherosolerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thromobocytopaenia or cancer), developmental circularly elsorders (e.g. Alzheimer disease, Parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune (inflammatory disorders (e.g. AlDS, (acquired immunodeficiency syndrome) allergies, asthma, autoimmune thy productive disorders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune (inflammatory disorders (e.g. AlDS, (acquired immunodeficiency syndrome) allergies, asthma, autoimmune thy productive disorders (e.g. infertility or a disruption in the contact dermatities, crohn's disease, disbetes mellitus, costeoporosis, pancreatitis, rheumatoid arthritis, osteoporosis, pancreatitis, rheumatoid arthritis, curbits, or viral, bacterial, thingal, parasitic, protozoal or helminthic infections. They are also useful in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid and mino acid acid and acid accidents.
                             (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to CGDD, a biologically active fragment or an immunogenic fragment. Also included are the polynucleotides encoding CGDD1-12, a recombinant polynucleotide comprising a promoter sequence operably linked to the CGDD polynucleotides, a cell transformed with the recombinant polynucleotide, a transformed with the recombinant polynucleotide, a transgenic organism comprising the recombinant polynucleotide, an anti-CGDD antibody, screening for compounds which bind to/modulate or are anti-agonists of CGDD or alter the expression of CGDD polynucleotide and a
        invention relates to an isolated polypeptide comprising CGDD1-12
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Sequence 8645 BP; 2060 A; 2494 C; 2319 G; 1771 T; 0 U; 1 Other;

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                                                                                                                                                                                          CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrIleAla
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                           Matches:
Conservative:
Mismatches:
               Length:
                                                                     Indels:
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100.00%
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US-10-029-020-14\_COPY\_750\_850 (1-101) x ABN85378 (1-8438)

Conservative: Mismatches: Matches:

1.97e-37 579.00 94.29% 93.33%

Best Local Similarity:

ABN85378 standard; DNA; 8438 BP

ABN85378 RESULT

(first entry)

21-OCT-2002

ABN85378;

HXXXH

Query Match:

Percent Similarity:

Alignment Scores:

Length:

Indels: Gaps:

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preventing or
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                                                           Immunosuppressive;
                                                                   Antiallergic, Haemostatic; Anti-HIV; Antidiabetic; Anorectic; Antiallergic, Haemostatic; Anti-HIV; Antidiabetic; Anorectic; Antibacterial; Nephrotropic; Hepatotropic; Nelaxant; Anticonvulsant; Gene Therapy; NOV; cancer; heart disease; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; asthma; IgA nephropathy; cirhosis; arthritis; AIDS; disease; infection; stroke; muscular dystrophy; epilepsy; wasting disorder; TEN-M4 like protein; chromosome 11; gene; ds.
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tissue typing or
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                                                Human; NOV1; cytostatic; Cardiant; Antiinflammatory;
                 Human NOV1, TEN-M4 like protein, coding sequence.
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                                                                                                                                                                                                                                                                                                                                                      /product= "NOV1 protein"
                                                                                                                                                                                                                                                                            Cocation/Qualifiers
4. 8395
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JAN-2001; 2001US-0260417P.
10-JAN-2001; 2001US-0260831P.
28-FEB-2001; 2001US-027338P.
09-MAR-2001; 2001US-0274876P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JAN-2002; 2002WO-US000554.
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                                                              CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrIle---
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ABQ82345 standard; cDNA; 8473 BP. RESULT

ABQ82345;

(first entry) 17-DEC-2002

Human NOV15c encoding cDNA SEQ ID NO:39.

Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; notropic; antidiabetic; antinflammatory; fungicide; antirhemmatic; antiarthritic; immunosuppressive; antiallergic; virucide; antianemnic; antibacterial; protozoacide; antihelminchic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemia; lymphoma; melanoma; neurological disorder; epilepsy; pick's disease; vesicular transport disease; Alzheimer's disease; altergy; pick's disease; vesicular transport disease; cystic fibrosis; goitre; ulcerative collitis; gastric disorder; dudodenal disorder; vaccine; ulcerative collitis; gene; craction; autoimmune disease; allergic reaction; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.

Homo sapiens

Location/Qualifiers 258. .8144 /\*tag= a /product= "NOV15c" /\*tag=

WO200262999-A2

15-AUG-2002

2000US-0258928P. 2001US-0259415P. 2001US-0259745P. 2001US-0259745P. 2001US-0279863P. 2001US-0279833P. 2001US-0279833P. 2001US-0279839P. 2001US-0283889P. 2001US-028989P. 2001US-029408P. 31-DEC-2001; 2001WO-US049976 02-JAN-2001; 2 04-JAN-2001; 2 20-FEB-2001; 2 09-MAR-2001; 29-MAR-2001; 13-APR-2001; 29-MAR-2001; ABQ82345

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29-MAY-2001; 16-AUG-2001; 17-AUG-2001;

18-APR-2001;

17-SEP-2001; 2001US-0322699P. 26-NOV-2001; 2001US-0333350P.

(CURA-) CURAGEN CORP

Li L, Wolenc AR, Vernet CAM, Libell ..., Gorman L;
, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;
Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K; Spytek KA, LLI L, Shinkets RA, Tchernev Malyankar U, Shinkets RA, Tchernev Kekuda R, Patturajan M, Gusev V, Rastelli L, Casman SJ, Boldog F, Camithson G, Millet I, Malyan... Kekuda R, Pact Pastelli L, Casman c., Smithson G,

WPI; 2002-732706/79. P-PSDB; ABP53588.

New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autolmmune of vesicul diseases.

Claim 8; Page 119-121; 444pp; English.

The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, corporated, anticonvulsant, cerebroprotective, nootropic, cardiovascular, antidiabetic, antiinflammatory, antitheumatic, antibacterial, fungicide, immunosuppressive, antianlergic, antitheumatic, antianthritic, virucide, immunosuppressive, antianlergic, and can be used in gene protozoacide and antihelminthic activities, and can be used in gene throughous proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a numma disease selected from NOVX-associated disorder. Such as cancers (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. cystic fibrosis, cysthemic cerebrovascular disease, Alzheimer's disease or Pick's disease), disorders of vesticular transport (e.g. cystic fibrosis, disorders (e.g. ulcerative colitis, or gastrointestinal disorders), autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be used in chromosome mapping, identifying individuals from minute cubelly and in forensic identification of a biological sample. The present sequence encodes human NOVISC, which is

C; 2145 G; 2006 T; 0 U; 4 Other; Sequence 8473 BP; 2301 A; 2017

8473 84 7 10 6 Conservative: Mismatches: Indels: Length: Matches: 3.22e-32 515.00 85.05% 78.50% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: .. 9

US-10-029-020-14\_COPY\_750\_850 (1-101) x ABQ82345 (1-8473)

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2322 GGAIGGAGAGGAGCAGGTGACGIAGCCAIGGAGACICTIIGCACAGAIAGCAAGGAC 2381
                                                                                                                                                                                                                                                                                        Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antinflammatory; fungicide; antirhematic; antiathritic; immunosuppressive; antialergic; virucide; antianaemic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy; pick's disease; vesicular transport disease; cystic fibrosis; goitre; diabetes mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X, J. Shimkets RA, Tchernev VT, Spaderna SK, Gorman L; Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S; Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K; Smithson G, Millet I, Macdougall JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune
GlyTrpArgGlyAlaGlyCysAspThrSerMetGluThrAlaCysGlyAspSerLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis; gene; chromosome 4; ss
                                                                                                                                                                                                                                                           Human NOV15b encoding cDNA SEQ ID NO:37.
                                                                                      Spytek KA, 11 1, ... Thermev Malyankar U, Shimkets RA, Tchermev Kekuda R, Patturajan M, Gusev V, Rastelli L, Casman SJ, Boldog F, ... Casman SJ, Millet I,
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151. .8316
                                                                 AsnAspGlyAspGlyLeuVal 101
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                                                                                                                                                            ABQ82344 standard; cDNA; 8645 BP.
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; 2001US-0279832P;
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16-AUG-2001; 2001US-0312915P.
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2001US-0259785P.
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26-NOV-2001; 2001US-0333350P
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29-MAR-2001;
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18-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                            ABQ82344;
                                                                                                                              RESULT 5
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The present live describes movel numban proteins designated Nova, where X is 1 to 20 e.g. NOVI. NoVX sequences can have neuroprotective, where X is 1 to 20 e.g. NOVI. NoVX sequences can have neuroprotective, cytostatic, antinicalmanatory, antinhematic, antinherbritic, virucide, immunosuppressive, antinicalmanaemic, antinhedretic, included, immunosuppressive, antinicalmanemic, antinhedretic, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, included, in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biological sample. The present sequence encodes human NOV15b, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CysAsnGlyAsnGlyArgCysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeu
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                                                                                                 The present invention describes novel human proteins designated NOVX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 ÇysArgAspGlyLyysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrlleAla
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Human NOV15a encoding cDNA SEQ ID NO:35.

29-MAY-2001; 16-AUG-2001; 17-AUG-2001; 17-SEP-2001; 26-NOV-2001; 

Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidabetic; antinflammatory; fungicide; antirhematic; antiallergic; fungicide; antiantamentory; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; prock; disease; lachemic cerebrovascular disease; Alzheimer's disease; plepsy; pick's disease; vesicular transport disease; cystic fibrosis; goitre; disortees mellitus; grave's disease; gastrointestinal disorder; vaccine; ulcerative collitis; gastric disorder; duodenal disorder; infection; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss.

sapiens. Ното

/\*tag= a /product= "NOV15a" /transl\_except= {pos:1249. .1251,aa:Ser} Location/Qualifiers .8328

WO200262999-A2

15-AUG-2002

31-DEC-2001; 2001WO-US049976

2001US-0279863P. 2001US-0279832P. 2001US-0279833P. 2001US-0283889P. 2001US-0284447P. 2001US-0286683P. 2001US-0259415P. 2001US-0259785P. 2001US-0269814P. 2001US-02940B0P. 2001US-0312915P. 2000US-0258928P 29-MAR-2001; 29-MAR-2001; 02-JAN-2001; 04-JAN-2001; 20-FEB-2001; 09-MAR-2001; 13-APR-2001; 18-APR-2001; 25-APR-2001; 29-DEC-2000;

(CURA-) CURAGEN CORP.

2001US-0313325P.

2001US-0322699P 2001US-0333350P Spytek KA, Li L, Wolenc AR, Vernet CAM, Eisen A, Liu X; Malyankar U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L; Kekuda R, Paturrajan M, Gusev V, Gangolli EA, Guo X, Shenoy S; Rastelli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K; Gunther E, Smithson G, Millet I, Macdougall JR;

WPI; 2002-732706/79. P-PSDB; ABP53586.

New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune di seases.

Claim 8; Page 110-112; 444pp; English.

The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOVI. NOVX sequences can have neuroprotective, cytostatic, antionvalsant, cerebroprotective, nootropic, cardiovascular, antidiabetic, antianflammatory, antitheumatic, antianthritic, virucide, immunosuppressive, antiallergic, antianaemic, antibacterial, fungicide, protozoacide and antihelminthic activities, and can be used in gene therapy. The NoVX proteins, nucleotides or antibodies can be used in the manufacture of a medicament for treating a syndrome associated with a human disease selected from NOVX-associated disorder, such as cancers (e.g. reutaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or Pick's

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disbease), disorders of vesicular transport (e.g. cystic fibrosis, diabetes mellitus, Grave's disease, or gottre), gastrointestinal disorders (e.g. ulcerative colitis, or gastric and duodenal disorders), autoimmune diseases (e.g. allergic reactions, autoimmune haemolytic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic and protozoal infections. The NOYX proteins can be used as immunogens to produce antibodies and as vaccines. The NOYX nucleotide sequences may be used in chromosome mapping, identifying individuals from minute biological samples (tissue typing), and in forensic identification of a biological sample. The present sequence encodes human NOVISa, which is
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Human; NOVX; cytostatic; neuroprotective; anticonvulsant; cardiovascular; cerebroprotective; nootropic; antidiabetic; antinflammatory; fungicide; antirheumatic; antiarthritic; immunosuppressive; antialergic; virucide; antitianemic; antibacterial; protozoacide; antihelminthic; gene therapy; cancer; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; stroke; ischaemic cerebrovascular disease; Alzheimer's disease; allergy; bick's disease; vesicular transport disease; cystic fibroats; golire; diabetess mellitus; Grave's disease; gastrointestinal disorder; vaccine; ulcerative colitis; gastric disorder; duodenal disorder; vaccine; autoimmune disease; allergic reaction; autoimmune haemolytic anaemia; rheumatoid arthritis; gene; chromosome 4; ss. Human NOV15d encoding cDNA SEQ ID NO:41. 

BP.

ABQ82346 standard; cDNA; 8487

ABQ82346 RESULT

(first entry)

17-DEC-2002

ABQ82346;

Homo sapiens

Key

Location/Qualifiers

Mon Aug 16 09:01:16 2004

Conservative:

Percent Similarity:

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3.03e-29
Alignment Scores:
         Pred. No.:
Score:
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Spytek KA, Li L, Wolenc AR, Vernet CAM, Bisen A, Liu X;
Malyankar U, Shimkets RA, Tchernev VT, Spaderna SK, Gorman L;
Kekuda R, Patturajan M, Gusev V, Gangolli EA, Guo X, Shenoy S;
Rastealli L, Casman SJ, Boldog F, Burgess CE, Edinger S, Ellerman K;
Gunther E, Smithson G, Millet I, Macdougall JR;
        /*tag= a
/product= "NOV15d"
                                                                                                                                      2001US-0284447P.
2001US-0286683P.
2001US-0294080P.
2001US-0312915P.
2001US-031325P.
2001US-0333350P.
                                                                                  2001US-0259415P.
2001US-0259785P.
2001US-0269814P.
2001US-0279863P.
                                                                                                                2001US-0279832P.
2001US-0279833P.
2001US-0283889P.
                                                           31-DEC-2001; 2001WO-US049976
  299. .8140
                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                              WPI; 2002-732706/79.
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                               WO200262999-A2
                                                                                                       09-MAR-2001;
29-MAR-2001;
29-MAR-2001;
13-APR-2001;
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20-FEB-2001;
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29-MAY-2001;
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17-SEP-2001;
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                                                                                   02-JAN-2001;
                                                                                                                                                            16-AUG-2001;
                                             L5-AUG-2002
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associated disorders, such as cancers, neurological disorders, disorders of vesicular transport, gastrointestinal disorders, and autoimmune New NOVX polypeptides and polynucleotides useful for treating NOVX-associated disorders, such as cancers, neurological disorders, diso

Claim 8; Page 123-125; 444pp; English.

diseases.

The present invention describes novel human proteins designated NOVX, where X is 1 to 20 e.g. NOV1. NOVX sequences can have neuroprotective, cytostatic, anticonvulsant, cerebroprotective, nootropic, cardiovascular, antidiabetic, antiinflammatory, antinhementic, antiarthritic, virucide, immunosuppressive, antiallergic, antianeamic, antiarthritic, virucide, protozoacide and antihemininhem cativities, and can be used in gene therapy. The NOVX proteins, nucleotides or antibodies can be used in the human disease selected from NOVX-associated disorder, such as cancers (e.g. leukaemia, lymphoma, melanoma or cancer of the liver, lung, muscle, ovary, testis and uterus), neurological disorders (e.g. epilepsy, stroke, ischaemic cerebrovascular disease, Alzheimer's disease or pick's disease), disorders of vesticular transport (e.g. cystic fibrosis, disorders of vesticular transport (e.g. cystic fibrosis, disorders of vesticular transport (e.g. cystic fibrosis, disorders of ulcerative collitis, or gastric and duodenal disorders), cutofimmune diseases (e.g. allergic reactions, autoimmune haemolytic anaemia, or rheumatoid arthritis), viral, bacterial, fungal, helminthic and protozoal infections. The NOVX proteins can be used as immunogens to produce antibodies and as vaccines. The NOVX nucleotide sequences may be biological samples (fissue typing), and in forensic identification of a biological samples (fissue typing), and in forensic identification of a biological samples (fissue typing), and in forensic manner. sample. The present sequence encodes human NOV15d, which chromosome 4 biological located on

Sequence 8487 BP; 2306 A; 2029 C; 2148 G; 2001 T; 0 U; 3 Other;

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Length:
Matches:
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2123 TGGACGGGCCCAACCTGTAATCAGAGAGCCTGCCACCCCGCTGTGCGAGGCACGGGACC 2182
                                                                                                                                                         recaaggaridecaagreraarideagceargecregaarideagagcacrideacrare--- 2239
                                                                                                                                                                                                  CysAspInrSerMetGluThrAlaCysGlyAspSerLysAspAsnAspGlyAspGlyLeu 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                 1 TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr
                                                                                                                                                                               41 HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyArg
                                                                                                                                                                                                                               CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGlyAlaGly
                                                                                                                                                                                                                                                                                             Prostate cancer; prostate tumour tissue; human; mammal; cytostatic; gene therapy; gene; ds.
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                                                          US-10-029-020-14_COPY_750_850 (1-101) x ABQ82346 (1-8487)
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            Mismatches:
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                          Indels:
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08-DEC-2000; 2000US-00733288.
08-DEC-2000; 2000US-00733742.
24-JAN-2001; 2001US-0263957F.
16-MAR-2001; 2001US-0276791P.
16-MAR-2001; 2001US-0276888P.
06-APR-2001; 2001US-0286214F.
30-APR-2001; 2001US-0286214F.
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          Best Local Similarity:
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2396 ATT 2398
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Cao Y; R, Wang

xu C, (

Liu C, Drmanac RT, Asundi V, Zhou P, X ao QA, Wang D, Wang J, Zhang J, Ren F, Yang Y, Wejhrman T, Goodrich R;

2000US-00654936. 2000US-00663561. 2000US-00693325.

2000US-00728422

-OCT-2000;

2000US-00560875. 2000US-00598075. 2000US-00620325.

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Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                      Tang YI, Liu C, Drmanac RI,
Ma Y, Zhao QA, Wang D, Wang
Xue AJ, Yang Y, Wejhrman T,
                                                                                                                                                                                                                                                                                                  in diagnosis and gene therapy
           05-FEB-2001; 2001WO-US004098
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                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                 20-JUN-2000; 2
19-JUL-2000; 2
01-SEP-2000; 2
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                                                    The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancerassociated polymucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polymucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals from the tissues of various organisms such as humans or other mammals concidence, sheep and dogs). The methods of the invention are useful for diagnosing or treating prostate cancer. The prostate cancer or agents that associated genes are useful for diagnosing or treating prostate cancer. The nucleic acid sequences are particularly cushlin gene therapy, as a vaccine or in antisense applications.

ABK92115-ABK92263 represent prostate cancer-associated polymucleotide
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Matches:
Conservative:
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                               Claim 22; Page 394-397; 436pp; English
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Best Local Similarity:
     prostate tissue
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2773 İĞCAATGITGICATĞƏAAATGCITTGIGGAGATAACTIGGACAATGATGAGAGATGGITIA 2832
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                                         The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynetides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leuvaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
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Mismatches:
Indels:
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Matches:
Claim 1; Page 1414-1426; 6221pp; English.
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WO200157190-A2 09-AUG-2001

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The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the nucleic acids encoding them. These sequences are useful for the treatment or prevention of numerous disorders including myelogenous leukaemia, carcinomas, melanomas, gliomas, astrocytomas, congenital neonatal alloimmune thrombocytopaenia, neurological disorders, neurodegenerative disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Marie —Tooth neuropathy, demyelinating Gardner syndrome, familial myelodysplastic syndrome, mental health conditions, immunological
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                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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            AAS14085 standard; DNA; 9826 BP
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06-MAR-2000; 2000US-0187293P.
06-MAR-2000; 2000US-0187294P.
17-MAR-2000; 2000US-0190400P.
07-APR-2000; 2000US-0196018P.
03-JAN-2001; 2001US-0259548P.
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                                                                           Human FCTR3b DNA sequence
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eosinophilia, lung diseases, reproductive disorders, infertility, male and female reproductive disorders, deafness, glycoprotein Ia deficiency, desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric disorders, pancreatic diseases such as diabetes, Schistosoma mansoni infection Spinocerebellar ataxia, Plasmodium falciparum parasitaemia, Corneal dystrophy-Greonouw type I, Corneal dystrophy-lattice type I and Paramia, Bucklers corneal dystrophy This sequence represents DNA encoding
disorders, allergy and infection, bronchial asthma, Avellino type
                                                                                                                                                                                                                                                                                                      Sequence 9826 BP; 2567 A; 2643 C; 2479 G; 2137 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                Wastrocytoma; congenital neonatal alloimmune thrombocytopaenia, infection;
Wastrocytoma; congenital neonatal alloimmune thrombocytopaenia, infection;
Wastrocytoma; congenital neonatal alloimmune thrombocytopaenia, infection;
familial myelodysplastic syndrome; Charcot Marie-Tooth neuropathy;
Gemyelinating Gardner syndrome; familial myelodysplastic syndrome;
Wental health condition; immunological disorder; allergy; infertility;
Wental health condition; immunological disorder; allergy; infertility;
Wental health condition; immunological disorder; dasorder; deafness;
Wencoductive disorder; reproductive disorder; glycoprotein Ia deficiency;
Gemoid disease; turcot syndrome; liver cirrhosis; hepatitis C; virucide;
Westrophy-Greonouw type Is; Corneal dystrophy-lattice type Is;
Reis-Bucklers corneal dystrophy; cytostatic; immunosuppressive;
Wentiallergic; antiathmatic, antiinfertility; antiinflammatory;
Wentialbetic; protozoacide; hepatotropic; virucide; ophthalmological;
Wentialbetic; protozoacide; hepatotropic; virucide; ophthalmological;
Wentiallergy; RCTR3b; neurestin-like protein.
                                                                                                                                                                                                                                                         Human; FCTRX; myelogenous leukaemia; carcinoma; melanoma; glioma; ds;
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8482. .9826
/*tag= c
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Conservative: Mismatches: Matches:

Length:

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Human; gene; ss; FCTR3b; colorectal cancer; adenomatous polyposis coli; myelogenous leukaemia; congenital neonatal autoimmune thrombocytopenia; worarian cancer; brain tumour; breast cancer; glioma; astrocytoma; worarian cancer; brain tumour; breast cancer; glioma; astrocytoma; worarian call carcinoma; melanoma; clear cell carcinoma; melanoma; neurological disorder; worariantar cell carcinoma; neurological disorder; worarial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy; Gardner syndrome; mental health condition; immunological disorder; worallergy; asthma; lung disease; reproductive disorder; deafness; glycoprotein deficiency; desmoid tumour; turcot syndrome; wordisorder; hepatitis C; gastric disorder; pancreatic disease; plasmodium falciparum infection; spinocerebellar ataxia; plasmodium falciparum infection; Groenouw's corneal dystrophy;
                                                                                                                                                                                                          2434 TGGACAGGCGCAGCGTGACCAGCGCGTGTGCCACCCCGCTGCATTGAGCACGGGACC 2493
                                                                                                                                                                                                                                                                                                            2494 IGTAAAGATGGCAAATGTGAATGCCGAGAGGGCTGGAATGGTGAACACTGGACCATTGGT 2553
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71
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                                                                                   Indels:
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3.49e-27
454.00
77.23%
70.30%
73.58%
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80

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Human, FCTRX; myelogenous leukaemia; carcinoma; melanoma; glioma; ds;

W astrocytoma; congenital neonatal alloimmune thrombocytopaenia; infection;

W astrocytoma; congenital neonatal alloimmune thrombocytopaenia; infection;

KW neurological disorder; neurodegenerative disorders; nerve trauma;

KW demyelinating Gardner syndrome; Charcot-Marie-Tooth neuropathy;

W demyelinating Gardner syndrome; familial myelodyeplastic syndrome;

KW mental health condition; immunological disorder; allorgy; infertility;

KW prondutive disorder; reproductive disorder; glycoprotein Ia deficiency;

KW desmoid disease; turcot syndrome; liver cirrhosis; hepatitis C; virucide;

KW gastric disorder; plasmodium falciparum parasitians disbetes;

KOTINGAL ASTROPHY-Greonouw type I; COTNEAL dystrophy-lattice type I;

KW corneal dystrophy-Greonouw type I; COTNEAL dystrophy-lattice type I;

KW antiallergic; antiasthmatic; antinifertility; immunosuppressalve;

KW antiallergic; antiasthmatic; antinifertility; immunosuppressalve;

KW gene therapy; FCTR3a; neurestin-like protein; FCTR3f.
                                                                                       2674 IGCAACGTIGCCAIGGAAACTICCIGIGCIGATAACAAGAIAATGAGGGAGAIGGCCIG 2733
                                  CysaspThrSerMetGluThrAlaCysGlyAspSerLysAspAspAspAspGlyAspGlyLeu
   CysThrLeuAspLeuAsnGlyTrpHisCysValCysGlnLeuGlyTrpArgGlyAlaGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
                                                                                                                                                                                                                                      AAS14089 standard; DNA; 9729 BP.
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03-MAR-2000; 2000US-018718P.
06-MAR-2000; 2000US-0187293P.
06-MAR-2000; 2000US-0187294P.
17-MAR-2000; 2000US-0190400P.
07-APR-2000; 2000US-0190400P.
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Macdougall J, Mishra V,
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P-PSDB; AAU08681.
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17-MAR-2000; 2
07-APR-2000; 2
03-JAN-2001; 2
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5'UTR
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                                                                                                                                                                                                                                                                                                                                                                                         New FCTRX polypeptide and encoding polynucleotide, useful for preventing or treating FCTRX-related disorders, such as cancer, autoimmune, neurodegenerative, gastrointestinal, reproductive and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2554 AGGCAAACGGCACCGAAACAGATGGCTGCCTGACTTGTGCAACGGTAACGGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2434 IGGACAGGCGCAGCGTGTGACCAGCGCGTGTGCCACCCCGCTGCATTGAGCACGGGACC
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                                                                                                                                                                                                                                                                                           Majumder K;
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Rastelli L;
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Matches:
Conservative:
Mismatches:
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Mezes PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 29-32; 155pp; English.
                                                               05-MAR-2001; 2001US-00800198.
                                                                                               03-MAR-2000; 2000US-0186592P.
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454.00
77.23%
70.30%
73.58%
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Macdougall J, Mishra V,
                                                                                                                                                               SHIMKETS R.
HERRMANN J.
MAJUMDER K.
MACDOUGALL J.
                                                                                                                                 VERMET C.
FERNANDES E.
                                                                                                                                                                                                                                                                                                                                               WPI; 2003-625633/59
                                                                                                                                                                                                                                                              RASTELLI L.
                                                                                                                                                                                                                              MISHRA V.
MEZES P S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity:
                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ADB32024.
US2003087816-A1
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                                08-MAY-2003.
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Majumder K;

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The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the nucleic acids encoding them. These sequences are useful for the treatment or prevention of numerous disorders including myelogenous leukaemia, carcinomas, melanomas, astrocytomas, congenital neonatal alloimmune thrombocytopaenia, neurological disorders, neurodegenerative disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Marie Tooth neuropathy, demyelinating Garddner syndrome, familial myelodysplastic syndrome, mental health conditions, immunological disorders, allergy and infection, bronchial asthma, Avellino type coshnophilia, lung diseases, reproductive disorders, infertility, male and female reproductive disorders, deafness, glyroprotein Ia deficiency, desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric disorders, pancreatic diseases such as diabetes, Schistosoma mansoni infection Spinocrebellar ataxia, Plasmodium falciparum parasitaemia, Corneal dystrophy-Greonouw type I, Corneal dystrophy-Jattice type I and Reis-Bucklers conneal dystrophy. This sequence represents DNA encoding the FCTR34 homologue FCTR3f
                           Novel polypeptides designated as FCTRX polypeptides, useful in detection, prevention and treatment of a broad range of pathological states.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9729 BP; 2548 A; 2629 C; 2438 G; 2114 T; 0 U; 0 Other;
                                                                                                               Claim 9; Page 37-39; 215pp; English.
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                                                                                                                                                                                             21 CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrlleAla 40
                                                                                                                                                                 2364 TGGACAGGCGCAGCGTGTGACCAGCGCGTGTGCCACCCCCGCTGCATTGAGCATGGGGACC
                                                                                                                                  1 TrpWetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr
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                                                                                                                                                                                                                                                                                                                                                                                                    2577 TGCAACGTTGCCATGGAAACTTCCTGTGGTAACAAGGATAATGAGGGGAGATGGCCTG
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                                Conservative:
Mismatches:
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    Length:
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9.7e-27
448.50
77.23$
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                                                            72.698
                                             Best Local Similarity:
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                               Percent Similarity:
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                                                            Query Match:
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Human, gene, se; FCTR3f; colorectal cancer; adenomatous polyposis coli; myelogenous leukaemia; congenital neonatal autoimmune thrombocytopenia; ovarian cancer; brain tumour; breast cancer; glioma; astrocytoma;

Human FCTR3f cDNA.

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The invention relates to FCTRX polypeptides and the polynucleotides

cnooding them. The sequences of the invention are useful for the

manufacture of a medicament for diagnosing and treating disorders

cassociated with the FCTRX polypeptide, such as colorectal cancer,

adenomatous polyposis coli, myelogenous leukaemia, congenital neonatal

cutoimmune thrombocytopenia, malignant ovarian tumours, malignant brain

cautoimmune thrombocytopenia, malignant ovarian tumours, malignant brain

cautoimmune thrombocytopenia, malignant ovarian tumours, malignant brain

carcinoma, breast adenocarcinoma, ovarian carcinoma, melanomas, clear

call and granular cell carcinoma, ovarian carcinoma, melanomas, clear

cell and granular cell carcinoma, neurological disorders,

cell and granular cell carcinoma, familial myelodysplastic

syndrome, Charcot Marie-Tooth neuropathy, Gardner syndrome, mental health

conditions, immunological disorders, allergy and infection, asthma, lung

diseases, male and female reproductive disorders, deafness, glycoprotein

deficiency, desmoid tumour, turcot syndrome, liver cirrhosis, hepatitis

c', gastric disorders, pancreatic diseases, diabetes, schistosoma mansoni

cinfection, spinocerebellar ataxia, plasmodium falciparum infection,

direction, scincerepersonered control corrections and strice corneal dystrophy. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New FCTRX polypeptide and encoding polynucleotide, useful for preventing or treating FCTRX-related disorders, such as cancer, autoimmune, neurodegenerative, gastrointestinal, reproductive and inflammatory
renal cell carcinoma; melanoma; clear cell carcinoma; granular cell carcinoma; neurological disorder; neurodegenerative disorder; nerve trauma; neurodegenerative disorder; nerve trauma; familial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy; Gardner syndrome; mental health condition; immunological disorder; allergy; asthma; lung disease; reproductive disorder; deafness; glycoprotein deficiency; desmoid tumour; turcot syndrome; liver cirrhosis; hepatitis C; gastric disorder; pancreatic disease; diabetes; schistosoma mansoni infection; spinocerebellar ataxia; plasmodium falciparum infection; Groenouw's corneal dystrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9729 BP; 2548 A; 2629 C; 2438 G; 2114 T; 0 U; 0 Other;
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Rastelli L;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mezes PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 34-37; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      03-MAR-2000; 2000US-0186592P.
                                                                                                                                                                                                                                                                                                                                                 05-MAR-2001; 2001US-00800198.
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448.50
77.23*
70.30*
72.69*
                                                                                                                                                                                              lattice corneal dystrophy.
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Macdougall J, Mishra V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHIMKETS R.
HERRMANN J.
MAJUMDER K.
MACDOUGALL J.
                                                                                                                                                                                                                                                                                                                                                                                                                              VERMET C.
FERNANDES E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-625633/59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISHRA V.
MEZES P S.
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(MAJU/)
(MACD/)
                                                                                                                                                                                                                                                                                                                                                                                                                            VERM/)
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1027 GACTTGTGCAAACGGTAACGGGAGATGCACTCGGTCAGAACAGCTGGCAGTGTGTCTGC 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel differentially regulated genes and polypeptides encoded by them. Sequences of the invention are useful in diagnosing, staging, monitoring, prognosticating, preventing, treating or determining the predisposition to diseases or conditions such as prostate cancer. They may be used as molecular markers, drug targets, vaccines, in gene therapy, research, clinical medicine or forensic science. The present sequence is a differentially regulated prostate cDNA, Pc099 which codes for teneurin-2. Pc099 gene is located on chromosome 5q34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnLeuGlyTrpArgGlyAlaGlyCysAspThrSerMetGluThrAlaCysGlyAspSer 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; cytostatic; gene therapy; antisense therapy; regulated; iscovery; clinical medicine; forensic medicine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 GlyLeuCysAsnGlyAsnGlyArgCysThrLeuAspLeuAsnGlyTrpHisCysValCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrCysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrlle
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                                                                                                                                                                                                     Sequence 4245 BP; 1035 A; 1132 C; 1115 G; 963 T; 0 U; 0 Other;
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Gaps:
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chromosome 5q33.3; ds.
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                                                                                      2364 Teleacadecelededeferencedecelegeneres de consecuentes de caracidades de 1423
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                                                                                                                                                CysArgAspGlyLysCysGluCysSerProGlyTrpAsnGlyGluHisCysThrIleAla 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulated protein; prevention; therapy; vaccine; therapy; Pc099; teneurin-2; chromosome 5q34; gene;
                                                                                                                                                                                                                                     HisTyrLeuAspArgValValLysGluGlyCysProGlyLeuCysAsnGlyAsnGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                       CysAspThrSerMetGluThrAlaCysGlyAspSerLysAspAspAspGlyAspGlyLeu
                                                              TrpMetGlyAlaAlaCysAspGlnArgAlaCysHisProArgCysAlaGluHisGlyThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Human Pc099
/note= "No start codon"
/partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ORIG-) ORIGENE TECHNOLOGIES INC
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07-NOV-2001; 2001US-0331042P.
18-DEC-2001; 2001US-0340251P.
07-JAN-2002; 2002US-0344791P.
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prostate cancer; gene
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P-PSDB; AAO29571.
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Kovacs KF,
      (ORIG-) ORIGENE TECHNOLOGIES INC.
14-MAY-2002; 2002US-00144194.
             Li X, Fan W,
                    WPI; 2003-381623/36.
                        P-PSDB; ABR58317
              Sun Z,
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Jay G;

New isolated human differentially-regulated breast cancer polymucleotide and polypeptide, useful for diagnosing, staging, prognosticating, preventing and/or treating diseases and conditions relating to breast cancer. Claim 2; SEQ ID NO 79; 127pp + Sequence Listing; English.

The invention relates to isolated polynucleotides which are differentially-regulated in breast cancer. The methods and compositions of the present invention are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and/or treating diseases and conditions relating to breast cancer, and may be used in gene therapy or alisenese therapy. They can also be used in research, drug discovery, clinical medicine and forensic medicine. Sequences given in records differentially-regulated in breast cancer. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pot\_sequences

Sequence 9058 BP; 2387 A; 2430 C; 2263 G; 1978 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: 3.67e-17 330.50 57.36% 46.51% 53.57% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.:

US-10-029-020-14\_COPY\_750\_850 (1-101) x ACC72051 (1-9058)

Search completed: August 14, 2004, 02:29:24 Job time : 200.323 secs

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APPLICANT: Alsobrook II, John et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE
FILE REFERENCE: 2402-568A
CURRENT APPLICATION NUMBER: 10510-30-06
PRIOR PILLING DATE: 2003-03-06
PRIOR FILLING DATE: 2001-12-19
PRIOR PLILING DATE: 2001-12-19
PRIOR PLILING DATE: 2002-03-20
PRIOR FILLING DATE: 2002-04-12
PRIOR PLILING DATE: 2002-06-14
PRIOR PLILING DATE: 2002-06-14
PRIOR PLILING DATE: 2002-06-14
PRIOR PLILING DATE: 2002-06-14
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PRIOR PLILING DATE: 2002-06-15
PRIOR PLILING DATE: 2002-06-15
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PRIOR PLILING DATE: 2002-06-15
PRIOR PLILING DATE: 2002-09-13
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Sequence 5, Appl
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1 US-10-029-020-13

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8 US-09-808-602-75

8 US-10-094-74-11-7

8 US-10-094-871-7

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8 US-09-808-602-74
     US-10-383-201-45
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Publication No. US20040029226A1
GENERAL INFORMATION:
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-Q=Cgn2 1/USPTO spool/US10029020/runat 06082004 112218 29331/app_query.fasta 1.3519
-Q=Cgn2 1/USPTO spool/US10029020/runat 06082004 112218 29331/app_query.fasta 1.3519
-DB=Published Applications Nh -QFWT=fastap -SUFFTX=p20.rnpb - MINMATCH=0.1
-LOOPCL=0 - LOOPEXX=0 - UNITS=bit s -STARR=1 - END=-1 - MATRIX=blosum62
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 -THR SCORE=pct - THR MAX=10
-THR MN=0 -ALIGN=15 - MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 - USR=US10029020 @CGN 1_1 2156 @runat - 06082004 112218 29331
-NCPU=6 - LOPU=3 -NO MMAP - LARGEQUERY - NEG SCORES=0 - WAIT - DSBELOCK=100
-LONGLOG -DEV_TIMEOUT=120 - WARN_TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5
-FGAPOP=6 - FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
                                                                                                                                                          ; Search time 142.298 Seconds (without alignments) 2448.158 Million cell updates/sec
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1 TFWRSQVFIDHPVHLKFNVS......RLLTQEARSLEGTFRQSRGT 71
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| Cgm2_6/ptodata/2/pubpna/US06_MW_PUB.seq:*
| Cgm2_6/ptodata/2/pubpna/US06_MW_PUB.seq:*
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| Cgm2_6/ptodata/2/pubpna/US07_NW_PUB.seq:*
| Cgm2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
| Cgm2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES

Query Match Length DB

Score

Result

3225727 seqs, 2453303834 residues

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

**BLOSUM62** 

Scoring table:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of

Searched:

Published\_Applications\_NA:\*

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US-10-029-020-14\_COPY\_450\_520

Perfect score:

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Sequence:

August 14, 2004, 01:33:47

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Run on:

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US-10-483-2014

| Sequence 41, Application US/10383201
| Publication No. US2004002922641
| Publication No. US2004002922641
| Sequence 41, Application No. US2004002922641
| GENERAL INFORMATION II. John et al.
| APPLICART: Alsobrook II. John et al.
| TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD |
| FILE REFRENCE: 12402-5684
| FILE REPRENCE: 2402-608-03-66
| PRIOR PILING DATE: 2001-02-10
| PRIOR APPLICATION NUMBER: 60/372,022
| PRIOR PILING DATE: 2002-04-12
| PRIOR FILING DATE: 2002-04-12
| PRIOR FILING DATE: 2002-06-14
| PRIOR FILING DATE: 2002-06-14
| PRIOR FILING DATE: 2002-06-13
| PRIOR FILING DATE: 2002-06-13
| PRIOR FILING DATE: 2002-06-13
| PRIOR FILING DATE: 2002-06-13
| PRIOR FILING DATE: 2002-06-13
| PRIOR FILING DATE: 2002-01-16
| PRIOR FILING DATE: 2002-01-16
| PRIOR FILING DATE: 2002-01-16
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SOFTWARE: CuraSeqList version 0.1
PRIOR FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 53
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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; LOCATION: (7)
US-10-383-201-53
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Sequence 53, Application US/10383201

Publication No. US20040029226A1

Sequence 53, Application US/10383201

Sublication No. US20040029226A1

APPLICANT: Alsobrook II, John et al.

TITLE OF INVENTION: THERABEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-568A

CURRENT APPLICATION NUMBER: US/10/383,201

PRIOR PILING DATE: 2003-03-06

PRIOR FILING DATE: 2002-03-20

PRIOR FILING DATE: 2002-04-20

PRIOR PILING DATE: 2002-04-12

PRIOR PILING DATE: 2002-06-14

PRIOR PILING DATE: 2002-06-13

PRIOR PILING DATE: 2002-06-13

PRIOR PILING DATE: 2002-09-13

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Matches:
Conservative:
Mismatches:
Indels:
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                 PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 10/051,874
PRIOR PILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 60/366,928
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 10/055,877
PRIOR APPLICATION NUMBER: 10/055,877
PRIOR FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SOFTWARE: CuraSeqList version 0.1
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372.00
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Best Local Similarity:
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; LOCATION: (1).
US-10-383-201-45
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Pred. No.:
Score:
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LENGTH: 1392
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US-10-383-201-53
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/290,578
FILING DATE: 08-No. US20030078389A1-2002
CLASSIFICATION: <un>

Unknown>

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Mismatches:
Indels:
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TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LeuGluGlyThrProArgGlnSerArgGlyThr
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APPLICATION NUMBER: US/08/891,845
FILING DATE: «Unknown»
APPLICATION NUMBER: 66/021640
FILING DATE: 12-Jul-96
        TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schaefer, Gabriele M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/10290578; Publication No. US20030078389A1; GENERAL INFORMATION:
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TELEFAX: 415/952-9881
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INFORMATION FOR SEQ ID NO: 11:
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Best Local Similarity:
Query Match:
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US-10-290-578-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinDatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/290,578

FILING DATE: 08-No. US200300783891-2002

CLASSIFICATION ATA:

APPLICATION NUMBER: US/08/891,845

FILING DATE: CURROWN.
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Mismatches:
Indels:
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Sliwkowski, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                          Length:
Matches:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFRAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/021640
FILING DATE: 12-Jul-96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10290578 Publication No. US20030078389A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1680 base pairs
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SEQUENCE CHARACTERISTICS:
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372.00
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ORGANISM: Homo sapiens
                                    ) NAME/KEY: CDS
; LOCATION: (1)..(1464)
US-10-383-201-41
                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                 Alignment Scores:
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US-10-290-578-3
                                                                                                                                                                                                               Query Match:
DB:
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61 LeuGluGlyThrProArgGlnSerArgGlyThr 71
                            61 LeuGluGlyThrProArgGlnSerArgGlyThr
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                                                                                                                                                                                                                                                      US-10-029-020-14_COPY_450_520 (1-71) x US-10-290-578-11 (1-2387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sliwkowski, Mark
APPLICANT: Kern, Jeffrey
TITILE OF INVENTION: Use of Heregulin as a Growth Factor
FILE REPERENCE: P1145R1
CURRENT APPLICATION NUMBER: US/09/773,517
FLOR APPLICATION NUMBER: 09/243,198
PRIOR FILING DATE: 1999-02-02
NUMBER: OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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TYPE: Nucleic Acid

STRANDEDNESS: Single

;

TOPOLOGY: Linear

;

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-290-578-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09773517 Patent No. US20010023241A1
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Best Local Similarity:
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Best Local Similarity:
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US-09-773-517-12
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DB:
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1681 ACTITCIGGAGAICTCAAGIGITCAIAGACCAICCIGIGCAICIGAAAITCAAIGIGICI 1740
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                                                                                                                                                                     Kern, Jeffrey
TITLE OF INVENTION: Use of Heregulin as a Growth Factor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
1861 CTAGAGGGGACCCGCGCCAGTCTCGGGGAACT 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/792,025
FILING DATE: 23-Feb-2001
CLASSIPICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/020,598
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: SCHWATIZ, Timothy R.
REGISTRATION NUMBER: 32.71
REFERENGE/DOCKET NUMBER: P1145
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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                                                                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                          Francisco
                                                                           US-09-792-025-12; Sequence 12, Application US/09792025; Patent No. US20020042087A1; GENERAL INFORMATION:
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                                                                                                                                                                  Mark
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STRANDEDNESS: Single
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SEQUENCE CHARACTERISTICS
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372.00
100.00%
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                     CITY: South San Fr
STATE: California
                                                                                                                                                                  APPLICANT: Sliwkowski,
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TYPE: DNA
CORGANISM: Homo sapiens
US-10-453-183-12
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-029-020-14_COPY_450_520 (1-71) x US-09-849-868-12 (1-3111)
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
1861 CTAGAGGGGACCCGGCGCCAGTCTCGGGGAACT 1893
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Sliwkowski, Mark
TITLE OF INVENTION: Gamma-Heregulin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STAREET: California
                                                                                      Sequence 12, Application US/09849868
Patent No. US20020081299A1
GENERAL INFORMATION:
APPLICANT: Generatech, Inc.
APPLICANT: Generatech, Inc.
TITLE OF INVENTION: HAIR CELL DISORDERS
FILE REFERENCE: GENERY: 035VPC
CURRENT APPLICATION NUMBER: US/09/849,868
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 3111
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Publication No. US20030078389A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                        US-09-849-868-12
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1681 ACTITCIGGAGAICTICAAGIGITCAIAGACCAICCIGIGCAICTIGAAAITCAAIGIGITCI 1740
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APPLICANT: Sliwkowski, Mark
TILE OF INVENTION: Use of Heregulin as a Growth Factor
TILE OF INVENTION: Use of Heregulin as a Growth Factor
FILE REFERENCE: Pl145R1
CURRENT APPLICATION NUMBER: US/10/453,183
CURRENT FILING DATE: 2003-06-03
PRIOR FILING DATE: 1999-02-02
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1998-02-04
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3111
71
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APPLICATION NUMBER: US/10/290,578
FILING DATE: 08-No. US20030078389A1-2002
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1861 CTAGAGGGGACCCCGCGCCAGTCTCGGGGAACT 1893
                 FILING DATE: 08-NO. US2003078389A1-.
CLASSIFICATION: CUNKNOWN-
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/891,845
FILING DATE: CUNKNOWN-
APPLICATION NUMBER: GO/021640
FILING DATE: 12-U1-96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1043
TELEPHONE: 415/225-1994
TELEPHONE: 415/225-1994
TELEPHONE: 415/225-1981
TELEPHONE: 415/225-1981
TELEPHONE: 415/225-1981
TELERX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE HRRACTERSTICS:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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Publication No. US20030199429A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3111 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Nucleic Acid
STRANDEDNESS: Single
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372.00
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7.7	DB:  US-10-029-020-14_COPY_450_520 (1-71) x US-10-383-201-43 (1-8354)  QY  1 ThrPheTrpArgSerGlnValPheIleAspHisProValHisLeuLySPheAsnValSer 20	21	rg.eu.eu.m.c.mo.ma.ar.gser 		0.10000	TITLE OF INVENTION: POLYPEPLIGES and Nucleic Acids Encoding Same	US-10-029-020-14_COPY_450_520 (1-71) x US-10-029-020-13 (1-8354) Ov 1 ThrPheTrpArdSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSer 20	1382 ACTTCTGGAGATCTCAAGTGTTCATAGACCATCTGTGCATCTGAAATTCAATGTGTCT 1 21 LeuGlyLysAlaAlaLeuValGlylleTyrGlyArgLysGlyLeuProProSerHisThr 4 21 LeuGlyLygAlaAlaAlaLeuValGlylleTyrGlyArgLysGlyLeuProProSerHisThr 4 1442 CTGGGAAAGGCAGCCCTGGTTGGCATTTATGGCAGAAAAGGCCTCCTTCACATACA 1
	Alignment Scores:  Pred. No.: Score: 372.00 Matches: 71 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 1100.00\$ DB: Gaps: 0	US-10-029-020-14_COPY_450_520 (1-71) x US-10-453-183-12 (1-3111)  Qy	Db 1681 ACTITCTGGAGATCTCAAGTGTTCATAGACCATCCTGGGATCTGAAATTCAATGTGTCT 1740  Qy 21 LeuGlyLysalaAlaLeuValGlylleTyrGlyArgLySGlyLeuProProSerHisThr 40	CATACA	Db   1801   CAGTTTGACTTTGTGGAGGTGCTGGATGGCAGGGGGCTCCTAACCCAGGAGGGGGGGG	REGULT 11  WEACHLY 11  WEACHLY 11  WEACHLY 11  WEACHLOATION NO. US70040029226A1  PUBLICATION NO. US70040029226A1  APPLICATION NO. WE US70040029226A1  APPLICATION NO. WEACHLOATION WHERE WEACHLOATION WHEN	; NAME/KEY: CDS ; LOCATION: (35)(8341) US-10-383-201-43	Alignment Scores: Pred. No.: Score: Score: Score: Alignment Jule-46 Matches: Town Matches: Percent Similarity: 100.00\$ Mismatches: Mismatc

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FILLE OF INVENTION: Using the Same

TITLE OF INVENTION: Using the Same

FILE REPRENCE: 21402-537

CURRENT APPLICATION NUMBER: US/10/042,865

CURRENT FILING DATE: 2002-05-17

PRIOR PAPLICATION NUMBER: 60/260,417

PRIOR PAPLICATION NUMBER: 60/260,831

PRIOR APPLICATION NUMBER: 60/260,831

PRIOR APPLICATION NUMBER: 60/272,338

PRIOR APPLICATION NUMBER: 60/272,338

PRIOR PILING DATE: 2001-01-01

PRIOR FILING DATE: 2001-02-29

PRIOR PILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/274,876

PRIOR APPLICATION NUMBER: 60/274,876

PRIOR APPLICATION NUMBER: 60/244,704

PRIOR APPLICATION NUMBER: 60/24-704

PRIOR APPLICATION NUMBER: 60/20-04-18

NUMBER OF SEQ ID NOS: 264

NUMBER OF SEQ ID NOS: 264
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1528 CTAGAGGGGACCCCGCGCCAGTCTCGGGGAACT 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                   Sequence 1, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       Casman, Stacte J
Shenoy, Suresh G
Spytek, Kimberly
Spytek, Kimberly
Zhong, Mei
Gangolli, Esha A
Burgess, Catherine B
Patturajan, Meera
Vernet, Corine A.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alsobrook II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
                                                                                                                                                                                                             APPLICANT: Padigaru, Muralidhara
APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
APPLICANT: Casman, Stacie J
APPLICANT: Speney, Suresh G
APPLICANT: Spytek, Kimberly
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MacDougail, John
Malyankar, Uriel M
Millet, Isabelle
Peyman, John
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Miller, Charles E
Guo, Xiaojia
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Grosse, William M
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Gunther, Erik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo
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APPLICANT:
APPLICANT:
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LENGTH: 84
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                                                                                                                                                                                                                                                                                                                                     GENERAL INVENTATION:

APPLICANT: Alsobrook II, John et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL

FILE REPERENCE: 2.042-5.684

CURRENT APPLICATION NUMBER: US/10/29020

PRIOR PLICATION NUMBER: US/025-920

PRIOR PLICATION NUMBER: US/035,984

PRIOR PLICATION NUMBER: 00/365,984

PRIOR PLILNG DATE: 2002-03-20

PRIOR PLILNG DATE: 2002-04-12

PRIOR PLILNG DATE: 2002-04-12

PRIOR PLILNG DATE: 2002-04-12

PRIOR PLILNG DATE: 2002-04-13

PRIOR PLILNG DATE: 2002-06-13

PRIOR PLILNG DATE: 2002-06-13

PRIOR PLILNG DATE: 2002-09-13

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                                              1502 CAGTITGACTITGIAGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGGAGGCGCGGAGC 1561
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             GlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSer
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                        LeuGluGlyThrProArgGlnSerArgGlyThr 71
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                                                                                                                                                                                                                        RESULT 13
US-10-383-201-55
Sequence 55, Application US/10383201
Publication No. US20040029226A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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; LOCATION: (1).
US-10-383-201-55
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; LENGTH: 8473 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-038-854-39

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PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: MacDougall, John R
ITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT PEPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-02
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
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PRIOR PRILING DATE: 2001-04-13
PRIOR PRILING DATE: 2001-04-13
                                                                                                                                                                                       LeuGluGlyThrProArgGlnSerArgGlyThr
                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
Patturajan, Meera
Gusev, Vladimir Y
Gangolli, Esha A
Guo, Xiaojia S
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Rastelli, Iuca
Casman, Stacie J
Boldog, Ferenc
Burgess, Catherine E
Edinger, Shlomit R
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Millet, Isabelle
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Wolenc, Adam R
Vernet, Corine
Eisen, Andrew J
Liu, Xiaohong
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Gunther, Erik
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                                                                                                                                               22 GlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThrGln
                                                                                                                                                                                           US-10-029-020-14_COPY_450_520 (1-71) x US-10-038-854-39 (1-8473)
        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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     3.1e-28
254.00
80.88%
70.59%
68.28%
                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

; Search time 832.674 Seconds (without alignments) 2546.273 Million cell updates/sec 372 1 TEWRSQVFIDHPVHLKENVS.....RLLTQEARSLEGTPRQSRGT 71 US-10-029-020-14\_COPY\_450\_520 August 14, 2004, 01:13:26 Perfect score: Sequence: Run on: Title:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext BLOSUM62 Scoring table:

27513289 segs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/Cogn2 1/UST029020/TVLDATE 06082004 112216 29287/app query.fasta\_1.3519
-D=/Cogn2 1/UST029020/TVLDATE 0.1 -LOOFUL=0 -LOOFXT=0
-DRATE 1= QFWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFUL=0 -LOOFXT=0
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

EST:\* Database :

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gb\_est3:\*
gb\_est4:\*
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em\_est6m:\* em gss hum:\* gss\_inv:\* \*:uld\_ss6 em\_estba:\* em\_esthum:\* em\_estov:\*
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em\_gss\_mam:\* em\_gss\_mus:\* em\_gss\_pro:\* em\_gss\_rod:\*
em\_gss\_phg:\*
em\_gss\_vrl:\*
gb\_gssl:\* gss\_vrt:\* fun: em gss eш 1165 ... 222 .

## gb\_gss2:\* 29:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

EST 24-JAN-2001

BG036207 870 bp mRNA linear EST 24-JAN-20602226960F1 NIH\_MGC\_91 Homo sapiens cDNA clone IMAGE:4428351 5', BG036207.1 GI:12431132 Homo sapiens (human) mRNA sequence. EST VERSION KEYWORDS SOURCE ORGANISM DEFINITION RESULT 1 BG036207 LOCUS ACCESSION

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 870)

REFERENCE

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20530913
11076861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="adenocarcinoma, cell line"
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/clone_lib="NIH_MGC_91"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                   Unpublished (1999)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CODNA Library Arraparation: Life Technologies, Inc.
CDNA Library Arraparation: Life Technologies, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://mage.lln.gov
Plate: LiAM10178 row: h column: 16
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.
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                            /dev_stage="9 days embryo" ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ....csp. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 GlybysalaalareuValGlyIleTyrGlyArgLysGlybeuProProSerHisThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 PheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSerLeu
                                                                                                                                                                                                                                                                               2627
48
9
11
3
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Insert Length: 10000 Std Error: 0.00
Plate: 0540 row: B column: 02
Seg primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 701.
Location/Qualifiers
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GSS.
                                                                                                                                                                                                                                                                     2.7e-22
248.50
80.28$
67.61$
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Fax: 801 585 7177
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                            No.:
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COMMENT
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KEYWORDS
SOURCE
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AZ661742
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                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                        Score:
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfy19114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clome: B930059M16 product:odd Oz/ten-m homolog 1 (Drogophila), full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 CIGGGGAAAGCAGCICIGGIIGGCAITIAIGGCAGAAAAGGCCIICCICCCIICCAIACI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 ACGITCIGGAGAICICAGGIGITCAIAGACCACCIGIACACCIGAAGITCAAIGIGICT 187
                                                 /lab host="B. Coli strain XL10-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ThrPheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSer
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Mismatches:
Indels:
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High-efficiency full-length cDNA cloning
Meth. Bnzymol. 303, 19-44 (1999)
99279253
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Matches:
clone="UUGC1M0540B02"
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HTC; CAP trapper.
Mus musculus (house mouse)
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228.00
83.93%
80.36%
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BQ257598 594 bp mRNA linear EST 06-MAY-2002 NISC kp04a02.q2 Baker mouse embryo e7.5 Mus musculus cDNA clone IMAGE:5408163, mRNA sequence.
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                                                                                                                                           FKFSEYCCOMBAPADSAQDMOSSPHNQFTFRPLPPPPPPPHACTCARKPPFTVDSLQR
RSMTTRSQPSPAAPAPPTSTQDSVHLHNSWVLNSNIPLETRHFLFKHGSGSSAIFSAA
SQNYPLTRSQPSPAAPAPPTSTQDSVHLHNSWVLNSNIPLETRHFLFKHGSGSSAIFSAA
SQNYPLTALFGLTWQLDPQQIYANGISNGNPGTFERMDTYSPFIGGRVSDKSEKKVFQVG
RAYLVHLFGLTWQLDPQQIYANGISNGNPGTFERMDTYSPFIGGRVSDKSEKKVPQVG
TATDTGPPDFVKLMOGKQLVKQDSKSSDDIQHSPRNLILTSLQETGFIEYMDQGPWYLAFY
NDGKKMBQVFVLTTAIGKLPCLLFEFTV"
                         /trānslation="WEQTDCKPYQPLSKVKHEMDLAYTSSSDESEDGRKPRQSFNSRE
TLHEYNQELRRNYNSQSRKRKDVEKSTQEIEPCETPPTLCSGYHTDMHSVSRHGYQLE
MGSDVDTETEGAASPDHALRMWIRGMKSEHSSCLSSRANSALSLTDTDHERKSDGENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2224 TITGAITICGIGAAAITAAIGGAIGGCAAACAGGTAAAAACAGGGCTCAAGAGCTCA 2283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2104 ITCTGGCGTTTCCAGATTACTATCCACCATCCTATATATCTGAAATTCAATATTTCTTTA 2163
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 GlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThrGln
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Conservative:
Mismatches:
Indels:
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/mol type="mRNA"
/strain="CD-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2284 GATGACATTCAGCACTCCCCAAGG 2307
xref="GI:26338766"
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Location/Qualifiers
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Mus musculus
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220.50
83.82%
54.41%
59.27%
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Direct Submission Joshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45-503-922, Tel:81-45
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
dev stage="10 days neonate"
                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishiia, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsuncto, H., Sakaguchi, S., Ikegami, T., Kashiwaji, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The FANTOW Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (Dases I to 3447)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Please visit our web site for further details.
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/strain="C57BL/6J"

/db_xref="PRANTOM DB:B930059M16"

/db_xref="MG1.2412967"

/db_xref="mG1.2412967"

/db_xref="taxon:10090"

/clone="B930059M16"
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/protein_id="BAC33054.1"
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                                                                                            /clone lib="Baker mouse embryo e7.5"
/note="Vector: pCS105; Site 1: Not1; Site 2: SalI; CDNA
mote="Vector: pCS105; Site 1: Not1; Site 2: SalI; CDNA
made by Oligo-dT priming. Directionally cloned into
SalI/Not1 sites using the following 5' adaptor:
5'-TCGACCCACGCGTCG-3'. Size-selected for average insert
size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
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1 (bases 1 to 519)
Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., et al.) Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSerLeuGlyLys 23
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Enail s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
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This clone (DKRZp779B1315) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GREMANY; Email: clone@rzpd.de.
Location/Qualifiers
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/clone="IMAGE:5408163"
/tissue_tvpe="embryo, late gastrula"
/dev_stage="embryo, 7.5 dpc"
/lab_host="XLI-Blue"
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DKFZp779B1315 5', mRNA sequence.
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VERSION
KEYWORDS
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JOURNAL
COMMENT
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with smusculus (nouse mouse)

Haracolus (nouse mouse)

Haracolus (nouse mouse)

Haracolus (hordata; Craniata; Vertebrata; Buteleostomi;

Hammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Marmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rammalinh.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Parayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project (BMAP))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF538752 306 bp mRNA linear EST 12-SEP-2003 UI-M-GIO-chf-i-06-0-UI.rl NIH BMAP_GIO Mus musculus cDNA clone IMAGE:30531941 5', mRNA sequence.
                                                             /tissue_type="liver"
/dev_stage="feral"
/dat_nost="bH10B"
/clone_lib="779 (synonym: hncc1)"
/note="Vector: pSportl_Sfi; Site_1: SfilA, Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 TICTGGTT-TTCCAGATTACTATCCACCATCCAATATATCTGAAGTTCAATATTTCTTTA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 GCCAAGGACTCTCTGCTGGGAATTTATGGCAGAAGAAACATTCCACCTACACATACTCAG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 TITGATITIGIAAACTAAIGGAIGGCAAACAGCIGGICAAGGAGGAGCTCT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 PheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSerLeu 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 GlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="whole_brain"
/dev_stage="embryol15.14.5,16.5,17.5dpc"
/lab_host="DHJOB (TI phage resistant)"
/clone_lib="NTH_BMARP_GIO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-029-020-14_COPY_450_520 (1-71) x BX494675 (1-519)
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
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/db_xref="taxon:9606"
/clone="DKFZp779B1315"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 GATGATACACACACTCCCCTCGG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:34590734
                                                                                                                                                                                                                                                                                                                              7.27e-17
201.00
77.94%
51.47%
54.03%
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E 6 (Dases 1 to 2/16)

S Adachi, J. Aizawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Haramato, K., Hiracka, T., Hirozane, T., Hayiseu, M., Hiramcto, K., Hiracka, T., Kiozane, T., Hori, F., Imctani, K., Ishii, Y., Itch, M., Kagawa, I., Kaukah, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakanura, M., Nishi, K., Nomura, K., Numaza, K., Numaza, K., Ohno, M., Ohsato, N., Okazaki, Y., Saito, B., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sago, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Tanachi, Shinshi, M., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Muramatsu, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, 
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/clone lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-UUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Submiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                 Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDMAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2716)
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                                                                                                                                                                                                                               The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium and the RIKEN Genome Exploration Research
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RIGA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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(MGD|MGI:1345184, GB|NM_011856, evidence: BLASTN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web site for further details.
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/mol type="mRNA"
/strain="C57BL/6"
/db_xref="FANIYOM"
/db_xref="FANIYOM"
/db_xref="MGI:2394397"
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1. .2716
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/clone="5930427L24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
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194.50
70.59%
55.88%
52.28%
                                                                                                                                                                                                                                                                    FANTOM Consortium.
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Best Local Similarity:
Query Match:
                                                                                                                                                                          11076861
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AUTHORS
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                                              TITLE
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      /note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarcs gel. First strand CDNA synthesis was primed with oligo-dr primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nerrous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930427L24 product:odd Oz/ten-m homolog 2 (Drosophila), full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuProProSerHisThrGlnPheAspPheValGluLeuLeuAspGlyArgArgLeuLeu 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 GCGAGAGGAGCGGAACCTGGTGGAGTCCGAAAGAGCCGGGCGGCGGCGAGA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 ThrGlnGluAlaArgSerieu-----GluGlyThrProArgGlnSerArg 69
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339
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Indels:
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Matches:
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AL710528

DKFZp686K106_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686K106_s', mRNA sequence.
                                                                                                               22 GlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThrGln 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. In Chases 1 to 247)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S. EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S. Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. wiemann@dkfz- heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GRRMANY; Email: clone@rzpd.de.
Location/Qualifiers
2 PheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSerLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No s1 sequence available.
This clone (DKFZp686K106) is available at the RZPD in
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Indels:
                                                                                                                                                                                                                  482 TATGACTTCATGGAACGTCTGGACGGAAG 511
                                                                                                                                                                         42 PheAspPheValGluLeuLeuAspGlyArg 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="DKFZp686K106"
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/lab_host="DH10B"
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AL710528.1 GI:19693883
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Best Local Similarity:
Query Match:
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JOURNAL
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/u.ganism="Homo sapiens"
/mol_type="mRNA"
/do xere="taxon:866"
/clone="IMAGE:5425486"
/clone="IMAGE:5425486"
/tissue_type="astrocytoma grade IV, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="MIH MGC 98"
/note="Organ: brain_ Vector: pOTB7; Site_1: Xhol; Site_2:
BcoR1; cDNA made by oligo-dT priming. Directionally
cloned into EcoR1/Xhol sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                           1172 TTTTGGAGGTCCCCAGATTCACATCAGTCAGCCTCAATTCTTAAAGTTCAACATCTCCCTG 1231
                                                                                                                               ----GAGAAATGGAGCGTG 1336
                                                                                                                                                                                                                                                                                                                                                                                                               BM017187 1013 bp mRNA linear EST 30-OCT-2001 603643790F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5425486 5',
                                                                                                                                                                                    42 PheAspPheValGluLeuLeuAspGlyArgArgLeuLeuThrGlnGluAlaArgSerLeu 61
                    21
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1. (bases 1 to 1013)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbe-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov.c. column: 23
http://image.llnl.gov.c. column: 23
High quality sequence stop: 565.
                                                                                                    22 GlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThrGln
             2 PheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSerLeu
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Matches:
Conservative:
Mismatches:
Indels:
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1292 TATGACTTCATGGAACGCCTGGATGGAAAG-
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                                                                                                                                                                                                                                                                                                           1337 GTCGAGTCGCCCAGGGAACGCCGG 1360
                                                                                                                                                                                                                                                                             62 GluGlyThrProArgGlnSerArg 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM017187.1 GI:16531541
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AUTHORS
TITLE
JOURNAL
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392 bp mRNA linear EST 18-MAR-1996
yzdsco6.sl Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:285994 3', mRNA sequence.
                                   BAC 230G8. 230G8 is Plasterk and N.V.
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1. (bases 1 to 392)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Morris, M., Parsons, J., Prange, C., Rikin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 288.
Location/Qualifiers
CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSerLeu
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                   This sequence was generated from the T7 end of part of the Daniokey BAC Library created by R. Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                           769
29
5
11
4
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                     http://www.sanger.ac.uk/Projects/D_rerio/
                                                                                                                                                                                                                                              /tissue_type="Testis"
/note="vector pIndigoBAC-536"
Campus, Hinxton, Cambridgeshire, C
humquery@sanger.ac.uk Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582 GIGCGCACAAGCTTTCTATTTACAGAA 556
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                                                                                                                                                            /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-230G8"
                                                                                                                          Location/Qualifiers
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Best Local Similarity:
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1. (bases 1 to 769)
Humphray, S. J., Huckle, E. and Durham, J. L.
Direct Submission
Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 13-MAR-2003
                                                                                                       GSS 28-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was generated from the T7 end of BAC 176110. 176110 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
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                                                                                                   BX172779 768 bp DNA linear GSS 28-JAN-Danic rerio genomic clone DKEY-176L10, genomic survey sequence.
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Danio rerio genomic clone DKEY-230GB, genomic survey sequence.
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Mismatches:
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/note="vector_pindigoBAC-536"
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Matches:
    TATGACTTCATGGAACGTCTGGACGGGAAG 245
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/db_xref="taxon:7955"
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Danio rerio
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340 bp DNA linear GSS 16-APR-2003
NDL.45P17.T7 Notre Dame Liverpool Aedes aegypti genomic clone
NDL.45P17, genomic survey sequence.
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/clone="NDL.45P17"
/clone="NDL.45P17"
/clone="Vector: pECBAC1; Site_1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and
                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
                                                                                                                                                                      22 GlyLysAlaAlaLeuValGlyIleTyrGlyArgLysGlyLeuProProSerHisThrGln
                                                                                                    PheTrpArgSerGlnValPheIleAspHisProValHisLeuLysPheAsnValSerLeu
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                                                                    US-10-029-020-14_COPY_450_520 (1-71) x BX178536 (1-749)
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Library was provided by David Severson
Seq primer: T7
Class: BAC ends.
   Mismatches:
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Aedes aegypti
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                       Indels:
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/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="liverpool"
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GSS.
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Hongbin Zhang"
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Fax: 301-838-0208
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                                                                                                                                             Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
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1 (bases 1 to 749)
Humphray, S.J., Huckle, E. and Durham, J.L.
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                                                                                                                /dev_stāge="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
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Location/Qualifiers
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/tissue_type="Testis"
/note="vector pindigoBAC-536"
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Matches:
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/db_xref="GDB:3893111"
/db_xref="taxon:9606"
/clone="IMAGB:285994"
/tissue_type="cochlea"
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/db_xref="taxon:7955"
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Search completed: August 14, 2004, 18:02:47 Job time : 842.674 secs

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CB532612 757081 MA
BU072782 in47902.y
BU270056 60436486
BU474934 603364860
AKO47423 MMS muscu
BQ735622 AGENCOURT
BU474512 603760992
                                                                                                                                                                                                                                                                              AK031199 Mus muscu
BK760112 BK760712
BK953105 QV3-NN020
AK050784 Mus muscu
BB657984 BB657984
BB655846 BB657984
CEF56467 tigr-GS8-
CEF76467 tigr-GS8-
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BF388169 UI-R-CA1-
CC178445 XCG49 BAY
BU172491 AGBNCOURT
BV1025342 603747714
CF225019 AGBNCOURT
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BU25930 603947544
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BU473055 603761665
CC514853 CST68836
BU461860 603773816
AL308788 Tetraodon
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BA111628 CH230-230
A7753786 cr16e09.x
BU921705 6093-12 M
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BG036207 602326960
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CB544750 AMGNNUC:T
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Ammania; Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
1 (bases 1 to 620)
               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CB532245 620 bp mRNA linear 756697 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
                                                           SUMMARIES
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BX760712
BF953105
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  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                     - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                 27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                   hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  BLOSUM62
Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bovoidea; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidea; Bovidea; Bovidea; Bovidea; Bovidea; Bosidea; Bovidea; Bosidea; Bovidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Bosidea; Boside
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Plate: LAMB014 ... COLUMN: 19
Seq primer: GTAATRGACTCACTATAGGG.
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/clone lib="Marc 6BOV"
/clone="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pitultary, and
92 AACACGGAGCCGATCACCCGGGCGGCCTGCAGAACCATTCTCGACTCCGGACACGCCC
                                                                                                                                                                                                                                                        620 bp mRNA linear
757081 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
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/mol type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
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                                                                                                                                                                                   VSDA, A6S, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4360
Final: smithdemail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
plate: LAM8014 row: K column: 19
Seq primer: TAGAAGGCAACTCAAGTCAAGG.
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                 Smith,T.P.L., Roberts.A.J., Bchternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
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/mol_type="mRNA"
/db xref="taxon:9913"
/tisbact="type="pooled"
/lab host="DH108"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
/notexy made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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Not1; Site_2: Xho1; CDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 566)
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
Obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melton,D., Brown,J., Kenty,G., Permutt,A., Iee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,B., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
ArgGluLeuGlyLeuGluGluValThrProProHisGlyThrLeuTyrArgThrAsplle
                                                                                                                GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp
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Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium
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/organism="Homo sapiens"
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COMMENT
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BU072782
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XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@ingate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            625 bp mRNA linear EST 25-NOV-2002 604158648F1 CSEQCHN03 Gallus gallus cDNA clone ChEST1010p11 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 623)
Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 CTCATTGAGATGGACATTCTCGGCGCCTCCCGCCATGATGGGGGTTACAGTGACGGGCAC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | PheLeuPheLysProGlyGlyThrSerProLeuPheCysThrThrSerProGlyTyrPro 304
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Gallus gallus
Gallus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 AspHisProGlyGlyLeuGlnAsnHisAlaArgLeuArgThrProProProLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisAlaHisThrProAsnGlnHisHisAlaAlaSerIleAsnSerLeuAsnArgGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheThrProArgSerAsnProSerProAlaProThrAspHisSerLeuSerGlyGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProAlaGlyGlyAlaGlnGluProAlaHisAlaGlnGluAsnTrpLeuLeuAsnSerAsn
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                                                                                                                                                                                                                                     566
162
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                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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//note="Grgan: ovary; Vector: pBluescript II KS(+); Site_1:
//note="Grgan: ovary; Vector: pBluescript II KS(+); Site_1:
//note="Grgan: ovary; Vector: pBluescript Inbrary was
Constructed from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Pollowing this first strand reaction, double-stranded
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom medified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-932 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                      BU474934 878 bp mRNA linear EST 30-NOV-2002
603364850F1 CSEQRBN21 Gallus gallus cDNA clone ChEST262c14 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 878)
Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
  160
                                                                                                                                                                                                                                                                                                                                             Gallus gallus (chicken)
(Gallus gallus
(Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                       140 gSerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                         177
                                                                                       160 uAsn-ThrGluThrAspHisProGlyGlyLeuGlnAsnHisAlaArgLeuArg
                                                                                                                878
141
12
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1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                      BU474934.1 GI:25968511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.13e-43
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92.73$
85.45$
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Tel: 01612008930
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Best Local Similarity:
                                                                                                                                                                                                                                                                               sequence.
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8
                                                                                                                                                                                                                                                        DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
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KEYWORDS
SOURCE
                                                                                                                                                                                            RESULT 5
BU474934
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                                                                                                                                                                                                                                                                                                                                                                /dev_stage="20-21"
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/lab_host="HD10B"
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Site l: ECORI; Site 2: NOt1; This normalized library was
Site l: ECORI; Site 2: NOt1; This normalized library was
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters; digested with
ECORI; size-selected, and cloned into the NotI and ECORI
compatible sites of a custom medified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysAspileValProGinGluAlaGluGluPheCysArgThrGlyAlaAsnPheThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetaspValLysGluArgLysProTyrArgSerLeuThrArgArgArgAspAlaGluArg
  12445392
Contact: Simon Hubbard
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
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151
13
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                                                                                                                                                                                                                                             /organism="Gallus gallus"
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Indels:
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Matches:
                                                                                                            PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                   Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                          Location/Qualifiers
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781.00
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Query Match:
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                           COMMENT
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Attary 12 of Lie moube transcriptome based on runctional annotation of 60,770 full-length cDNas

State (bases 1 to 3447)

R ddachi, J. Alzawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, W., Hiraoka, T., Hirozane, T., Hori, F., Imclani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nushi, K., Natsuyama, T., Miyazaki, A., Murata, M., Nakamura, K., Saitoh, H., Sakai, K., Sakazume, N., Saro, H., Saski, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, Sano, H., Saski, D., Shibata, K., Shinagawa, A., Shiraki, T., Direct Submission

M Direct Submission

M Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Genome Exploration Research Group, RIKEN Genome Exploration Research Group, RIKEN Genome Exploration Research Group, Rikes Genere Exploration Research Group, Rikes Genome Exploration Research Group, Rikes Genome Exploration Research Group, Rikes Genome Exploration Research Group, Rikes Genome Exploration Research Group, Rikes Genome Exploration Research Group, Rikes Genome Exploration Research Group, Rikes Genome Exploration Research Group, Rikes Genome Tesseger Criken, Go. jp, 197. Herrital Function Research Group, Ranagawa 230-0045, Japan (E-mail-genome-research Rose Criken, Go. jp, 197. Herrital Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive Functive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation
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SQNYPLTSWTYSPPRPLPRSTFSRPAFTFNKPRCCNWKCTALSATAITVTLALLL
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THTQPDFVKLMDGKQLVKQDSKSSDDIQHSPRULILISLQETGFIEYNDQGPWYLAFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="cerebellum"
clone_lib="RIKEN full-length enriched mouse cDNA library"
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MGSDVDTETEGAASPDHALRMWIRGMKSEHSSCLSSRANSALSLTDTDHERKSDGENG
FKFSPVCCDMEAPADSAQDMQSSPHNQFTFRPLPPPPPPPPPACTCARKPPPTVDSLQR
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                                                                                                                                                                                                                 The RIKEN Genome Exploration Research Group Phase II Team and the
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(Drosophila) (MGD|MGI:1345185, GB|NM_011855, evidence
BLASTN, 99%, match=3037)
                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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        pipeline with 384 multicapillary sequencer
. 10 (11), 1757-1771 (2000)
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URL:http://fantom.gsc.riken.go.jp/.
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| db_xref="MG1:241296"
| db_xref="taxon:10090"
| clone="B930059M16"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
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/dev_stage="embryo, stage 31-32"
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/lab_host="mbLOB" (phage-resistant)"
/clone lib="NLCBH (phage-resistant)"
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/notes="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1:
/notes="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1:
/notes="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1:
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Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.

1 (bases 1 to 884)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                    ThrSerSerThrValTyrSerProProProArgProLeuProArgSerThrPheAlaArg
                                                                                                                                                                                                                            326 ProblapheAsnLeuLysLysProSerLysTyrCysAsnTrpLysCysAlaAlaLeuSer
                                                                                                                                                                                                                                                                                                  346 AlalleVallleSerAlaThrLeuVallleLeuLeuAlaTyrPheValAlaMetHisLeu
                                                                                                                                                                                                                                                         267 GluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAspGlyHisPheLeu
                                                                        PhelysProGly --- GlyThrSerProLeuPheCysThrThrSerProGlyTyrProLeu
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BQ735622
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/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="teaxon:8355"
/clone="IMAGE:5542655"
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Matches:
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Tissue Procurement: Dr. Igor Dawid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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               NDGKKMEQVFVLTTAIGKLPCLLFEFTV"
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603760992F1 CSEQREN21 Gallus gallus cDNA clone ChEST679924 5', mRNA
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                                        US-10-029-020-14_COPY_1_400 (1-400) x BQ735622 (1-884)
   Mismatches:
               Indels:
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32.62%
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sequence. BU474512 BU474512.1 GI:25968089

DEFINITION

ACCESSION VERSION

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/clone_libe=CSEORBN21"
//olone_libe=CSEORBN21"
//olone_libe=CSEORBN21"
//olote="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated con the first strand reaction.
Following this first strand reaction, double-stranded cDNA
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified McS of the
pBluescript (KS+) vector. The library was normalized in z
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
reannealing hybridization was used."
                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 799)

Boardman, P. B., Sanz-Erquerro, J., Overton, I.M., Burt, D.W., Bosch, E. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. Ourrenensive Collection of Chicken CDNAs
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                                                                                                                                                                                                                                                                            Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                                                                                                                                     PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
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/organism="Gallus gallus"
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/clone="ChEST679g24"
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/strain="Layer"
Gallus gallus (chicken)
Gallus gallus
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AMGNNUC:TRYP1-00009-A5-A tryp1 (10582) Rattus norvegicus cDNA clone tryp1-00009-a5 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysaspilevalProginglualagluglupheCysargThrGlyAlaAsnPheThrLeu
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                                                                                                                                                                                                                            SerSerGluThrLeulysAlaTyrAspGlnAspAlaArgLeuAlaTyrGlySerArgVal
                                                                                                                                             MetAspVallysGluArgLysProTyrArgSerLeuThrArgArgArgAspAlaGluArg
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
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            4.68e-40
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Best Local Similarity:
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// clone lib-"CSEQCHL16"
// note="Organ: brain; Vector: pBluescript II KS(+); Site 1:
Chote="Organ: brain; Vector to general pBluescript II KS(+)
ECORI; Site 2: Not1; Modification of pBluescript II KS(+)
[Stratagenel vector to accommodate cDNA produced with the
[Stratagenel vector to accommodate cDNA produced with the
cloned protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
ligate in double stranded adaptor containing Bsg1 and
BamHI sites [5/ggccgcgtgcgccccggtagaaaaaaag]
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Boardman, P.B., San-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Boardman,P.E., San-Ezquerro,J., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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603143046F1 CSEQCHL16 Gallus gallus cDNA clone ChEST137111 5', mRNA
                                                                                                                                             ThrvalLeuSerProGluHisProValArgLeuTrpGlyArgSerThrArgSerGlyArg 140
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Gallus gallus
Gallus Gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                        SerSer-CysleuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThrGluHisGl
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                                                                                 GlyLeuProGlnCysGlyTyrSerMetGlyAlaGlySerAspAlaAspMetGluAlaAsp
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="not cerebrum or cerebellum"
dev stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PO BOX 88, Manchester, M60 1QD, UK Tel: 01612008930 Fax: 01612360409 Email: Simon. Hubbaxd@umist.ac.uk. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
BU119163
BU119163.1 GI:25328007
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                                                                                                                                                                                                                                                                               160 uAsnThrGluThr 164
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6 (bases 1 to 4556)

8 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,T.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
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Sano,H., Saaki,D., Shibata,T., Takahashi,F., Takaku-Akahira,S.,
Muramatsu,M. and Hayashizaki,Y., Takahashi,F., Takaku-Akahira,S.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission Noshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
Kanagawa 230-0045, Japan (E-mail:genome-resegec.riken.go.jp,
Pax:Bl-45-503-9222,
Physical Brose-Liken.go.jp/, Tel:Bl-45-503-9222,
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                                                                                                               Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Panamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashinagi, K., Yoneda, Y., Ishikawa, T., Ogawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group phase I for I Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.

Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research
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1. .4556
/note="add Oz/ten-m homolog 1 (Drosophila)
(MCD|MGI:1345185, GB|NM_011855, evidence: BLASIN, 99%, match=3037)"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
1. .4556
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   Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeulyslysProSerlysTyrCysAsnTrpLysCysAlaAlaLeuSerAlaileValIle 349
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HTC; CAP trapper.
Mus musculus (house mouse)
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/clone lib="trypl (10582)"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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126
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Conservative:
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
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685.00
99.22*
97.67*
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Best Local Similarity:
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ORGANISM
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DEFINITION

RESULT 11

ò S AK034286

ACCESSION VERSION KEYWORDS

REFERENCE AUTHORS TITLE JOURNAL MEDLINE

PUBMED REFERENCE AUTHORS

TITLE

Db 1764CATTTCCTG 1772		326 1893 346	1953	Db 2013 ATTCTATGTGTCTGTTTTTTAACCTGCTGTTTTGTTTGCAGIGGGGTAGGAGT 2012  Qy 370 pHisLeuGlnProMetGluGlyGlnMetTyrGluIle 382  Db 2013 TCACTCTCAATGTGGACAAATTTGTAGCATA 2109	RESULT 12 AL922332/c LOCUS AL922332 AL922332 AL922332 AL922332 DEFINITION AL922332 DEFINITION AL922332 AL9223232 AL922332 AL922332 AL922332 AL922332 AL922332 AL922332 AL92232	ACCESSION AL922332.1 GI:23188912 VERSTWORDS EST: SOURCE Danio rerio (zebrafish) ORGANISM Danio rerio	Eukaryota; Metazoa; Chordada; Cidilada; Vercepida; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  REFERENCE 1 (bases 1 to 490) 7 ii. P Push H Run A. He.Y., Ma.W.,	Lo, J., Lee, S., Xu, M., Liu, F., Nam, M., Jenney, W., Wen, Z. and Peng, J. 15000 unique zebrafish EST clusters and their future unicroarray for profiling gene expression patterns duri	AL ED	COMMENT Lobitational Genomics Lab of Functional Genomics Institute of Molecular and Cell Biology 30 Medical Drive, Singapore, 117609, Singapore Email: penglivemach a-star.edu.sg	FEATURES Location/Qualifiers source /organism="Danio rerio"	/mol_type="mRNA" /strain="local wildtype" /db_xref="taxon:7955" /clone="109-E12-2" /clone="109-E12-2"	/tissue_cype="whote cmulyour /dev_stage="mixed stages" /clone_lib="PUR-21+22"	nt Scores: 8.72e-34 Length:	ore: Similarity: 82.10% recent Similarity: 71.60% ery Match:	. פעף
ORIGIN	Alignment Scores: 5.91e-37 Length: 4556 Pred. No.: 659.00 Matches: 163 Score: 659.00 Matches: 163 Percent Similarity: 49.65% Conservative: 52 Best Local Similarity: 37.64% Mismatches: 109 Ouery Match: 11 Gaps: 14	US-10-029-020-14_COPY_1_400 (1-400) x AK034286 (1-4556) QY	20 ArgArgTyrThrSerSerSerAlaAspSerGluGluGlyLysAlaProGlnLysSerTyr	Qy 40 SerSerSerGluThrLeuLysAlaTyrAspGlnAspAlaArgLeuAalTyrAspGlnAspAlaArgLeuAalTyrGryser 50	1167 AGTAC 76 AlaAs	DB 1221TyrArgThrAspIleGlyLeuProGlnCysGlyTyrSerMetGlyAla 111 Qy 96TyrArgThrAspIleGlyLeuProGlnCysGlyTyrSerMetGlyAla 111	Oy 112 GlySerAspAlaAspMetGluAlaAspThrValLeuSerProGluHisProValArgLeu 131	Qy 132 TrpGlyArgSerThrArgSerGlyArgSerSerCysLeuSerSerArgAlaAsnSerAsn 151	Oy 152 LeuThrLeuThrAspThrGluHisGluAsnThrGluThrAspHisProGlyGlyLeuGln 171	Qy 171 171  Db 1473 TTCTCTCTGTTTGTGACATGGAGGCTCCAGCTGATTCGGCTCAAGACATGCAAAGC 1532	AGCCCACACACAGTTCACCTTCAGACCCCTCCCACCACCACCACCTCCTCCACATGCC	187	rccrecrccrcca	Oy 227 GlyGlyAlaGluProAlaHisAlaGluGluAsnTrpLeuLeuAsnSerAsnIlePro 246	Qy 247 LeuGluThrArgAsnLeuGlyLysGlnProPheLeuGlyThrLeuGlnAspAsnLeulle 266	, Qy 267 GluMetAspIleLeuGlyAlaSerArgHisAspGlyAlaTyrSerAspGlyHisPheLeu 286

g ò qq ò qq ò g à a ò g à a

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/clone lib="NIH_MGC 91"
/note="Corgan: prostate; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; ollgo-dr primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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1 (bases 1 to 511)

Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Homo sapiens HCM2175 gene, VIRTUAL TRANSCRIPT, partial sequence,
DAVAGESO,
                                                                                                                                                                                                                                                                                                                                                                                         2 GGCACCTCCCCGCTCTTCTGCACCACATCACCAGG-TACCCACTGACGTCCAGGACGAGG
                                                                                                                                                                                                                                                                                                                                                                291 GlyThrSerProteuPheCysThrThrSerProGlyTyrProteuThrSerSerThrval
                                                                                                                                                                                                                                                                                                                                                                                                                                          311 TyrSerProProArgProLeuProArgSerThrPheAlaArgProAlaPheAsnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 511)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanembaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
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109
1109
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Matches:
Conservative:
Mismatches:
Indels:
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602326960F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4428351 5',
                                       VallysGluargLysProTyrArgSerLeuThrArgArgAspAlaGluargArgTyr 22
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 870)
                                                                                                               ThrSerSarSerAlaAspSerGluGluGlYLYsAlaProGlnLysSerTyrSerSer
                                                                                                                                                                                       43 GluThrieutysalaTyrAspGlnAspAlaArgLeuAlaTyrGlySerArgValLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
DNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.h column: 16
High quality sequence stop: 713.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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US-10-029-020-14_COPY_1_400 (1-400) x AL922332 (1-490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 870
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BG036207.1 GI:12431132
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RESULT 13 BG036207

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REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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241 TTTACCCTAAGGCAGTTAGGAGTTTGTGAACCAGCAACTCGAAGAGGACTGGCATTTTGT 300
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Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                      (Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Matches:
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Science 302 (5652), 1960-1963 (2003)
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AV405292
AY405292.1 GI:39761266
GSS.
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Pan troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Pan.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Clark,A.G., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J.,
Adams,M.D. and Cargill,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 SerGlyArgSerSerCysLeuSerSerArgAlaAsnSerAsnLeuThrLeuThrAspThr 157
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                                                             /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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                         d on alignment.
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